



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 218755

TO: Patricia Duffy  
Location: REM-3B05&3C18  
Art Unit: 1645  
Thursday, March 29, 2007

Case Serial Number: 10/063561

From: Deirdre Arnold  
Location: Biotech-Chem Library  
REM 1A55  
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

### Search Notes

SPDI (final results are not available on SCORE)

*Please feel free to contact me if you have any questions or would like to rework the search.*

Thank you for using STIC services.

Regards,  
Deirdre Arnold

218755

From: Duffy, Patricia  
Sent: Tuesday, March 20, 2007 12:06 PM  
To: STIC-Biotech/ChemLib  
Subject: SPDI SEARCH

DEAR STIC, 03-1050

IN RE:10/063,561  
PLEASE SEARCH SEQ ID NO:52  
SPDI SEARCH.

Patricia A. Duffy, Ph.D.  
Primary Patent Examiner  
571-272-0855,  
Remsen 3B05,  
Mailbox: 3C18

72448

440AFA

CRFE

520  
52Pub-Main  
Pub-New1500 hits  
0 align

Geneseg

1500 hits  
1500 align

ISS

PDR  
Uniprot1500 hits  
15 align

D-14

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Searcher: Arnold  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: 3/28/07  
Date completed: \_\_\_\_\_  
Searcher Prep Time: 2A  
Online Time: 2A

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# 1  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

Spdi:  
C

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

OM Protein - Protein search, using sw model  
Run on: March 28, 2007, 20:56:15; Search time 219 Seconds  
(without alignments)

US-10-063-561-52 983.136 Million cell updates/sec

Title: US-10-063-561-52  
Perfect score: 2363  
Sequence: 1 MKFGPIACLLALCLGSGE.....KLGFINDAIKQRRSRIP 440  
Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5  
Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Database: Listing first 1500 summaries

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No. Score Match Length DB ID Description

RESULT 1 ID AAY9354 standard; protein; 440 AA.

DE Human PRO1411 (UNQ729) amino acid sequence SEQ ID NO:52.

PN WO200012708-A2.

PD 09-MAR-2000.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 3; Length 440;

Pred. No. 3.1e-137;

RESULT 2 ID AAB6103 standard; protein; 440 AA.

DE Protein of the invention #15.

PN WO200078961-A1.

PD 28-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 4; Length 440;

Pred. No. 3.1e-137;

RESULT 3 ID AAB31205 standard; protein; 440 AA.

DE Amino acid sequence of human polypeptide PRO1411.

PN WO200077037-A2.

PD 21-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 4; Length 440;

Pred. No. 3.1e-137;

RESULT 4 ID AAU29124 standard; protein; 440 AA.

DE Human PRO polypeptide sequence #101.

PN WO200168848-A2.

PD 20-SEP-2001.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 4; Length 440;

Pred. No. 3.1e-137;

RESULT 5 ID AAB87551 standard; protein; 440 AA.

DE Human PRO1411.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 4; Length 440;

Pred. No. 3.1e-137;

RESULT 6 ID AAU8369 standard; protein; 440 AA.

DE Human PRO protein, Seq ID NO 156.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 5; Length 440;

Pred. No. 3.1e-137;

RESULT 7 ID ABG5876 standard; protein; 440 AA.

DE Human secreted/transmembrane protein PRO1411.

PN US2002119130-A1.

PD 29-AUG-2002.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 5; Length 440;

Pred. No. 3.1e-137;

RESULT 8 ID ABB84891 standard; protein; 440 AA.

DE Human PRO1411 protein sequence SEQ ID NO:150.

PN WO200200690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 5; Length 440;

Pred. No. 3.1e-137;

RESULT 9 ID ABB95497 standard; protein; 440 AA.

DE Human angiogenesis related protein PRO1411 SEQ ID NO: 150.

PN WO200208284-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERB/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MASTERS S A.

PA (PANJ/) PAN J.

PA (PRON/) PRONT N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

Query Match Best Local Similarity 100.0%; Score 2363; DB 5; Length 440;

Pred. No. 3.1e-137;

RESULT 10 ID ADY31896 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.

PN WO200193983-A1.

PD 13-DEC-2001.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 5; Length 440;

Pred. No. 3.1e-137;

RESULT 11 ID ABU58500 standard; protein; 440 AA.

DE Human PRO polypeptide #101.

PN US2003027272-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;

Pred. No. 3.1e-137;

RESULT 12 ID ABU88048 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.

PN US2003032127-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;

Pred. No. 3.1e-137;

RESULT 13 ID ABU84363 standard; protein; 440 AA.

DE Human secreted/transmembrane protein (PRO) #101.

PN US2003032112-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;

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Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 14
ID ABR66237 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 15
ID ABR65627 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 16
ID ABR9567 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 17
ID ABR82806 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 18
ID ABR8927 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 19
ID ABR68176 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 20
ID ABR96229 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 21
ID ABR92660 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 22
ID ABR98016 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 23
ID ABR08737 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 24
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

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ID ABR02789 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 25
ID ABR74943 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 26
ID ABR94705 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 27
ID ABR25176 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO141.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 28
ID ABR033782 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 29
ID ABR85678 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 30
ID ABR98938 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 31
ID ABR98053 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 32
ID ABR91759 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 33
ID ABR89452 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 34
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

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ID ABU86293 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 35  
ID ABU67506 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 36  
ID ABU80534 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 37  
ID ABU90901 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 38  
ID ABO33960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO411.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 39  
ID ABR99452 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 40  
ID ABR9842 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 41  
ID ABO16365 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 42  
ID ABR92265 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 43  
ID ABO16906 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 44  
ID ABR78327 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 45  
ID ABU1977 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 46  
ID ABU85063 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 47  
ID ABO0202 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 48  
ID ABO11534 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 49  
ID ABO02179 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 50  
ID ABU88753 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 51  
ID ABU67294 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 52  
ID ABU83448 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 53  
ID ABO06249 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 54  
ID ABR5285 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 55  
ID ABO09347 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 56  
ID ABO19211 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 57  
ID ABO11229 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 58  
ID ABR66847 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 59  
ID ABO16060 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 60  
ID ABO13766 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 61  
ID ABU71531 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 62  
ID ABU65669 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein, SEQ ID 202.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 63  
ID ABO07517 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

RESULT 64  
ID ABO03704 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 65  
ID ABR67152 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 66  
ID ABO15755 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 67  
ID ABU56036 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein, PRO1411.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 68  
ID ABU72312 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 69  
ID ABU65364 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 70  
ID ABU95309 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 71  
ID ABU71212 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 72  
ID ABO07822 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 73  
ID ABR70063 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

RESULT 74  
ID ABR69396 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 75  
ID ABO01537 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 76  
ID ABU81339 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 77  
ID ABR60136 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 78  
ID ABU90985 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 79  
ID ABR67871 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 80  
ID ABR65259 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 81  
ID ABR68481 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 82  
ID ABR71893 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 83  
ID ABU85373 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 84  
ID ABU89063 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 85  
ID ABU83143 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 86  
ID ABU94999 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 87  
ID ABU90547 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 88  
ID ABU84058 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 89  
ID ABU93709 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 90  
ID ABR64954 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 91  
ID ABR68786 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 92  
ID ABO06602 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 93  
ID ABR99147 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 94  
ID ABU57031 standard; protein; 440 AA.

DE Human PRO polypeptide #101.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 95  
ID ABU72062 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 96  
ID ABU85983 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 97  
ID ABU82270 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 98  
ID ABU87281 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 99  
ID ABU67163 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 100  
ID ABU83753 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 101  
ID ABO08127 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 102  
ID ABU92501 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 103  
ID ABU81838 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 104  
ID ABU66002 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 105  
ID ABU81171 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 106  
ID ABU59831 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 107  
ID ABU94019 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 108  
ID ABU99872 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 109  
ID ABU82125 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 110  
ID ABU66542 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 111  
ID ABR90960 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 112  
ID ABO53286 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 113  
ID ABU94387 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 114

ID ABU79269 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABU86598 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABU86903 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABU94692 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABO04619 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABR70368 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABU96533 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US20030322301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 30-JAN-2003.  
ID ABR65932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 20-FEB-2003.  
ID ABR6649 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032126-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 06-FEB-2003.  
ID ABU79574 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABU92965 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABU9144 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 20-FEB-2003.  
ID ABU90237 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 20-FEB-2003.  
ID ABO09652 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 06-MAR-2003.  
ID ABO10924 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 20-FEB-2003.  
ID ABR0978 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 27-FEB-2003.  
ID ABU98288 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 05-DEC-2002.  
ID ABU87586 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 30-JAN-2003.  
ID ABU91454 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
PD 13-FEB-2003.  
ID ABU89293 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036634-A1.  
PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 135  
ID ABU84668 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 136  
ID ABR69758 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 137  
ID ABU80135 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 138  
ID ABU82500 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 139  
ID ABU93404 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 140  
ID ABO0957 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 141  
ID ABO09042 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 142  
ID ABU96464 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 143  
ID ABU10610 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein #101.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 144  
ID ABU72134 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 145  
ID ABU95619 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 146  
ID ABU79805 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 147  
ID ABU96828 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 148  
ID ABR70673 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 149  
ID ABO05024 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 150  
ID ABO08432 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 151  
ID ABO05639 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 152  
ID ABR74028 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 153  
ID ABR95620 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 154  
ID ABR80917 standard; protein; 440 AA.

DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN	US2003049741-A1.
PD	13-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 155	
ID	ABR81222 standard; protein; 440 AA.
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN	US2003049743-A1.
PD	13-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 156	
ID	ABM00918 standard; protein; 440 AA.
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN	US2003049769-A1.
PD	13-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 157	
ID	ABR88520 standard; protein; 440 AA.
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN	US2003068743-A1.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 158	
ID	ABM77341 standard; protein; 440 AA.
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN	US2003054479-A1.
PD	20-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 159	
ID	ABO28825 standard; protein; 440 AA.
DE	Human secreted/transmembrane protein (PRO) #101.
PN	US2003068685-A1.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 160	
ID	ABO31570 standard; protein; 440 AA.
DE	Human secreted/transmembrane protein (PRO) #101.
PN	US2003068725-A1.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 161	
ID	ABM07987 standard; protein; 440 AA.
DE	Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN	US2003068752-A1.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 162	
ID	ABO40467 standard; protein; 440 AA.
DE	Human secreted/transmembrane protein (PRO) #101.
PN	US2003068682-A1.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%; Pred. No. 3.1e-137;
RESULT 163	
ID	ABO35892 standard; protein; 440 AA.
DE	Human PRO polypeptide #101.

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RESULT 173
ID ADB17109 standard; protein; 440 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 174
ID ABO21553 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 175
ID ABR97817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 176
ID ABR87605 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 177
ID ABM77646 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 178
ID ABM27876 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 179
ID ABM06157 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 180
ID ABM03663 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 181
ID ABM35114 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 182
ID ABM26351 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 183
ID ABO48133 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 184
ID ABR92875 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 185
ID ABO24636 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 186
ID ABM1647 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 187
ID ABM02748 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 188
ID ABM16044 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 189
ID ABO27605 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 190
ID ABM29096 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 191
ID ABM07072 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2363; DB 6; Length 440;
    Best Local Similarity 100.0%; Pred. No. 3.1e-137;
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Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 201		
ID ABO03399 standard; protein; 440 AA.		
DE Human secreted/transmembrane protein (PRO) #101.		
PN US2003036127-A1.		
PD 20-FEB-2003.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 202		
ID ABO02484 standard; protein; 440 AA.		
DE Human secreted/transmembrane protein (PRO) #101.		
PN US2003040061-A1.		
PD 27-FEB-2003.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 203		
ID ABO44264 standard; protein; 440 AA.		
DE Human secreted/transmembrane polypeptide PRO 1411.		
PN US2003018172-A1..		
PD 23-JAN-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 204		
ID ABR930655 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.		
PN US2003036130-A1.		
PD 20-FEB-2003.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 205		
ID ABR73723 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.		
PN US2003054468-A1.		
PD 20-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 206		
ID ABO16975 standard; protein; 440 AA.		
DE Human secreted/transmembrane protein (PRO) #101.		
PN US2003054470-A1.		
PD 20-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 207		
ID ABR94400 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.		
PN US2003044917-A1.		
PD 06-MAR-2003.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 208		
ID ABR75907 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.		
PN US2003044929-A1.		
PD 06-MAR-2003.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 209		
ID ABR71283 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.		
PN US2003059880-A1.		
PD 27-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2363; DB 6; Length 440;
Best Local Similarity	100.0%;	Pred. No. 3.1e-137;
RESULT 210		
ID ABR93180 standard; protein; 440 AA.		
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.		
PN US200306465-A1.		
PD 03-APR-2003.		

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 211  
ID ABR03485 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 212  
ID ABR07910 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 213  
ID ABO33596 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 214  
ID ABO27910 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 215  
ID ABO30045 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 216  
ID ABO33254 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 217  
ID ABO04942 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 218  
ID ABO08902 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 219  
ID ABO36502 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 220  
ID ABO35587 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 221  
ID ABO39552 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 222  
ID ABO10427 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 223  
ID ABO11952 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 224  
ID ABO52098 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 225  
ID ABO52403 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 226  
ID ADA1914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 227  
ID ABO23721 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 228  
ID ADA17297 standard; protein; 440 AA.  
DE Human transmembrane PRO polypeptide (Segid 52).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

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RESULT 229
ID ABR97207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 230
ID ABR6995 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 231
ID ABM11037 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 232
ID ABM28181 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 233
ID ABO32180 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 234
ID ABM15307 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 235
ID ABM06462 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 236
ID ABM04273 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 237
ID ABM23386 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 238
ID ABM18484 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 239
ID ABO04314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 240
ID ABM35419 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 241
ID ABM33182 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 242
ID ABO52708 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 243
ID ABO50268 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 244
ID ABU9262 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 245
ID ABO04314 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 246
ID ABO05944 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 247
ID ABM18484 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
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Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 248  
ID ABR97512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 249  
ID ABR80612 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 250  
ID ABM01223 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 251  
ID ABR88825 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 252  
ID ABM13477 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 253  
ID ABM20861 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 254  
ID ABO41992 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 255  
ID ABO42602 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 256  
ID ABM10122 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

RESULT 257  
ID ABO38637 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 258  
ID ABM32877 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 259  
ID ABM22691 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 260  
ID ABM74902 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 261  
ID ADA79746 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 262  
ID ABR96292 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 263  
ID ABM02443 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 264  
ID ABR86385 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 265  
ID ABR86690 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 266  
ID ABM16654 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064448-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 267  
ID ABM29706 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 268  
ID ABO29130 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US200306893-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 269  
ID ABM23911 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 270  
ID ABM23301 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 271  
ID ADA47278 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 272  
ID ABM22081 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 273  
ID ABO37722 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 274  
ID ABM28486 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 275  
ID ABM28791 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 276  
ID ABM66435 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 277  
ID ABM75817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 278  
ID ABM34097 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 279  
ID ABM34402 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 280  
ID ABO20333 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 281  
ID ABO21248 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 282  
ID ABO22163 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 283  
ID ADA20086 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 284  
ID ABR96597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 285  
ID ABR85775 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

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PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 286
ID ABR99757 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 287
ID ABM00613 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 288
ID ABM00308 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 289
ID ABO29740 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 290
ID ABM23606 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 291
ID ABM29401 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US200306879-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 292
ID ABO38332 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 293
ID ABO45632 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 294
ID ABM20556 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 295
ID ADA81473 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 296
ID ABO16670 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 297
ID ABO18296 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 298
ID ABO22723 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 299
ID ABO23028 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 300
ID ABR92570 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 301
ID ABR81527 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 302
ID ABM77951 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 303
ID ABR89740 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 304
ID ABM26656 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
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PN US2003032121-A1.  
ID 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 305  
ID ABM13782 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 306  
ID ABO28520 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 307  
ID ABO30350 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 308  
ID ABO07377 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 309  
ID ABM03968 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 310  
ID ABO37112 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 311  
ID ABO41687 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 312  
ID ABO35282 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 313  
ID ABM5131 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104540-A1.  
PD 05-JUN-2003.

Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 314  
ID ABO47523 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 315  
ID ABO47828 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 316  
ID ABO48438 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 317  
ID ABO51488 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 318  
ID ABO51793 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 319  
ID ABO50573 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 320  
ID ABR79697 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 321  
ID ABM16959 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 322  
ID ABO17991 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
Pred. No. 3.1e-137;  
RESULT 323

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ID ABO20943 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 324  
ID ABR96902 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 325  
ID ABRM12257 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 326  
ID ABRM16349 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 327  
ID ABRM24216 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 328  
ID ABRM14697 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 329  
ID ABRM04578 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 330  
ID ABRM06767 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 331  
ID ABRM02207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 332  
ID ABO39247 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 333  
ID ABR75512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 334  
ID ABRM25436 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 335  
ID ABRM19946 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 336  
ID ABO46852 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 337  
ID ABO47157 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 338  
ID ADA83271 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 339  
ID ABR71588 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 340  
ID ABR72198 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 341  
ID ABR98537 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 342  
ID ABO06907 standard; protein; 440 AA.
```



DE Human secreted/transmembrane protein (PRO) #101.  
ID US2003040053-A1.  
PN 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 343  
ID ABR84860 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 344  
ID ABR73418 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 345  
ID ABR76512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 346  
ID ABR73113 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 347  
ID ABJ72433 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 348  
ID ABM18179 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 349  
ID ABO20638 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 350  
ID ABO25381 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 351  
ID ABO25686 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

RESULT 352  
ID ABR94095 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 353  
ID ABR80002 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 354  
ID ABM11342 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 355  
ID ABO32949 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 356  
ID ABO30655 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 357  
ID ABO30960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 358  
ID ABM27266 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 359  
ID ABM30011 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 360  
ID ABM05547 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 361  
ID ABM15612 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003068698-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 362  
 ID ABM08597 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003068759-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 363  
 ID ABO42297 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049748-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 364  
 ID ABO38027 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003068765-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 365  
 ID ABO45937 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049754-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 366  
 ID ABM6740 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003068688-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 367  
 ID ADB20314 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003082767-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 368  
 ID ABM19641 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003104552-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 369  
 ID ABO49353 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049774-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 370  
 ID ABO49658 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049775-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 371  
 ID ABO49658 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049775-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 372  
 ID ABO34328 standard; protein; 440 AA.  
 DE Human secreted/transmembrane polypeptide PRO 1411.  
 PN US2003044934-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 373  
 ID ABR88215 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003068720-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 374  
 ID AD00383 standard; protein; 440 AA.  
 DE Human secreted/transmembrane polypeptide PRO 411.  
 PN US2003027992-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 375  
 ID ABM26961 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003068739-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 376  
 ID ABO03358 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003068763-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 377  
 ID ABO39857 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003068689-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 378  
 ID ABO49963 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049776-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 379  
 ID ABO50878 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049780-A1.  
 PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 380  
ID ABO05334 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 381  
ID ABR74638 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 382  
ID ABO4449 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 383  
ID ABR77117 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 384  
ID ABM1874 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 385  
ID ABR95925 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 386  
ID ABO21858 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 387  
ID ABO20028 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 388  
ID ABO24331 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 389  
ID ABR86080 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049759-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 390  
ID ABR10732 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 391  
ID ABM76731 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 392  
ID ABR9435 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 393  
ID ABM12562 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 394  
ID ABM05852 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 395  
ID ABO34977 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 396  
ID ABM03053 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 397  
ID ABM19031 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 398  
ID ABM19336 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 399  
ID ABO46547 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 400  
ID ABO49048 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 401  
ID ABR69091 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 402  
ID ABR89130 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 403  
ID ABR72503 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 404  
ID ABR74333 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 405  
ID ABO18601 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 406  
ID ABR80307 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 407  
ID ABO1528 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 408  
ID ABO2138 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 409  
ID ABR87300 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 410  
ID ABR12867 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 411  
ID ABR30621 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 412  
ID ABR24521 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 413  
ID ABO29435 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 414  
ID ABO31265 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 415  
ID ABR14392 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 416  
ID ABR09817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 417  
ID ABO38942 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068774-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 418  
ID ABM34707 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 419  
ID ABO51183 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 420  
ID ABO04009 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 421  
ID ABO10479 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 422  
ID ABR77722 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 423  
ID ABR7932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 424  
ID ABO24026 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 425  
ID ABR93790 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 426  
ID ABM0183 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 427  
ID ABM78256 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 428  
ID ABO33473 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 429  
ID ABR90045 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 430  
ID ABM27571 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 431  
ID ABM3172 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 432  
ID ABO31875 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 433  
ID ABM14087 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 434  
ID ABM08292 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 435  
ID ABO40162 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 436  
ID ABM74597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096351-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 437  
ID ABM33792 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 438  
ID ABM20251 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 439  
ID ABO48743 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 440  
ID ABR72808 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 441  
ID ABO15450 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 442  
ID ABR85165 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 443  
ID ABO15145 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 444  
ID ABO17280 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 445  
ID ABO19863 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 446  
ID ABM17569 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 447  
ID ABJ72135 standard; protein; 440 AA.  
DE Human membrane bound receptor/protein PRO1411 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 448  
ID ABR85470 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 449  
ID ABM77036 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 450  
ID ABO28215 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 451  
ID ABM22996 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 452  
ID ABM30316 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 453  
ID ABM21776 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 454  
ID ABM21471 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 455  
ID ABM15002 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068766-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 456  
ID ABO41077 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 457  
ID ABO36807 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 458  
ID ABO37417 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 459  
ID ABM75207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 460  
ID ABM33487 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 461  
ID ABO46242 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 462  
ID ADA82637 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 463  
ID AD885625 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 464  
ID ADB83646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 465  
ID ADB80752 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 466  
ID ADB73293 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 467  
ID ABM31841 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 468  
ID ADB78375 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 469  
ID ABM31231 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 470  
ID ADB85023 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 471  
ID ADB78129 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 472  
ID AD885945 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 473  
ID ABM32146 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 474  
ID ADB83646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;

Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 474  
ID ABM32451 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 475  
ID ADB87195 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 476  
ID ADB84777 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 477  
ID ADB68304 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 478  
ID ADB68111 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 479  
ID ABM31536 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 480  
ID ABM30926 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 481  
ID ADB83892 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 482  
ID ADB73047 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

RESULT 483  
ID ADB90928 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 484  
ID ADC07008 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 485  
ID ADC17921 standard; protein; 440 AA.  
DE Human PRO polypeptide #15.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 486  
ID ADC17187 standard; protein; 440 AA.  
DE Mammalian PRO polypeptide (Segid 52).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 487  
ID ADC14885 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 488  
ID ADC36885 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 489  
ID ADC52380 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 490  
ID ADC21875 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 491  
ID ADC49906 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 492  
ID ADC14885 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;



ID ADC49105 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 493  
ID ADC49622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 494  
ID ADC47483 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 495  
ID ADC47228 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 496  
ID ADC78103 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 497  
ID ADD06338 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 498  
ID ADD05675 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 499  
ID ADD10439 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 500  
ID ADC71857 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 501  
ID ADD11399 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 502  
ID ADD50820 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 503  
ID ADD51066 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 504  
ID ADD70567 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US200309625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 505  
ID ADD39644 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 506  
ID ADD70090 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 507  
ID ADD37192 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 508  
ID ADD36056 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 509  
ID ADD38211 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 510  
ID ADD39167 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.

PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 511  
ID ADD50547 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 512  
ID ADD50301 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 513  
ID ADD38690 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 514  
ID ADD40121 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 515  
ID ADD51312 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 516  
ID ADE50342 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 517  
ID ADE19954 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003092885-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 518  
ID ADE49865 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 519  
ID ADE21423 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 520  
ID ADF29848 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 521  
ID ADF55741 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 522  
ID ADG01057 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 523  
ID ADG08610 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 524  
ID ADG02670 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 525  
ID ADG01377 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 526  
ID ADF95552 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 527  
ID ADF95231 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 528  
ID ADG12367 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207392-A1.  
PD 06-NOV-2003.

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Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 529
ID ADH24084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 530
ID ADH34110 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 531
ID ADH29943 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 532
ID ADH23914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 533
ID ADH09027 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 534
ID ADG85318 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 535
ID ADH24594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 536
ID ADH37450 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO1411.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 537
ID ADH02039 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 538
ID ADH37620 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO1411.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 539
ID ADG85658 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 540
ID ADH24254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 541
ID ADH38548 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 542
ID ADG63787 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 543
ID ADG83669 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 544
ID ADH29477 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 545
ID ADH27593 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 546
ID ADH37790 standard; protein; 440 AA.
DE Human secreted and transmembrane protein PRO1411.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
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RESULT 547  
ID ADH37967 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 548  
ID ADH57387 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 549  
ID ADH53529 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 550  
ID ADH5369 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 551  
ID ADH52035 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 552  
ID ADH4990 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 553  
ID ADI25400 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 554  
ID ADH90193 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 555  
ID ADI25570 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 556  
ID ADH98594 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 557  
ID ADH99245 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 558  
ID ADI03592 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 559  
ID ADI11949 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 560  
ID ADH90023 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 561  
ID ADH8424 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 562  
ID ADI11099 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 563  
ID ADI11609 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 564  
ID ADH98254 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 565  
ID ADH98594 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 566  
ID ADH98084 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 567  
ID ADI05072 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 568  
ID ADI03422 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO411.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 569  
ID ADI04617 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 570  
ID ADH78271 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 571  
ID ADI19615 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 572  
ID ADH90363 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 573  
ID ADI03082 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 574  
ID ADH77931 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003191290-A1.

PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 575  
ID ADH97914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 576  
ID ADI01299 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 577  
ID ADI01994 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 578  
ID ADI03252 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 579  
ID ADI11439 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 580  
ID ADI02341 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 581  
ID ADI11779 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 582  
ID ADI05416 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 583  
ID ADH79488 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191290-A1.

PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 584  
ID ADI19445 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 585  
ID ADI05246 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 586  
ID ADH79658 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 587  
ID ADI01484 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 588  
ID ADI01654 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 589  
ID ADI01824 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 590  
ID ADH79828 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 591  
ID ADI04646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 592  
ID ADI02782 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 593  
ID ADH78101 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 594  
ID ADI25740 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 595  
ID ADI25910 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 596  
ID ADK65422 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 597  
ID ADH98764 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 598  
ID ADH80005 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 599  
ID ADM30342 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 600  
ID ADI93736 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 601  
ID ADC48859 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 602
ID ADCE52190 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 603
ID ADE21030 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 604
ID ADE05874 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 605
ID ADD75103 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 606
ID ADD75849 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 607
ID ADD85081 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 608
ID ADD86907 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 609
ID ADE20784 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 610
ID ADE39081 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 611
ID ADE05628 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 612
ID ADD73613 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 613
ID ADD78453 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 614
ID ADE41400 standard; protein; 440 AA.
DE Human secreted/transmembrane PRO polypeptide #75.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 615
ID ADE74339 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 616
ID ADE21276 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 617
ID ADD77391 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 618
ID ADE20538 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 619
ID ADD75603 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 620
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ID ADD74119 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 621
ID ADD74365 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 622
ID ADD76095 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 623
ID ADD85587 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 624
ID ADE05136 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 625
ID ADD75349 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 626
ID ADD76893 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 627
ID ADD86661 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 628
ID ADE41201 standard; protein; 440 AA.
DE Human secreted/transmembrane polypeptide PRO1411.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 629
ID ADD78129 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 630
ID ADE74951 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 631
ID ADD77637 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 632
ID ADD77883 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 633
ID ADD85341 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 634
ID ADD73873 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 635
ID ADD74611 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 636
ID ADD77139 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 637
ID ADD85833 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.1e-137;
RESULT 638
ID ADE05382 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003100723-A1.
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PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 639  
ID ADD74857 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 640  
ID AD96425 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 641  
ID AD75736 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 642  
ID AD724635 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 643  
ID AD729371 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 644  
ID AD96902 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 645  
ID ADG0569 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 646  
ID ADG27223 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 647  
ID AD796164 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215909-A1.  
PD 20-NOV-2003.

Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 648  
ID ADG11266 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 649  
ID ADG04435 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 650  
ID ADG12065 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 651  
ID ADG00595 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 652  
ID AD74622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 653  
ID ADG06718 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 654  
ID ADH06622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 655  
ID ADH06452 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 656  
ID ADG68873 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;

Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 657  
ID ADH27763 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 658  
ID ADH25104 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 659  
ID ADH33736 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 660  
ID ADG82851 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 661  
ID ADH02940 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 662  
ID ADH02379 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 663  
ID ADH07986 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 664  
ID ADG6383 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 665  
ID ADH39204 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

RESULT 666  
ID ADH03894 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 667  
ID ADH03417 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 668  
ID ADH26132 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 669  
ID ADG83944 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 670  
ID ADH39062 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 671  
ID ADG85488 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 672  
ID ADG63636 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 673  
ID ADH06282 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 674  
ID ADH30112 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 675  
ID ADH30112 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

ID ADH24424 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 676  
ID ADH3101 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 677  
ID ADG6953 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 678  
ID ADH07816 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 679  
ID ADG85828 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 680  
ID ADH39374 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 681  
ID ADH33566 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 682  
ID ADH33906 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 683  
ID ADH01116 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 684  
ID ADG69723 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 685  
ID ADH02209 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 686  
ID ADG69213 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 687  
ID ADG85998 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 688  
ID ADH24934 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 689  
ID ADH39551 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 690  
ID ADH02549 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 691  
ID ADG69043 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 692  
ID ADH07646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 693  
ID ADG86168 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

PN US2003180863-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 694  
 ID ADH24764 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003180908-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 695  
 ID ADH25812 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003180911-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 696  
 ID ADH28378 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003180922-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 697  
 ID ADH57217 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003181642-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 698  
 ID ADH43583 standard; protein; 440 AA.  
 DE Human PRO polypeptide #75.  
 PN US2003224984-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 699  
 ID ADH52323 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003180921-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 700  
 ID ADG34152 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2004006206-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 701  
 ID ADH04371 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein PRO1411.  
 PN US2004005626-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 702  
 ID ADH4571 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003180857-A1.

PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 703  
 ID ADH90533 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003181700-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 704  
 ID ADI11269 standard; protein; 440 AA.  
 DE Human PRO polypeptide #26.  
 PN US2003181683-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 705  
 ID ADH98934 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003190698-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 706  
 ID ADI33622 standard; protein; 440 AA.  
 DE Human PRO polypeptide #78.  
 PN US2003096960-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 707  
 ID ADI02164 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003190699-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 708  
 ID ADH69716 standard; protein; 440 AA.  
 DE Human PRO polypeptide #78.  
 PN US2004019183-A1.  
 PD 29-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 709  
 ID ADH61372 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein PRO1411.  
 PN US2004014130-A1.  
 PD 22-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 710  
 ID ADH90703 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003181701-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
 RESULT 711  
 ID ADI29877 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003096961-A1.  
 PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 712  
ID ADJ54640 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 713  
ID ADJ98578 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 714  
ID ADJ98748 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 715  
ID ADJ78907 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 716  
ID ADJ99141 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 717  
ID ADJ99311 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 718  
ID ADJ98929 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 719  
ID ADJ79077 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 720  
ID ADK00937 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 721  
ID ADK14458 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 722  
ID ADM27274 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 723  
ID ADK82928 standard; protein; 440 AA.  
DE Human PRO polypeptide #75.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 724  
ID ADJ64611 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 725  
ID ADK66632 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US200404180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 726  
ID ADM31507 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 727  
ID ADM36554 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 728  
ID ADM40359 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 729  
ID ADM80907 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 730  
ID ADM80907 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;

Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 730  
ID ADL94571 standard; protein: 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 731  
ID ADN37967 standard; protein: 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 732  
ID ADU68160 standard; protein: 440 AA.  
DE Human CNGH0010 variant 2 protein SegID5.  
PN WO2004098502-A2.  
PD 18-NOV-2004.  
PA (CENZ ) CENTOCOR INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 733  
ID ADV77747 standard; protein: 440 AA.  
DE Neoplastic disease detection protein PRO1411.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (EATO/) EATON D L.  
PA (FLIV/) FLIVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2363; DB 9; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 734  
ID AED44958 standard; protein: 440 AA.  
DE Human secreted/transmembrane protein PRO1411, SEQ:52.  
PN US2005181478-A1.  
PD 18-AUG-2005.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2363; DB 9; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 735  
ID AED50197 standard; protein: 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2005163766-A1.  
PD 28-JUL-2005.  
PA (GRIM/) GRIMALDI J C.  
Query Match 100.0%; Score 2363; DB 9; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 736  
ID AEF12578 standard; protein: 440 AA.  
DE Human PRO1411 protein SEQ ID NO:52.  
PN US200608901-A1.  
PD 12-JAN-2006.  
PA (WATA/) WATANABE C K.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 737

ID AEF74267 standard; protein: 440 AA.  
DE Human PRO1411 protein SEQ ID NO:52.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATO/) EATON D L.  
PA (FLIV/) FLIVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 738  
ID AEG62889 standard; protein: 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2006073544-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 739  
ID AEG72712 standard; protein: 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2006074226-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 740  
ID AEG62277 standard; protein: 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2006073545-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 741  
ID AEG88194 standard; protein: 440 AA.  
DE Human PRO protein amino acid sequence - SEQ ID 202.  
PN US2006074227-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 742  
ID AEF17510 standard; protein: 440 AA.  
DE Human tumor overexpressed cdna protein product PRO1411 SEQ ID NO: 202.  
PN US2006094864-A1.  
PD 04-MAY-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 743  
ID AEF43605 standard; protein: 440 AA.  
DE PRO1411 protein sequence, SEQ ID 52.  
PN US2006099657-A1.  
PD 11-MAY-2006.  
PA (EATO/) EATON D L.  
PA (FLIV/) FLIVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 744  
ID AEF49342 standard; protein: 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:156.  
PN EPI659177-A2.  
PD 24-MAY-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 745  
ID AE11930 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2006160186-A1.  
PD 20-JUL-2006.  
PA (EATO/) EATON D L.  
PA (FLV/) FLVAKOPF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 746  
ID AEK48377 standard; protein; 440 AA.  
DE Human PRO1411 amino acid sequence.  
PN EPI686174-A1.  
PD 02-AUG-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 747  
ID AEK62970 standard; protein; 440 AA.  
DE Human PRO1411 polypeptide, SEQ ID NO: 156.  
PN EPI700867-A2.  
PD 13-SEP-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 748  
ID AEK56724 standard; protein; 440 AA.  
DE Human PRO polypeptide SEQ ID NO:142.  
PN WO2006098887-A2.  
PD 21-SEP-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 749  
ID AE117010 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:156.  
PN EPI702928-A2.  
PD 20-SEP-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 10; Length 440;  
Best Local Similarity 100.0%; Pred. No. 3.1e-137;  
RESULT 750  
ID ADL32808 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 2357; DB 7; Length 440;  
Best Local Similarity 99.8%; Pred. No. 7.2e-137;  
RESULT 751  
ID ADU68195 standard; protein; 608 AA.  
DE Human CNGH0010 protein embedded in SegID1.  
PN WO2004098502-A2.  
PD 18-NOV-2004.  
PA (CENZ ) CENTOCOR INC.  
Query Match 97.3%; Score 2299; DB 8; Length 608;  
Best Local Similarity 91.6%; Pred. No. 3.6e-133;  
RESULT 752  
ID ADU68158 standard; protein; 555 AA.

DE Human CNGH0010 variant 1 protein SegID3.  
PN WO2004098502-A2.  
PD 18-NOV-2004.  
PA (CENZ ) CENTOCOR INC.  
Query Match 95.9%; Score 2266.5; DB 8; Length 555;  
Best Local Similarity 94.9%; Pred. No. 3.3e-131;  
RESULT 753  
ID AAB38324 standard; protein; 387 AA.  
DE Human secreted protein encoded by gene 4 clone HKAJK47.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 85.9%; Score 2030; DB 3; Length 387;  
Best Local Similarity 87.5%; Pred. No. 7.8e-117;  
RESULT 754  
ID AAY50941 standard; protein; 479 AA.  
DE Human adult skin cDNA clone v04\_1 derived protein.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 85.1%; Score 1963; DB 6; Length 476;  
Best Local Similarity 87.1%; Pred. No. 1.2e-114;  
RESULT 755  
ID AEC32634 standard; protein; 476 AA.  
DE Human keratinocyte-related protein #2.  
PN WO2005083075-A1.  
PD 09-SEP-2005.  
PA (EISA ) EISAI CO LTD.  
Query Match 84.5%; Score 1963; DB 6; Length 372;  
Best Local Similarity 84.5%; Pred. No. 9.8e-113;  
RESULT 756  
ID ABO27306 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO411.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 83.1%; Score 1963; DB 6; Length 372;  
Best Local Similarity 84.5%; Pred. No. 9.8e-113;  
RESULT 757  
ID ABO34192 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 83.1%; Score 1963; DB 6; Length 372;  
Best Local Similarity 84.5%; Pred. No. 9.8e-113;  
RESULT 758  
ID AAY50940 standard; protein; 369 AA.  
DE Human adult skin cDNA clone v03\_1 derived protein #2.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 81.5%; Score 1925.5; DB 3; Length 369;  
Best Local Similarity 83.4%; Pred. No. 2e-110;  
RESULT 759  
ID AAY50939 standard; protein; 358 AA.  
DE Human adult skin cDNA clone v03\_1 derived protein #1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 71.6%; Score 1692; DB 3; Length 358;  
Best Local Similarity 95.8%; Pred. No. 4.2e-96;  
RESULT 760  
ID AEC32630 standard; protein; 517 AA.  
DE Murine keratinocyte-related protein #2.  
PN WO2005083075-A1.  
PD 09-SEP-2005.  
PA (EISA ) EISAI CO LTD.  
Query Match 44.1%; Score 1043; DB 9; Length 517;  
Best Local Similarity 48.9%; Pred. No. 4.4e-56;  
RESULT 761  
ID ADP07783 standard; protein; 186 AA.  
DE Human secreted protein, seq id 266.

PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 37.1%; Score 875.5; DB 8; Length 186;  
Best Local Similarity 92.3%; Pred. No. 3.2e-46;  
RESULT 762  
ID ADU68164 standard; protein; 149 AA.  
DE Human CNGH0010 variant 4 protein SeqID9.  
PN WO2004098502-A2.  
PD 18-NOV-2004.  
PA (CENZ-) CENTOCOR INC.  
Query Match 29.4%; Score 695; DB 8; Length 149;  
Best Local Similarity 98.5%; Pred. No. 3.2e-35;  
RESULT 763  
ID AAY60056 standard; protein; 230 AA.  
DE Human endometrium tumour EST encoded protein 116.  
PN DE19817948-A1.  
PD 21-OCT-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 28.3%; Score 669; DB 2; Length 230;  
Best Local Similarity 98.4%; Pred. No. 1.9e-33;  
RESULT 764  
ID ADU68162 standard; protein; 253 AA.  
DE Human CNGH0010 variant 3 protein SeqID7.  
PN WO2004098502-A2.  
PD 18-NOV-2004.  
PA (CENZ-) CENTOCOR INC.  
Query Match 28.0%; Score 661; DB 8; Length 253;  
Best Local Similarity 97.6%; Pred. No. 6.5e-33;  
RESULT 765  
ID ABO23519 standard; protein; 1079 AA.  
DE Mycobacterium tuberculosis outlier protein #3.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S. K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 19.1%; Score 450.5; DB 7; Length 1079;  
Best Local Similarity 30.5%; Pred. No. 2.2e-19;  
RESULT 766  
ID ABB91435 standard; protein; 1079 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:145.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 19.1%; Score 450.5; DB 9; Length 1079;  
Best Local Similarity 30.5%; Pred. No. 2.2e-19;  
RESULT 767  
ID ABB91429 standard; protein; 1306 AA.  
DE Protein encoded by Prokaryotic essential gene #22008.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 18.6%; Score 439.5; DB 6; Length 1306;  
Best Local Similarity 30.9%; Pred. No. 1.3e-18;  
RESULT 768  
ID ABB91429 standard; protein; 1306 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:139.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 18.6%; Score 439.5; DB 9; Length 1306;  
Best Local Similarity 30.9%; Pred. No. 1.3e-18;  
RESULT 769  
ID AAO16495 standard; protein; 400 AA.  
DE Kukulcania hibernalis spider silk protein #2.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 18.4%; Score 434; DB 6; Length 400;  
Best Local Similarity 33.4%; Pred. No. 8.8e-19;  
RESULT 770  
ID ABB36971 standard; protein; 1381 AA.  
DE Protein encoded by Prokaryotic essential gene #22498.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.6%; Score 415.5; DB 6; Length 1381;  
Best Local Similarity 29.9%; Pred. No. 3.9e-17;  
RESULT 771  
ID ABB91428 standard; protein; 1381 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:138.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 17.6%; Score 415.5; DB 9; Length 1381;  
Best Local Similarity 29.9%; Pred. No. 3.9e-17;  
RESULT 772  
ID ABB15873 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis mycobacterial antigen protein SEQ ID NO:111.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 17.5%; Score 412.5; DB 6; Length 484;  
Best Local Similarity 33.6%; Pred. No. 2.2e-17;  
RESULT 773  
ID ABB36943 standard; protein; 484 AA.  
DE Protein encoded by Prokaryotic essential gene #22470.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.5%; Score 412.5; DB 6; Length 484;  
Best Local Similarity 33.6%; Pred. No. 2.2e-17;  
RESULT 774  
ID ABO23518 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis outlier protein #2.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S. K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 17.5%; Score 412.5; DB 7; Length 484;  
Best Local Similarity 33.6%; Pred. No. 2.2e-17;  
RESULT 775  
ID ABB91460 standard; protein; 484 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:170.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 17.5%; Score 412.5; DB 9; Length 484;  
Best Local Similarity 33.6%; Pred. No. 2.2e-17;  
RESULT 776  
ID AAM16105 standard; protein; 357 AA.  
DE Peptide #253 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 777  
ID ABB35090 standard; peptide; 357 AA.  
DE Peptide #2596 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 778  
ID AAM28596 standard; protein; 357 AA.  
DE Peptide #2633 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;



Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 779  
ID ABB29912 standard; peptide; 357 AA.  
DE Peptide #2563 encoded by breast cell single exon nucleic acid probe.  
PN W0200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 780  
ID ABB20509 standard; protein; 357 AA.  
DE Protein #2508 encoded by probe for measuring heart cell gene expression.  
PN W0200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 781  
ID AAM6282 standard; protein; 357 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28588.  
PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 782  
ID AAM55912 standard; protein; 357 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28017.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 783  
ID AAG4940 standard; peptide; 357 AA.  
DE Human liver peptide; SEQ ID NO 28588.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 784  
ID AAM03832 standard; protein; 357 AA.  
DE Peptide #2514 encoded by probe for measuring breast gene expression.  
PN W0200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 785  
ID ABB7823 standard; peptide; 357 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27488.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3.9e-17;  
RESULT 786  
ID ABB91425 standard; protein; 1901 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:135.  
PN W02005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) CONUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 17.2%; Score 406; DB 9; Length 1901;  
Best Local Similarity 29.7%; Pred. No. 2.1e-16;  
RESULT 787  
ID ABB36734 standard; protein; 532 AA.  
DE Protein encoded by Prokaryotic essential gene #22261.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.1%; Score 404.5; DB 6; Length 532;  
Best Local Similarity 32.2%; Pred. No. 7.5e-17;

RESULT 788  
ID AAP80940 standard; protein; 1177 AA.  
DE SlpIII protein comprising the gagags of silk fibroin.  
PN W080803533-A.  
PD 19-MAY-1988.  
PA (SYTR-) SYNTRO CORP.  
Query Match 17.0%; Score 402.5; DB 1; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 789  
ID AAR05307 standard; protein; 1177 AA.  
DE SLP IIT (Silk-fibroin like protein).  
PN W09005177-A.  
PD 17-MAY-1990.  
PA (SYTR-) SYNTRO CORP.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 790  
ID AAR95105 standard; protein; 1177 AA.  
DE Silk like protein (SLP)IIT.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 791  
ID AAM26342 standard; protein; 1177 AA.  
DE Silk-like protein SlpIIT.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 792  
ID AAY78277 standard; peptide; 1177 AA.  
DE SlpIIT amino acid sequence SEQ ID NO:64.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 3; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 793  
ID AAB63995 standard; protein; 1177 AA.  
DE SlpIIT protein sequence SEQ ID 31.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 4; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 794  
ID AAB72725 standard; protein; 1177 AA.  
DE Repetitive protein polymer protein sequence #25.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 4; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 795  
ID ABB69267 standard; protein; 1177 AA.  
DE Silk-like protein SLP.IIT.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 5; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 796  
ID ABB44959 standard; protein; 1177 AA.  
DE Silk fibroin protein repeating peptide related protein seq id 64.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 7; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
RESULT 797

ID AAR41007 standard; protein; 1178 AA.  
 DE S1k-like protein s1p-III multimer.  
 PN US5243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 17.0%; Score 402.5; DB 2; Length 1178;  
 Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
 RESULT 798  
 ID AAW53518 standard; protein; 1178 AA.  
 DE Amino acid sequence of the synthetic S1P1II protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 17.0%; Score 402.5; DB 2; Length 1178;  
 Best Local Similarity 30.4%; Pred. No. 2.1e-16;  
 RESULT 799  
 ID AAP82962 standard; protein; 1059 AA.  
 DE SEPI4 protein comprising gagags of silk fibroin.  
 PN WO8803533-A.  
 PD 19-MAY-1988.  
 PA (SYTR) SYNTRO CORP.  
 Query Match 17.0%; Score 401; DB 1; Length 1059;  
 Best Local Similarity 30.4%; Pred. No. 2.4e-16;  
 RESULT 800  
 ID AEB91436 standard; protein; 1538 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:146.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 16.9%; Score 400.5; DB 9; Length 1538;  
 Best Local Similarity 32.4%; Pred. No. 3.6e-16;  
 RESULT 801  
 ID ADV78697 standard; protein; 572 AA.  
 DE Human-derived cell attachment protein - SEQ ID 161.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 16.9%; Score 399.5; DB 9; Length 572;  
 Best Local Similarity 30.9%; Pred. No. 1.6e-16;  
 RESULT 802  
 ID AEB91439 standard; protein; 853 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:149.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 16.9%; Score 399.5; DB 9; Length 853;  
 Best Local Similarity 31.2%; Pred. No. 2.4e-16;  
 RESULT 803  
 ID AAW53524 standard; protein; 1023 AA.  
 DE Amino acid sequence of the S1P4 protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 2; Length 1023;  
 Best Local Similarity 30.4%; Pred. No. 3.1e-16;  
 RESULT 804  
 ID AAR41013 standard; protein; 1059 AA.  
 DE S1P4 multimeric protein.  
 PN US5243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 2; Length 1059;  
 Best Local Similarity 30.4%; Pred. No. 3.2e-16;  
 RESULT 805  
 ID AAW26348 standard; protein; 1059 AA.  
 DE S1P4 synthetic protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 2; Length 1059;  
 Best Local Similarity 30.4%; Pred. No. 3.2e-16;  
 RESULT 806  
 ID AAY78283 standard; protein; 1101 AA.

DE S1P4 amino acid sequence SEQ ID NO:83.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 3; Length 1101;  
 Best Local Similarity 30.4%; Pred. No. 3.3e-16;  
 RESULT 807  
 ID ABG69273 standard; protein; 1101 AA.  
 DE S1k/Elastin-like protein S1P4.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 5; Length 1101;  
 Best Local Similarity 30.4%; Pred. No. 3.3e-16;  
 RESULT 808  
 ID ADK44978 standard; protein; 1101 AA.  
 DE Recombinant structural protein S1P4 protein seg id 83.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 7; Length 1101;  
 Best Local Similarity 30.4%; Pred. No. 3.3e-16;  
 RESULT 809  
 ID AE116231 standard; protein; 741 AA.  
 DE Cell adhesion polypeptide Pronectin F.  
 PN JP2006150072-A.  
 PD 15-JUN-2006.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 16.8%; Score 397.5; DB 10; Length 741;  
 Best Local Similarity 30.3%; Pred. No. 2.8e-16;  
 RESULT 810  
 ID AEB91427 standard; protein; 1660 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:137.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 16.7%; Score 395; DB 9; Length 1660;  
 Best Local Similarity 30.0%; Pred. No. 8.5e-16;  
 RESULT 811  
 ID AEB98982 standard; protein; 616 AA.  
 DE Epstein-Barr virus EBNA-1 deletion mutant protein (delta65-89).  
 PN US2005260564-A1.  
 PD 24-NOV-2005.  
 PA (SUCD) SUCDEN B.  
 PA (WANG) WANG J.  
 PA (KENN) KENNEDY G D.  
 Query Match 16.6%; Score 392.5; DB 9; Length 616;  
 Best Local Similarity 31.2%; Pred. No. 4.7e-16;  
 RESULT 812  
 ID ABJ36550 standard; protein; 923 AA.  
 DE Protein encoded by Prokaryotic essential gene #22077.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT) ELITRA PHARM INC.  
 Query Match 16.6%; Score 392.5; DB 6; Length 923;  
 Best Local Similarity 27.7%; Pred. No. 6.9e-16;  
 RESULT 813  
 ID AEB91437 standard; protein; 923 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:147.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 16.6%; Score 392.5; DB 9; Length 923;  
 Best Local Similarity 27.7%; Pred. No. 6.9e-16;  
 RESULT 814  
 ID AEB91445 standard; protein; 731 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:155.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 16.6%; Score 392; DB 9; Length 731;  
 Best Local Similarity 32.2%; Pred. No. 6e-16;  
 RESULT 815

ID AEB91426 standard; protein; 1329 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:136.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL.) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 16.6%; Score 392; DB 9; Length 1329;  
Best Local Similarity 28.5%; Pred. No. 1.1e-15;  
RESULT 816  
ID AE116238 standard; protein; 767 AA.  
DE Cell adhesion polypeptide Pronectin Y.  
PN JP2006150072-A.  
PD 15-JUN-2006.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 16.8%; Score 391.5; DB 10; Length 767;  
Best Local Similarity 29.8%; Pred. No. 6.7e-16;  
RESULT 817  
ID ABP53453 standard; protein; 1062 AA.  
DE Pre-gelated protein polymer SUP3 related amino acid sequence #2.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPELLLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 16.4%; Score 386.5; DB 5; Length 1062;  
Best Local Similarity 31.5%; Pred. No. 1.9e-15;  
RESULT 818  
ID ABU36827 standard; protein; 778 AA.  
DE Protein encoded by Prokaryotic essential gene #22354.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 16.3%; Score 386; DB 6; Length 778;  
Best Local Similarity 31.2%; Pred. No. 1.5e-15;  
RESULT 819  
ID AEB91434 standard; protein; 778 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:144.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL.) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 16.3%; Score 386; DB 9; Length 778;  
Best Local Similarity 31.2%; Pred. No. 1.5e-15;  
RESULT 820  
ID ADV78696 standard; protein; 382 AA.  
DE Human-derived cell attachment protein - SEQ ID NO:160.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 16.3%; Score 385.5; DB 9; Length 382;  
Best Local Similarity 31.4%; Pred. No. 8e-16;  
RESULT 821  
ID AEB91444 standard; protein; 767 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:154.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL.) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 16.2%; Score 383.5; DB 9; Length 767;  
Best Local Similarity 29.5%; Pred. No. 2.1e-15;  
RESULT 822  
ID AAY28843 standard; protein; 641 AA.  
DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1).  
PN WO947647-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 16.2%; Score 383; DB 2; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 823  
ID AAY95856 standard; protein; 641 AA.  
DE Epstein Barr virus nuclear antigen 1 protein (EBNA1).  
PN WO200047778-A1.  
PD 17-AUG-2000.  
PA (PHAR-) PHARMACOEPIA INC.  
Query Match 16.2%; Score 383; DB 3; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 824

ID AAB62332 standard; protein; 641 AA.  
DE EBV tethering protein EBNA1.  
PN WO200125484-A2.  
PD 12-APR-2001.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 16.2%; Score 383; DB 4; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 825  
ID ABP72663 standard; protein; 641 AA.  
DE Epstein-Barr virus nuclear antigen 1.  
PN WO2003018754-A2.  
PD 06-MAR-2003.  
PA (NEUR-) NEURONZ LTD.  
PA (NEUR-) NEURONZ BIOSCIENCES INC.  
Query Match 16.2%; Score 383; DB 6; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 826  
ID AAB34812 standard; protein; 641 AA.  
DE Epstein-Barr virus nuclear antigen 1 (EBNA1).  
PN WO200290558-A1.  
PD 14-NOV-2002.  
PA (FITB-) FIT BIOTECH OXY PLC.  
Query Match 16.2%; Score 383; DB 6; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 827  
ID ADK65581 standard; protein; 641 AA.  
DE Human herpesvirus 4 nuclear antigen-1 protein.  
PN DE10207135-A1.  
PD 11-SEP-2003.  
PA (EURO-) EUROIMMUN GMBH.  
Query Match 16.2%; Score 383; DB 7; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 828  
ID AD575052 standard; protein; 641 AA.  
DE Epstein-Barr virus nuclear antigen 1.  
PN WO2004007536-A2.  
PD 22-JAN-2004.  
PA (AFPI-) AFFINITUM PHARM INC.  
Query Match 16.2%; Score 383; DB 8; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 829  
ID ADP12515 standard; protein; 641 AA.  
DE Protein encoded by mRNA of the invention #125.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 16.2%; Score 383; DB 8; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 830  
ID ADQ94586 standard; protein; 641 AA.  
DE Epstein-Barr virus EBNA1 protein.  
PN US2004141995-A1.  
PD 22-JUL-2004.  
PA (WANG/) WANG R.  
PA (VOOK/) VOOK K.  
Query Match 16.2%; Score 383; DB 8; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 831  
ID ADV68156 standard; protein; 641 AA.  
DE Epstein-Barr virus EBNA1 protein.  
PN US2004248081-A1.  
PD 09-DEC-2004.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 16.2%; Score 383; DB 9; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 832  
ID ADP80000 standard; protein; 641 AA.  
DE Epstein-Barr virus NRP-related nuclear antigen 1 protein.  
PN WO2005042561-A2.  
PD 12-MAY-2005.  
PA (NEUR-) NEUREN PHARM LTD.  
PA (NEUR-) NEUREN PHARM INC.  
Query Match 16.2%; Score 383; DB 9; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 833

Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 833  
ID AEB68217 standard; protein: 641 AA.  
DE Epstein-Barr virus EBNA1 amino acid sequence.  
PN CN1584593-A.  
PD 23-FEB-2005.  
PA (HONG-) HONGKONG SHENNONG CO LTD.  
Query Match 16.2%; Score 383; DB 9; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 834  
ID AEB89872 standard; protein: 641 AA.  
DE Epstein-Barr virus EBNA-1 protein.  
PN US2005260564-A1.  
PD 24-NOV-2005.  
PA (SUGD/) SUGDEN B.  
PA (WANG/) WANG J.  
PA (KENN-) KENNEDY G D.  
Query Match 16.2%; Score 383; DB 9; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 835  
ID AEB29091 standard; protein: 641 AA.  
DE EBV-encoded nuclear antigen 1 (EBNA1) amino acid sequence, SEQ ID 1.  
PN JP2006121995-A.  
PD 18-MAY-2006.  
PA (UYTY ) UNIV TOKYO.  
Query Match 16.2%; Score 383; DB 10; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 836  
ID AEB60518 standard; protein: 641 AA.  
DE Epstein Barr virus nuclear antigen 1 (EBNA1).  
PN WO2006096989-A2.  
PD 21-SEP-2006.  
PA (CANA ) NAT RES COUNCIL CANADA.  
Query Match 16.2%; Score 383; DB 10; Length 641;  
Best Local Similarity 31.0%; Pred. No. 1.9e-15;  
RESULT 837  
ID AEB56250 standard; protein: 755 AA.  
DE Partial B. mori fibroin-H (Fib-H)-C-terminal SEQ ID NO 20.  
PN WO2006083514-A2.  
PD 10-AUG-2006.  
PA (UYFL ) UNIV FLORIDA.  
Query Match 16.2%; Score 383; DB 10; Length 755;  
Best Local Similarity 31.1%; Pred. No. 2.2e-15;  
RESULT 838  
ID AEB91451 standard; protein: 741 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:161.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL ) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 16.1%; Score 381.5; DB 9; Length 741;  
Best Local Similarity 29.0%; Pred. No. 2.7e-15;  
RESULT 839  
ID AEB36438 standard; protein: 837 AA.  
DE Protein encoded by Prokaryotic essential gene #21965.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 16.1%; Score 380.5; DB 6; Length 837;  
Best Local Similarity 30.5%; Pred. No. 3.4e-15;  
RESULT 840  
ID AEB91449 standard; protein: 837 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:159.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL ) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 16.1%; Score 380.5; DB 9; Length 837;  
Best Local Similarity 30.5%; Pred. No. 3.4e-15;  
RESULT 841  
ID AEB16241 standard; protein: 705 AA.  
DE Cell adhesion polypeptide P2-1.  
PN JP2006150072-A.  
PD 15-JUN-2006.  
PA (SANN ) SANYO CHEM IND LTD.

Query Match 16.0%; Score 379; DB 10; Length 705;  
Best Local Similarity 31.8%; Pred. No. 3.6e-15;  
RESULT 842  
ID AEB53456 standard; protein: 996 AA.  
DE Pre-gelled protein polymer SLP4 related amino acid sequence #2.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 16.0%; Score 379; DB 5; Length 996;  
Best Local Similarity 31.8%; Pred. No. 5e-15;  
RESULT 843  
ID AEB18319 standard; protein: 1002 AA.  
DE Silk-like protein, SLP4.  
PN WO200200016-A1.  
PD 03-JAN-2002.  
PA (LUMI-) LUMINIS PTY LTD.  
PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.  
Query Match 16.0%; Score 379; DB 5; Length 1002;  
Best Local Similarity 31.8%; Pred. No. 5.1e-15;  
RESULT 844  
ID AEB36945 standard; protein: 588 AA.  
DE Protein encoded by Prokaryotic essential gene #22472.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 16.0%; Score 378; DB 6; Length 588;  
Best Local Similarity 30.1%; Pred. No. 3.5e-15;  
RESULT 845  
ID ADM40790 standard; protein: 588 AA.  
DE Mycobacterial disease detection method related RVJ367 protein.  
PN WO2003073101-A2.  
PD 04-SEP-2003.  
PA (UYNY ) UNIV NEW YORK STATE.  
Query Match 16.0%; Score 378; DB 7; Length 588;  
Best Local Similarity 30.1%; Pred. No. 3.5e-15;  
RESULT 846  
ID AAW27178 standard; protein: 646 AA.  
DE Nephila clavipes spider silk protein.  
PN WO9708315-A1.  
PD 06-MAR-1997.  
PA (BASE/) BASEL R M.  
PA (ELIO/) ELION G R.  
Query Match 16.0%; Score 378; DB 2; Length 646;  
Best Local Similarity 29.0%; Pred. No. 3.8e-15;  
RESULT 847  
ID ADB61321 standard; protein: 646 AA.  
DE Spider silk related Maspi protein.  
PN WO2003060099-A2.  
PD 24-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
PA (ALMA/) ALMATTARI A.  
Query Match 16.0%; Score 378; DB 7; Length 646;  
Best Local Similarity 31.5%; Pred. No. 3.8e-15;  
RESULT 848  
ID ADC35240 standard; protein: 646 AA.  
DE Maspi silk protein, SEQ ID 1.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 16.0%; Score 378; DB 7; Length 646;  
Best Local Similarity 31.5%; Pred. No. 3.8e-15;  
RESULT 849  
ID ADM46149 standard; protein: 646 AA.  
DE Nephila clavipes spideroin 1 (Maspi) protein.  
PN WO2003057720-A2.  
PD 17-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 16.0%; Score 378; DB 7; Length 646;  
Best Local Similarity 31.5%; Pred. No. 3.8e-15;  
RESULT 850  
ID ADT93270 standard; protein: 646 AA.  
DE Nephila clavipes (spider) Maspi protein - SEQ ID 27.

PN WO2004090205-A2.  
PD 21-OCT-2004.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 15.0%; Score 378; DB 8; Length 646;  
Best Local Similarity 31.5%; Pred. No. 3.8e-15;  
RESULT 851  
ID ABB91438 standard; protein; 749 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:148.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 15.9%; Score 376.5; DB 9; Length 749;  
Best Local Similarity 30.2%; Pred. No. 5.5e-15;  
RESULT 852  
ID AAR95107 standard; protein; 1038 AA.  
DE Fibronectin cell binding seq. contg. silk like protein (SLP)III.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.9%; Score 376.5; DB 2; Length 1038;  
Best Local Similarity 28.5%; Pred. No. 7.5e-15;  
RESULT 853  
ID AAB63997 standard; protein; 1038 AA.  
DE RCB-SLP protein from PSY1521 SEQ ID 36.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.9%; Score 376.5; DB 4; Length 1038;  
Best Local Similarity 28.5%; Pred. No. 7.5e-15;  
RESULT 854  
ID AAB72727 standard; protein; 1038 AA.  
DE Repetitive protein polymer protein sequence #27.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.9%; Score 376.5; DB 4; Length 1038;  
Best Local Similarity 28.5%; Pred. No. 7.5e-15;  
RESULT 855  
ID ADO08760 standard; protein; 452 AA.  
DE Novel surgical dressing-related protein SeqID47.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN-) SANYO CHEM IND LTD.  
Query Match 15.9%; Score 375.5; DB 8; Length 452;  
Best Local Similarity 29.9%; Pred. No. 3.9e-15;  
RESULT 856  
ID ADV78654 standard; protein; 452 AA.  
DE Human-derived cell attachment protein - SEQ ID 118.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN-) SANYO CHEM IND LTD.  
Query Match 15.9%; Score 375.5; DB 6; Length 452;  
Best Local Similarity 29.9%; Pred. No. 3.9e-15;  
RESULT 857  
ID ABU36682 standard; protein; 914 AA.  
DE Protein encoded by Prokaryotic essential gene #22209.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.9%; Score 375; DB 6; Length 914;  
Best Local Similarity 33.0%; Pred. No. 8.2e-15;  
RESULT 858  
ID ABB91450 standard; protein; 914 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:160.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 15.9%; Score 375; DB 9; Length 914;  
Best Local Similarity 33.0%; Pred. No. 8.2e-15;  
RESULT 859  
ID AAM50037 standard; protein; 1255 AA.  
DE N. clavipes spidroin synthetic homologue SOISO1 protein.

PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPRP-) IPR INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.8%; Score 374; DB 5; Length 1255;  
Best Local Similarity 30.5%; Pred. No. 1.3e-14;  
RESULT 860  
ID AAM50039 standard; protein; 1880 AA.  
DE N. clavipes spidroin synthetic homologue SOISO101 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPRP-) IPR INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.8%; Score 374; DB 5; Length 1880;  
Best Local Similarity 30.5%; Pred. No. 1.9e-14;  
RESULT 861  
ID AAO16497 standard; protein; 520 AA.  
DE Arctopis trifasciata spider silk protein #1.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UWVY-) UNIV WYOMING.  
Query Match 15.8%; Score 373.5; DB 6; Length 520;  
Best Local Similarity 30.0%; Pred. No. 5.9e-15;  
RESULT 862  
ID ABU36979 standard; protein; 584 AA.  
DE Protein encoded by Prokaryotic essential gene #22506.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.8%; Score 373.5; DB 6; Length 584;  
Best Local Similarity 32.3%; Pred. No. 6.6e-15;  
RESULT 863  
ID ABU36570 standard; protein; 667 AA.  
DE Protein encoded by Prokaryotic essential gene #22097.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.8%; Score 373.5; DB 6; Length 667;  
Best Local Similarity 28.5%; Pred. No. 7.5e-15;  
RESULT 864  
ID ADE28209 standard; protein; 203 AA.  
DE Human MDDT protein - SEQ ID 59.  
PN WO2003046152-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.8%; Score 373; DB 7; Length 203;  
Best Local Similarity 58.9%; Pred. No. 2.6e-15;  
RESULT 865  
ID ABU36802 standard; protein; 694 AA.  
DE Protein encoded by Prokaryotic essential gene #22329.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.7%; Score 372; DB 6; Length 694;  
Best Local Similarity 30.3%; Pred. No. 9.6e-15;  
RESULT 866  
ID ABB91448 standard; protein; 694 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:158.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 15.7%; Score 372; DB 9; Length 694;  
Best Local Similarity 30.3%; Pred. No. 9.6e-15;  
RESULT 867  
ID AEF65782 standard; protein; 942 AA.  
DE Spider flagelliform protein Flag-N.  
PN WO2006008163-A2.  
PD 26-JAN-2006.  
PA (UYMU-) UNIV TECH MUENCHEN.  
Query Match 15.7%; Score 372; DB 10; Length 942;  
Best Local Similarity 30.8%; Pred. No. 1.3e-14;  
RESULT 868  
ID ABU36862 standard; protein; 615 AA.  
DE Protein encoded by Prokaryotic essential gene #22389.  
PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELITRA) ELITRA PHARM INC.  
Query Match 15.7%; Score 371; DB 6; Length 615;  
Best Local Similarity 31.0%; Pred. No. 9.8e-15;  
RESULT 869  
ID AAB91442 standard; protein; 615 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:152.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 15.7%; Score 371; DB 9; Length 615;  
Best Local Similarity 31.0%; Pred. No. 9.8e-15;  
RESULT 870  
ID AAY40097 standard; protein; 651 AA.  
DE Spider silk protein spidroine major 1.  
PN PR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.7%; Score 371; DB 2; Length 651;  
Best Local Similarity 30.1%; Pred. No. 1e-14;  
RESULT 871  
ID AAU11781 standard; protein; 651 AA.  
DE Spider natural silk protein Spidroin 1.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E. I.  
Query Match 15.7%; Score 371; DB 5; Length 651;  
Best Local Similarity 30.1%; Pred. No. 1e-14;  
RESULT 872  
ID AAR14308 standard; protein; 718 AA.  
DE N.clavipes dragline silk protein-1.  
PN EP452925-A.  
PD 23-OCT-1991.  
PA (UYWY-) UNIV OF WYOMING.  
Query Match 15.7%; Score 371; DB 2; Length 718;  
Best Local Similarity 30.1%; Pred. No. 1.1e-14;  
RESULT 873  
ID AAM53346 standard; protein; 718 AA.  
DE Nephila clavipes spider silk protein.  
PN US572810-A.  
PD 17-MAR-1998.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.7%; Score 371; DB 2; Length 718;  
Best Local Similarity 30.1%; Pred. No. 1.1e-14;  
RESULT 874  
ID AAY59070 standard; protein; 718 AA.  
DE N. clavipes spider silk protein 1.  
PN US598984-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.7%; Score 371; DB 3; Length 718;  
Best Local Similarity 30.1%; Pred. No. 1.1e-14;  
RESULT 875  
ID AUB36634 standard; protein; 491 AA.  
DE Protein encoded by prokaryotic essential gene #2261.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITRA) ELITRA PHARM INC.  
Query Match 15.7%; Score 370.5; DB 6; Length 491;  
Best Local Similarity 28.3%; Pred. No. 8.5e-15;  
RESULT 876  
ID AAR81318 standard; protein; 980 AA.  
DE Adhesion protein.  
PN WO9519793-A1.  
PD 27-JUL-1995.  
PA (USNA) US SEC OF NAVY.  
Query Match 15.7%; Score 370.5; DB 2; Length 980;  
Best Local Similarity 29.6%; Pred. No. 1.6e-14;  
RESULT 877  
ID AAR05312 standard; protein; 1066 AA.  
DE Sequence encoding SLP-L1 monomer (similar to silk fibroin).  
PN WO9005177-A.

PD 17-MAY-1990.  
PA (SYTR) SYNTRO CORP.  
Query Match 15.7%; Score 370; DB 2; Length 1066;  
Best Local Similarity 27.9%; Pred. No. 1.9e-14;  
RESULT 878  
ID AAM50038 standard; protein; 989 AA.  
DE N. clavipes spidroin synthetic homologue S01SM12 protein.  
PN DE1013781-A1.  
PD 13-DEC-2001.  
PA (IRKP-) IRK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.6%; Score 369.5; DB 5; Length 989;  
Best Local Similarity 30.8%; Pred. No. 1.9e-14;  
RESULT 879  
ID AAR41010 standard; protein; 2025 AA.  
DE SLP1 multimeric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.6%; Score 369; DB 2; Length 2025;  
Best Local Similarity 27.4%; Pred. No. 4.1e-14;  
RESULT 880  
ID AAR82959 standard; protein; 2107 AA.  
DE SLP1 protein comprising gagags of silk fibroin and gvygp of elastin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR) SYNTRO CORP.  
Query Match 15.6%; Score 369; DB 1; Length 2107;  
Best Local Similarity 27.4%; Pred. No. 4.2e-14;  
RESULT 881  
ID AAY78287 standard; protein; 1011 AA.  
DE SLPF amino acid sequence SEQ ID NO:94.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 367; DB 3; Length 1011;  
Best Local Similarity 26.9%; Pred. No. 2.8e-14;  
RESULT 882  
ID AAG69277 standard; protein; 1011 AA.  
DE Silk/Elastin-like protein SLPF.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 367; DB 5; Length 1011;  
Best Local Similarity 26.9%; Pred. No. 2.8e-14;  
RESULT 883  
ID ADB44989 standard; protein; 1011 AA.  
DE Recombinant structural protein SLPF protein seq id 94.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 367; DB 7; Length 1011;  
Best Local Similarity 26.9%; Pred. No. 2.8e-14;  
RESULT 884  
ID AAW26351 standard; protein; 1170 AA.  
DE SLPF synthetic protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 367; DB 2; Length 1170;  
Best Local Similarity 26.9%; Pred. No. 3.2e-14;  
RESULT 885  
ID AAB67896 standard; protein; 610 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 30480.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 15.5%; Score 366; DB 4; Length 610;  
Best Local Similarity 32.5%; Pred. No. 2e-14;  
RESULT 886  
ID AAB36887 standard; protein; 691 AA.  
DE Dolomedes tenebrosus fibroin 2 protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.

PA (UTW-) UNIV WYOMING.  
Query Match 15.5%; Score 366; DB 6; Length 691;  
Best Local Similarity 27.0%; Pred. No. 2.2e-14;  
RESULT 887  
ID AAM53526 standard; protein; 695 AA.  
DE Amino acid sequence of FCB-SLP111 protein.  
PN W09810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 2; Length 695;  
Best Local Similarity 27.3%; Pred. No. 2.2e-14;  
RESULT 888  
ID AAM26349 standard; protein; 766 AA.  
DE FCB-SLP111 (57 kDa) synthetic protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 2; Length 766;  
Best Local Similarity 27.3%; Pred. No. 2.5e-14;  
RESULT 889  
ID AAY78285 standard; peptide; 766 AA.  
DE FCB-SLP111 amino acid sequence SEQ ID NO:88.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 3; Length 766;  
Best Local Similarity 27.3%; Pred. No. 2.5e-14;  
RESULT 890  
ID AAG69275 standard; protein; 766 AA.  
DE Fibronectin FCB portion/silk-like protein, FCB-SLP111 #1.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 5; Length 766;  
Best Local Similarity 27.3%; Pred. No. 2.5e-14;  
RESULT 891  
ID ADE44983 standard; protein; 766 AA.  
DE Recombinant structural protein FCB-SLP111 protein seq id 88.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 7; Length 766;  
Best Local Similarity 27.3%; Pred. No. 2.5e-14;  
RESULT 892  
ID AAY78286 standard; protein; 979 AA.  
DE FCB-SLP111 amino acid sequence SEQ ID NO:89.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 3; Length 979;  
Best Local Similarity 27.3%; Pred. No. 3.1e-14;  
RESULT 893  
ID AAG69276 standard; protein; 979 AA.  
DE Fibronectin FCB portion/silk-like protein, FCB-SLP111 #2.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 5; Length 979;  
Best Local Similarity 27.3%; Pred. No. 3.1e-14;  
RESULT 894  
ID ADE44984 standard; protein; 979 AA.  
DE Recombinant structural protein FCB-SLP111 protein seq id 89.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 7; Length 979;  
Best Local Similarity 27.3%; Pred. No. 3.1e-14;  
RESULT 895  
ID AEB05675 standard; protein; 980 AA.  
DE Cell adhesive amino acid sequence SEQ ID NO:89.  
PN JP2005263631-A.  
PD 29-SEP-2005.  
PA (SANN) SANTO CHEM IND LTD.

Query Match 15.5%; Score 366; DB 9; Length 980;  
Best Local Similarity 27.3%; Pred. No. 3.1e-14;  
RESULT 896  
ID AAM26350 standard; protein; 1050 AA.  
DE FCB-SLP111 (72 kDa) synthetic protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 2; Length 1050;  
Best Local Similarity 27.3%; Pred. No. 3.3e-14;  
RESULT 897  
ID ADV78691 standard; protein; 1051 AA.  
DE Human-derived cell attachment protein - SEQ ID 155.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANTO CHEM IND LTD.  
Query Match 15.5%; Score 366; DB 9; Length 1051;  
Best Local Similarity 27.3%; Pred. No. 3.3e-14;  
RESULT 898  
ID AAM53527 standard; protein; 1170 AA.  
DE Amino acid sequence of SELPF protein.  
PN W09810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.5%; Score 366; DB 2; Length 1170;  
Best Local Similarity 26.9%; Pred. No. 3.7e-14;  
RESULT 899  
ID AAM50042 standard; protein; 630 AA.  
DE N. clavipes spideroin synthetic homologue S01 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.5%; Score 365.5; DB 5; Length 630;  
Best Local Similarity 29.6%; Pred. No. 2.2e-14;  
RESULT 900  
ID AAM50047 standard; protein; 676 AA.  
DE N. clavipes spideroin synthetic homologue S01 protein #2.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.5%; Score 365.5; DB 5; Length 676;  
Best Local Similarity 29.6%; Pred. No. 2.3e-14;  
RESULT 901  
ID ABU36623 standard; protein; 576 AA.  
DE Protein encoded by Prokaryotic essential gene #22150.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.4%; Score 365; DB 6; Length 576;  
Best Local Similarity 30.2%; Pred. No. 2.2e-14;  
RESULT 902  
ID AEB91454 standard; protein; 576 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:164.  
PN W02005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 15.4%; Score 365; DB 9; Length 576;  
Best Local Similarity 30.2%; Pred. No. 2.2e-14;  
RESULT 903  
ID ABU36439 standard; protein; 591 AA.  
DE Protein encoded by Prokaryotic essential gene #21966.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.4%; Score 365; DB 6; Length 591;  
Best Local Similarity 29.4%; Pred. No. 2.2e-14;  
RESULT 904  
ID AEB91456 standard; protein; 801 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:166.  
PN W02005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 15.4%; Score 364.5; DB 9; Length 801;

Best Local Similarity 26.4%; Pred. No. 3.2e-14;  
 RESULT 905  
 ID AAF65783 standard; protein; 907 AA.  
 DE Spider flagelliform protein Flag-C.  
 PN WO2006008163-A2.  
 PD 26-JAN-2006.  
 PA (UNIV-) UNIV TECH MUENCHEN.  
 Query Match 15.4%; Score 364.5; DB 10; Length 907;  
 Best Local Similarity 28.4%; Pred. No. 3.6e-14;  
 RESULT 906  
 ID ABG69270 standard; protein; 2018 AA.  
 DE SLP-L1 protein SEQ ID 49.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364.5; DB 5; Length 2018;  
 Best Local Similarity 27.4%; Pred. No. 7.7e-14;  
 RESULT 907  
 ID ADE44975 standard; protein; 2018 AA.  
 DE Recombinant structural protein SLP1 protein seq id 80.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364.5; DB 7; Length 2018;  
 Best Local Similarity 27.4%; Pred. No. 7.7e-14;  
 RESULT 908  
 ID AAY78280 standard; peptide; 2100 AA.  
 DE SLP1 amino acid sequence SEQ ID NO:80.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364.5; DB 3; Length 2100;  
 Best Local Similarity 27.4%; Pred. No. 8e-14;  
 RESULT 909  
 ID ABU36540 standard; protein; 606 AA.  
 DE Protein encoded by Prokaryotic essential gene #22067.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 15.4%; Score 364; DB 6; Length 606;  
 Best Local Similarity 29.8%; Pred. No. 2.6e-14;  
 RESULT 910  
 ID AEB91453 standard; protein; 606 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:163.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 15.4%; Score 364; DB 9; Length 606;  
 Best Local Similarity 29.8%; Pred. No. 2.6e-14;  
 RESULT 911  
 ID AAR95112 standard; protein; 649 AA.  
 DE SLP-L1 protein (SLP)-L2.  
 PN US5514581-A.  
 PD 07-MAY-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 2; Length 649;  
 Best Local Similarity 27.7%; Pred. No. 2.8e-14;  
 RESULT 912  
 ID AAB64002 standard; protein; 649 AA.  
 DE SLP-L1 protein SEQ ID 49.  
 PN US6140072-A.  
 PD 31-OCT-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 4; Length 649;  
 Best Local Similarity 27.7%; Pred. No. 2.8e-14;  
 RESULT 913  
 ID AAB72732 standard; protein; 649 AA.  
 DE Repetitive protein polymer protein sequence #32.  
 PN US6184348-B1.  
 PD 06-FEB-2001.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 4; Length 649;  
 Best Local Similarity 27.7%; Pred. No. 2.8e-14;  
 RESULT 914  
 ID AAR95111 standard; protein; 784 AA.  
 DE SLP-L1 protein (SLP)-L1.  
 PN US5514581-A.  
 PD 07-MAY-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 2; Length 784;  
 Best Local Similarity 31.3%; Pred. No. 3.3e-14;  
 RESULT 915  
 ID AAB64001 standard; protein; 784 AA.  
 DE SLP-L1 protein SEQ ID 48.  
 PN US6140072-A.  
 PD 31-OCT-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 4; Length 784;  
 Best Local Similarity 31.3%; Pred. No. 3.3e-14;  
 RESULT 916  
 ID AAB72731 standard; protein; 784 AA.  
 DE Repetitive protein polymer protein sequence #31.  
 PN US6184348-B1.  
 PD 06-FEB-2001.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 4; Length 784;  
 Best Local Similarity 31.3%; Pred. No. 3.3e-14;  
 RESULT 917  
 ID AAR05309 standard; protein; 946 AA.  
 DE SLP-L2 polymer (similar to silk fibroin).  
 PN WO9005177-A.  
 PD 17-MAY-1990.  
 PA (SYTR-) SYNTRO CORP.  
 Query Match 15.4%; Score 364; DB 2; Length 946;  
 Best Local Similarity 27.7%; Pred. No. 4e-14;  
 RESULT 918  
 ID AAW01496 standard; protein; 1018 AA.  
 DE SLP-L1 protein SLP-L3.0 polymer.  
 PN WO9501998-A2.  
 PD 19-JAN-1995.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 2; Length 1018;  
 Best Local Similarity 30.5%; Pred. No. 4.3e-14;  
 RESULT 919  
 ID AAW26345 standard; protein; 2107 AA.  
 DE SLP1 synthetic elastomeric protein.  
 PN US6641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 2; Length 2107;  
 Best Local Similarity 27.4%; Pred. No. 8.6e-14;  
 RESULT 920  
 ID AAW53521 standard; protein; 2107 AA.  
 DE Amino acid sequence of the SLP1 protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.4%; Score 364; DB 2; Length 2107;  
 Best Local Similarity 27.4%; Pred. No. 8.6e-14;  
 RESULT 921  
 ID ABU36685 standard; protein; 639 AA.  
 DE Protein encoded by Prokaryotic essential gene #22212.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 15.4%; Score 363; DB 6; Length 639;  
 Best Local Similarity 30.5%; Pred. No. 3.2e-14;  
 RESULT 922  
 ID AEB91455 standard; protein; 639 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:165.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 15.4%; Score 363; DB 9; Length 639;  
 Best Local Similarity 30.5%; Pred. No. 3.2e-14;  
 RESULT 923



ID AAR99057 standard; protein; 604 AA.  
DE Spider dragline variant, DB-1B.16 polymer.  
PN W09429450-A2.  
PD 22-DEC-1994.  
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.  
Query Match 15.3%; Score 362; DB 2; Length 604;  
Best Local Similarity 29.7%; Pred. No. 3.5e-14;  
RESULT 924  
ID AAR95109 standard; protein; 1332 AA.  
DE Silk like protein (SLP)-C.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 2; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 7.4e-14;  
RESULT 925  
ID AAB63999 standard; protein; 1332 AA.  
DE SLP-C protein sequence SEQ ID 41.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 4; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 7.4e-14;  
RESULT 926  
ID AAB72729 standard; protein; 1332 AA.  
DE Repetitive protein polymer protein sequence #29.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 4; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 7.4e-14;  
RESULT 927  
ID ADV78708 standard; protein; 569 AA.  
DE Human-derived cell attachment protein - SEQ ID 172.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN ) SANYO CHEM IND LTD.  
Query Match 15.3%; Score 360.5; DB 9; Length 569;  
Best Local Similarity 31.3%; Pred. No. 4e-14;  
RESULT 928  
ID AAP82960 standard; protein; 2055 AA.  
DE SLP2 protein comprising gagags of silk fibroin and gvygv of elastin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR ) SYNTRO CORP.  
Query Match 15.3%; Score 360.5; DB 1; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 929  
ID ABU36590 standard; protein; 562 AA.  
DE Protein encoded by Prokaryotic essential gene #22117.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 360; DB 6; Length 562;  
Best Local Similarity 28.9%; Pred. No. 4.3e-14;  
RESULT 930  
ID AAB76672 standard; protein; 655 AA.  
DE Protein related to Bombyx mori silk fibroin.  
PN WO200240528-A1.  
PD 23-MAY-2002.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 15.2%; Score 360; DB 5; Length 655;  
Best Local Similarity 28.7%; Pred. No. 5e-14;  
RESULT 931  
ID AEI16235 standard; protein; 767 AA.  
DE Cell adhesion polypeptide Pronectin L.  
PN JP2006150072-A.  
PD 15-JUN-2006.  
PA (SANN ) SANYO CHEM IND LTD.  
Query Match 15.2%; Score 360; DB 10; Length 767;  
Best Local Similarity 29.7%; Pred. No. 5.8e-14;  
RESULT 932  
ID ABU36665 standard; protein; 1011 AA.

DE Protein encoded by Prokaryotic essential gene #22192.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 359.5; DB 6; Length 1011;  
Best Local Similarity 31.2%; Pred. No. 8.1e-14;  
RESULT 933  
ID AAE36926 standard; protein; 490 AA.  
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #1.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 490;  
Best Local Similarity 27.9%; Pred. No. 4.3e-14;  
RESULT 934  
ID AAO16492 standard; protein; 525 AA.  
DE Phidippus audax fibronin 1 protein.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 525;  
Best Local Similarity 28.9%; Pred. No. 4.6e-14;  
RESULT 935  
ID AAE36893 standard; protein; 525 AA.  
DE Phidippus audax fibroin 1 protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 525;  
Best Local Similarity 28.9%; Pred. No. 4.6e-14;  
RESULT 936  
ID AAE36886 standard; protein; 854 AA.  
DE Dolomedes tenebrosus fibroin 1 protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 854;  
Best Local Similarity 26.2%; Pred. No. 7.4e-14;  
RESULT 937  
ID AAY40099 standard; protein; 615 AA.  
DE Spider silk protein spidroine minor 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA ) L'OREAL SA.  
Query Match 15.2%; Score 358.5; DB 2; Length 615;  
Best Local Similarity 28.7%; Pred. No. 5.8e-14;  
RESULT 938  
ID AAR41011 standard; protein; 2055 AA.  
DE SLP2 multicentric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.8e-13;  
RESULT 939  
ID AAM26346 standard; protein; 2055 AA.  
DE SLP2 synthetic elastomeric protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.8e-13;  
RESULT 940  
ID AAM53522 standard; protein; 2055 AA.  
DE Amino acid sequence of the SLP2 protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.8e-13;  
RESULT 941  
ID AAY78281 standard; peptide; 2055 AA.  
DE SLP2 amino acid sequence SEQ ID NO:81.

PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 3; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.8e-13;  
RESULT 942  
ID ADE44976 standard; protein; 2055 AA.  
DE Recombinant structural protein SLP2 protein seq id 81.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 7; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.8e-13;  
RESULT 943  
ID AAR9053 standard; protein; 606 AA.  
DE Spider dragline variant, DP-1A.9 polymer.  
PN W09429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 29.2%; Pred. No. 6.1e-14;  
RESULT 944  
ID AAR9055 standard; protein; 606 AA.  
DE Spider dragline variant, DP-1B.9 polymer.  
PN W09429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 6.1e-14;  
RESULT 945  
ID AAY40101 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 6.1e-14;  
RESULT 946  
ID AAY40102 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 6.1e-14;  
RESULT 947  
ID AAY40100 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 6.1e-14;  
RESULT 948  
ID AAU11793 standard; protein; 809 AA.  
DE Dragline protein 1 analogue DP-1B 8mer.  
PN W0200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 809;  
Best Local Similarity 30.3%; Pred. No. 8e-14;  
RESULT 949  
ID AAU11797 standard; protein; 818 AA.  
DE Dragline protein 1 analogue DP-1B/his tag 8mer.  
PN W0200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 818;  
Best Local Similarity 30.3%; Pred. No. 8.1e-14;  
RESULT 950  
ID AAU11794 standard; protein; 1617 AA.  
DE Dragline protein 1 analogue DP-1B 16mer.  
PN W0200190389-A2.

PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 1617;  
Best Local Similarity 30.3%; Pred. No. 1.6e-13;  
RESULT 951  
ID AAU11798 standard; protein; 1626 AA.  
DE Dragline protein 1 analogue DP-1B/his tag 16mer.  
PN W0200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 1626;  
Best Local Similarity 30.3%; Pred. No. 1.6e-13;  
RESULT 952  
ID AA016494 standard; protein; 761 AA.  
DE Kukulcania hibernalis spider silk protein #1.  
PN W0200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.1%; Score 357; DB 6; Length 761;  
Best Local Similarity 28.1%; Pred. No. 8.7e-14;  
RESULT 953  
ID ABG69271 standard; protein; 2055 AA.  
DE Silk/Elaeclin-like protein SLP2.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.0%; Score 354.5; DB 5; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 3.2e-13;  
RESULT 954  
ID AAW01494 standard; protein; 945 AA.  
DE Silk-like protein SLP-P9 polymer.  
PN W09501998-A2.  
PD 19-JAN-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES.  
Query Match 15.0%; Score 354; DB 2; Length 945;  
Best Local Similarity 25.1%; Pred. No. 1.6e-13;  
RESULT 955  
ID ADV78700 standard; protein; 578 AA.  
DE Human-derived cell attachment protein - SEQ ID 164.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 15.0%; Score 353.5; DB 9; Length 578;  
Best Local Similarity 26.1%; Pred. No. 1.1e-13;  
RESULT 956  
ID ADV78705 standard; protein; 376 AA.  
DE Human-derived cell attachment protein - SEQ ID 169.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 14.9%; Score 353; DB 9; Length 376;  
Best Local Similarity 29.3%; Pred. No. 7.8e-14;  
RESULT 957  
ID ABU34417 standard; protein; 505 AA.  
DE Protein encoded by Prokaryotic essential gene #19944.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 353; DB 6; Length 505;  
Best Local Similarity 32.4%; Pred. No. 1e-13;  
RESULT 958  
ID ADV78706 standard; protein; 561 AA.  
DE Human-derived cell attachment protein - SEQ ID 170.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 14.9%; Score 353; DB 9; Length 561;  
Best Local Similarity 29.3%; Pred. No. 1.1e-13;  
RESULT 959  
ID AAP82961 standard; protein; 2257 AA.  
DE SLP3 protein comprising gagags of silk fibroin and gvyrv of elastin.  
PN W08803533-A.  
PD 19-MAY-1988.

PA (SYTR ) SYNTRO CORP.  
Query Match 14.9%; Score 352.5; DB 1; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 4.7e-13;  
RESULT 960  
ID ABU36613 standard; protein; 603 AA.  
DE Protein encoded by Prokaryotic essential gene #22140.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 352; DB 6; Length 603;  
Best Local Similarity 30.0%; Pred. No. 1.4e-13;  
RESULT 961  
ID AAR80254 standard; peptide; 1056 AA.  
DE Polymer SELP3.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.9%; Score 351.5; DB 2; Length 1056;  
Best Local Similarity 26.5%; Pred. No. 2.6e-13;  
RESULT 962  
ID ABP53475 standard; protein; 1056 AA.  
DE Protein polymer SELP3 polymer block amino acid sequence.  
PN US2002045367-A1.  
PD 18-APR-2002.  
PA (CAP/) CAPPELO J. R.  
PA (STED/) STEDRONSKY E R.  
Query Match 14.9%; Score 351.5; DB 5; Length 1056;  
Best Local Similarity 26.5%; Pred. No. 2.6e-13;  
RESULT 963  
ID ABU36613 standard; protein; 957 AA.  
DE Protein encoded by Prokaryotic essential gene #21964.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 351; DB 6; Length 957;  
Best Local Similarity 28.0%; Pred. No. 2.5e-13;  
RESULT 964  
ID ABU36626 standard; protein; 461 AA.  
DE Protein encoded by Prokaryotic essential gene #22353.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.8%; Score 350.5; DB 6; Length 461;  
Best Local Similarity 31.3%; Pred. No. 1.4e-13;  
RESULT 965  
ID AAR41012 standard; protein; 2257 AA.  
DE SELP3 multimeric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 6.2e-13;  
RESULT 966  
ID AAW26347 standard; protein; 2257 AA.  
DE SELP3 synthetic elastomeric protein.  
PN US641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 6.2e-13;  
RESULT 967  
ID AAW53523 standard; protein; 2257 AA.  
DE Amino acid sequence of the SELP3 protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 6.2e-13;  
RESULT 968  
ID AAV78282 standard; peptide; 2257 AA.  
DE SELP3 amino acid sequence SEQ ID NO:82.  
PN US6018030-A.  
PD 25-JAN-2000.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.8%; Score 350.5; DB 3; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 6.2e-13;  
RESULT 969  
ID ABG69272 standard; protein; 2257 AA.  
DE Silk/Elastin-like protein SELP3.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.8%; Score 350.5; DB 5; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 6.2e-13;  
RESULT 970  
ID ADE44977 standard; protein; 2257 AA.  
DE Recombinant structural protein SELP3 protein seq id 82.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.8%; Score 350.5; DB 7; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 6.2e-13;  
RESULT 971  
ID ADQ19957 standard; protein; 316 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2777.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 14.8%; Score 350; DB 8; Length 316;  
Best Local Similarity 35.3%; Pred. No. 1e-13;  
RESULT 972  
ID AEB17598 standard; protein; 316 AA.  
DE Human lorixin protein Segid12.  
PN JP2005110602-A.  
PD 28-APR-2005.  
PA (SUMO) SUMITOMO SEIYAKU KK.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 14.8%; Score 350; DB 9; Length 316;  
Best Local Similarity 35.3%; Pred. No. 1e-13;  
RESULT 973  
ID ABU36684 standard; protein; 618 AA.  
DE Protein encoded by Prokaryotic essential gene #22211.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.8%; Score 349; DB 6; Length 618;  
Best Local Similarity 29.9%; Pred. No. 2.2e-13;  
RESULT 974  
ID AEB91440 standard; protein; 618 AA.  
DE Microbial pathogen adhesion protein sequence, SEQ ID NO:150.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 14.8%; Score 349; DB 9; Length 618;  
Best Local Similarity 29.9%; Pred. No. 2.2e-13;  
RESULT 975  
ID AAB82611 standard; protein; 528 AA.  
DE Spider recombinant silk protein PRTNCD5.  
PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MELL/) MELLO C M.  
PA (ARCI/) ARCIDIACONO S.  
PA (BURL/) BUTLER M M.  
PA (USSA) US SEC OF ARMY.  
Query Match 14.7%; Score 348.5; DB 4; Length 528;  
Best Local Similarity 29.0%; Pred. No. 2.1e-13;  
RESULT 976  
ID AAB80166 standard; protein; 831 AA.  
DE PMISS1 Misp spider silk protein insert product.  
PN WO9525165-A1.  
PD 21-SEP-1995.  
PA (UWVY-) UNIV WYOMING.  
Query Match 14.7%; Score 348.5; DB 2; Length 831;  
Best Local Similarity 28.1%; Pred. No. 3.2e-13;  
RESULT 977  
ID AEU11639 standard; protein; 561 AA.

DE 15mer-R5 fusion protein sequence.  
PN MO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT) TUFTS COLLEGE.  
PA (USAF) US SEC OF AIR FORCE.  
PA (UNIT) UNIV ILLINOIS FOUN.  
Query Match 14.7%; Score 348; DB 10; Length 561;  
Best Local Similarity 28.9%; Pred. No. 2.3e-13;  
RESULT 978  
ID AEJ1618 standard; protein; 518 AA.  
DE Spidrotein 1 fibrous domain repeat comprising protein fragment.  
PN MO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT) TUFTS COLLEGE.  
PA (USAF) US SEC OF AIR FORCE.  
PA (UNIT) UNIV ILLINOIS FOUN.  
Query Match 14.7%; Score 347; DB 10; Length 518;  
Best Local Similarity 29.0%; Pred. No. 2.5e-13;  
RESULT 979  
ID AEJ1625 standard; protein; 568 AA.  
DE 15mer-BSP fusion protein sequence.  
PN MO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT) TUFTS COLLEGE.  
PA (USAF) US SEC OF AIR FORCE.  
PA (UNIT) UNIV ILLINOIS FOUN.  
Query Match 14.7%; Score 347; DB 10; Length 568;  
Best Local Similarity 29.0%; Pred. No. 2.7e-13;  
RESULT 980  
ID AAE3869 standard; protein; 648 AA.  
DE Argiopo trifasciata major ampullate spidroin 1 (Maspi) protein.  
PN MO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYW-) UNIV WYOMING.  
Query Match 14.6%; Score 346; DB 6; Length 648;  
Best Local Similarity 27.3%; Pred. No. 3.6e-13;  
RESULT 981  
ID ADO08772 standard; protein; 441 AA.  
DE Novel surgical dressing-related protein SegID59.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 14.6%; Score 345.5; DB 8; Length 441;  
Best Local Similarity 27.2%; Pred. No. 2.6e-13;  
RESULT 982  
ID ADV78665 standard; protein; 441 AA.  
DE Human-derived cell attachment protein - SEQ ID 129.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 14.6%; Score 345.5; DB 9; Length 441;  
Best Local Similarity 27.2%; Pred. No. 2.6e-13;  
RESULT 983  
ID AAM3853 standard; protein; 898 AA.  
DE Mycobacterium tuberculosis 77 kda protein.  
PN MO9741252-A2.  
PD 06-NOV-1997.  
PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.  
Query Match 14.6%; Score 344.5; DB 2; Length 898;  
Best Local Similarity 26.8%; Pred. No. 6e-13;  
RESULT 984  
ID AAM17023 standard; protein; 283 AA.  
DE Peptide #3457 encoded by probe for measuring cervical gene expression.  
PN MO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 985  
ID ABB36017 standard; peptide; 283 AA.  
DE Peptide #3523 encoded by human foetal liver single exon probe.  
PN MO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 986  
ID AAM29514 standard; protein; 283 AA.  
DE Peptide #3551 encoded by probe for measuring placental gene expression.  
PN MO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 987  
ID ABB30839 standard; peptide; 283 AA.  
DE Peptide #3490 encoded by breast cell single exon nucleic acid probe.  
PN MO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 988  
ID ABB21422 standard; protein; 283 AA.  
DE Protein #3421 encoded by probe for measuring heart cell gene expression.  
PN MO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 989  
ID AAM69190 standard; protein; 283 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29496.  
PN MO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 990  
ID AAM56810 standard; protein; 283 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28915.  
PN MO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 991  
ID ABB50867 standard; peptide; 283 AA.  
DE Human liver peptide, SEQ ID NO 29515.  
PN MO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 992  
ID AAM04731 standard; protein; 283 AA.  
DE Peptide #3413 encoded by probe for measuring breast gene expression.  
PN MO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 4; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 993  
ID ABB38794 standard; peptide; 283 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28459.  
PN MO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.6%; Score 344; DB 5; Length 283;  
Best Local Similarity 34.4%; Pred. No. 2.1e-13;  
RESULT 994  
ID ABB36839 standard; protein; 525 AA.  
DE Protein encoded by Prokaryotic essential gene #22366.  
PN MO20027183-A2.  
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.6%; Score 344; DB 6; Length 525;  
Best Local Similarity 30.4%; Pred. No. 3.9e-13;  
RESULT 995  
ID AAB3684 standard; protein: 651 AA.  
DE Argiome trifasciata flagelliform silk protein (Flag).  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 14.6%; Score 344; DB 6; Length 651;  
Best Local Similarity 26.7%; Pred. No. 4.7e-13;  
RESULT 996  
ID AAB91447 standard; protein: 783 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:157.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 14.6%; Score 344; DB 9; Length 783;  
Best Local Similarity 28.4%; Pred. No. 5.6e-13;  
RESULT 997  
ID AEU11619 standard; protein: 527 AA.  
DE Spidroin 1 fibrous domain repeat and linker comprising protein fragment.  
PN WO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT-) TUFTS COLLEGE.  
PA (USAF-) US SEC OF AIR FORCE.  
PA (UNIT-) UNIV ILLINOIS FOUNO.  
Query Match 14.5%; Score 343; DB 10; Length 527;  
Best Local Similarity 29.1%; Pred. No. 4.5e-13;  
RESULT 998  
ID AEU11638 standard; protein: 551 AA.  
DE CRGD-15mer-R5 fusion protein sequence.  
PN WO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT-) TUFTS COLLEGE.  
PA (USAF-) US SEC OF AIR FORCE.  
PA (UNIT-) UNIV ILLINOIS FOUNO.  
Query Match 14.5%; Score 343; DB 10; Length 551;  
Best Local Similarity 29.1%; Pred. No. 4.6e-13;  
RESULT 999  
ID AEU11626 standard; protein: 578 AA.  
DE CRGD-15mer-BSP fusion protein sequence.  
PN WO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT-) TUFTS COLLEGE.  
PA (USAF-) US SEC OF AIR FORCE.  
PA (UNIT-) UNIV ILLINOIS FOUNO.  
Query Match 14.5%; Score 343; DB 10; Length 578;  
Best Local Similarity 29.1%; Pred. No. 4.9e-13;  
RESULT 1000  
ID AEU11623 standard; protein: 675 AA.  
DE CRGD-15mer-CMP1 fusion protein sequence.  
PN WO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT-) TUFTS COLLEGE.  
PA (USAF-) US SEC OF AIR FORCE.  
PA (UNIT-) UNIV ILLINOIS FOUNO.  
Query Match 14.5%; Score 343; DB 10; Length 675;  
Best Local Similarity 29.1%; Pred. No. 5.6e-13;  
RESULT 1001  
ID AAB82609 standard; protein: 681 AA.  
DE Spider recombinant silk protein PQE((SP1)4/(SP2)1)4.  
PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MELI/) MELLO C M.  
PA (ARCI/) ARCIDIAONO S.  
PA (BUTL/) BUTLER M M.  
PA (USGA-) US SEC OF ARMY.  
Query Match 14.5%; Score 343; DB 4; Length 681;  
Best Local Similarity 28.3%; Pred. No. 5.7e-13;  
RESULT 1002  
ID AAB82610 standard; protein: 691 AA.  
DE Spider recombinant silk protein PBT((SP1)4/(SP2)1)4.

PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MELI/) MELLO C M.  
PA (ARCI/) ARCIDIAONO S.  
PA (BUTL/) BUTLER M M.  
PA (USGA-) US SEC OF ARMY.  
Query Match 14.5%; Score 343; DB 4; Length 691;  
Best Local Similarity 28.3%; Pred. No. 5.8e-13;  
RESULT 1003  
ID AEU11624 standard; protein: 992 AA.  
DE CRGD-15mer-DMP1 fusion protein sequence.  
PN WO2006076711-A2.  
PD 20-JUL-2006.  
PA (TUFT-) TUFTS COLLEGE.  
PA (USAF-) US SEC OF AIR FORCE.  
PA (UNIT-) UNIV ILLINOIS FOUNO.  
Query Match 14.5%; Score 343; DB 10; Length 992;  
Best Local Similarity 29.1%; Pred. No. 8.2e-13;  
RESULT 1004  
ID ADB61323 standard; protein: 629 AA.  
DE Spider silk related ADF-3 protein.  
PN WO2003060099-A2.  
PD 24-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
PA (ALMA/) ALMATTARI A.  
Query Match 14.5%; Score 342.5; DB 7; Length 629;  
Best Local Similarity 29.5%; Pred. No. 5.7e-13;  
RESULT 1005  
ID ADC35242 standard; protein: 629 AA.  
DE ADF-3 silk protein, SEQ ID 3.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 14.5%; Score 342.5; DB 7; Length 629;  
Best Local Similarity 29.5%; Pred. No. 5.7e-13;  
RESULT 1006  
ID ADM46151 standard; protein: 629 AA.  
DE Nepilia clavipes ADF-3 protein.  
PN WO2003057720-A2.  
PD 17-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 14.5%; Score 342.5; DB 7; Length 629;  
Best Local Similarity 29.5%; Pred. No. 5.7e-13;  
RESULT 1007  
ID ADP93272 standard; protein: 629 AA.  
DE Nepilia clavipes (Spider) ADF-3 protein - SEQ ID 29.  
PN WO2004090205-A2.  
PD 21-OCT-2004.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 14.5%; Score 342.5; DB 8; Length 629;  
Best Local Similarity 29.5%; Pred. No. 5.7e-13;  
RESULT 1008  
ID AEB48113 standard; protein: 636 AA.  
DE Spider dragline silk protein wild-type ADF-3 protein SEQ ID NO:3.  
PN EP1609801-A1.  
PD 28-DEC-2005.  
PA (UYMU-) UNIV TECH MUENCHEN.  
Query Match 14.5%; Score 342.5; DB 10; Length 636;  
Best Local Similarity 29.5%; Pred. No. 5.7e-13;  
RESULT 1009  
ID AAF65784 standard; protein: 636 AA.  
DE Spider dragline silk protein ADF-3 wild-type sequence.  
PN WO2006080163-A2.  
PD 26-JAN-2006.  
PA (UYMU-) UNIV TECH MUENCHEN.  
Query Match 14.5%; Score 342.5; DB 10; Length 636;  
Best Local Similarity 29.5%; Pred. No. 5.7e-13;  
RESULT 1010  
ID AEU56249 standard; protein: 636 AA.  
DE A. diadematus fibroin-3 (ADF-3) C-terminal region SEQ ID NO 19.  
PN WO2006083514-A2.  
PD 10-AUG-2006.  
PA (UYFL-) UNIV FLORIDA.

Query Match 14.5%; Score 342.5; DB 10; Length 636;  
 Best Local Similarity 29.5%; Pred. No. 5.7e-13;  
 RESULT 1011  
 ID AAM50045 standard; protein: 773 AA.  
 DE N. clavipes spideroin homologue SM12-70xELP for plant expression.  
 PN DB10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 14.5%; Score 342.5; DB 5; Length 773;  
 Best Local Similarity 29.4%; Pred. No. 6.9e-13;  
 RESULT 1012  
 ID AAM50046 standard; protein: 777 AA.  
 DE N. clavipes spideroin homologue SM12-70xELP for E. coli expression.  
 PN DB10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 14.5%; Score 342.5; DB 5; Length 777;  
 Best Local Similarity 29.4%; Pred. No. 6.9e-13;  
 RESULT 1013  
 ID AD008787 standard; protein: 482 AA.  
 DE Novel surgical dressing-related protein SegID74.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 14.5%; Score 342; DB 8; Length 482;  
 Best Local Similarity 27.1%; Pred. No. 4.7e-13;  
 RESULT 1014  
 ID ADV78680 standard; protein: 482 AA.  
 DE Human-derived cell attachment protein - SEQ ID 144.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 14.5%; Score 342; DB 9; Length 482;  
 Best Local Similarity 27.1%; Pred. No. 4.7e-13;  
 RESULT 1015  
 ID ABU36689 standard; protein: 515 AA.  
 DE Protein encoded by Prokaryotic essential gene #22216.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.5%; Score 342; DB 6; Length 515;  
 Best Local Similarity 29.3%; Pred. No. 5e-13;  
 RESULT 1016  
 ID AEF65778 standard; protein: 671 AA.  
 DE Spider dragline silk protein ADF-4.  
 PN WO2006008163-A2.  
 PD 26-JAN-2006.  
 PA (UYMU-) UNIV TECH MUENCHEN.  
 Query Match 14.4%; Score 340; DB 10; Length 671;  
 Best Local Similarity 28.7%; Pred. No. 8.6e-13;  
 RESULT 1017  
 ID ABU36423 standard; protein: 487 AA.  
 DE Protein encoded by Prokaryotic essential gene #21950.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.4%; Score 339.5; DB 6; Length 487;  
 Best Local Similarity 29.9%; Pred. No. 6.8e-13;  
 RESULT 1018  
 ID AEF65777 standard; protein: 653 AA.  
 DE Spider dragline silk protein ADF-3.  
 PN WO2006008163-A2.  
 PD 26-JAN-2006.  
 PA (UYMU-) UNIV TECH MUENCHEN.  
 Query Match 14.3%; Score 339; DB 10; Length 653;  
 Best Local Similarity 30.0%; Pred. No. 9.6e-13;  
 RESULT 1019  
 ID AAE36885 standard; protein: 1002 AA.  
 DE Argiope trifasciata flag protein fragment.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYMY-) UNIV WYOMING.

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Query Match 14.3%; Score 337; DB 6; Length 1002;  
 Best Local Similarity 29.9%; Pred. No. 1.9e-12;  
 RESULT 1020  
 ID AAE18320 standard; protein: 968 AA.  
 DE Silk elastin combination protein, SELP3.  
 PN WO200200016-A1.  
 PD 03-JAN-2002.  
 PA (LUMI-) LUMINIS PTY LTD.  
 Query Match 14.2%; Score 336.5; DB 5; Length 968;  
 Best Local Similarity 29.6%; Pred. No. 2e-12;  
 RESULT 1021  
 ID ADV78659 standard; protein: 404 AA.  
 DE Human-derived cell attachment protein - SEQ ID 158.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 14.2%; Score 336; DB 9; Length 404;  
 Best Local Similarity 29.4%; Pred. No. 9.3e-13;  
 RESULT 1022  
 ID AEE05671 standard; protein: 404 AA.  
 DE Cell adhesive amino acid sequence SEQ ID NO:85.  
 PN JP2005263631-A.  
 PD 29-SEP-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 14.2%; Score 336; DB 9; Length 404;  
 Best Local Similarity 29.4%; Pred. No. 9.3e-13;  
 RESULT 1023  
 ID ABP53479 standard; protein: 1169 AA.  
 DE Protein polymer SELPF polymer block amino acid sequence.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAP/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match 14.2%; Score 336; DB 5; Length 1169;  
 Best Local Similarity 30.5%; Pred. No. 2.6e-12;  
 RESULT 1024  
 ID AEB91457 standard; protein: 434 AA.  
 DE Microbial pathogen adhesin protein sequence, SEQ ID NO:167.  
 PN WO2005076010-A2.  
 PD 18-AUG-2005.  
 PA (COUL-) COUNCIL SCI & IND RES SOUTH AFRICA.  
 Query Match 14.2%; Score 335; DB 9; Length 434;  
 Best Local Similarity 30.0%; Pred. No. 1.1e-12;  
 RESULT 1025  
 ID AD008775 standard; protein: 482 AA.  
 DE Novel surgical dressing-related protein SegID62.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 14.2%; Score 335; DB 8; Length 482;  
 Best Local Similarity 30.6%; Pred. No. 1.3e-12;  
 RESULT 1026  
 ID ADV78658 standard; protein: 482 AA.  
 DE Human-derived cell attachment protein - SEQ ID 132.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 14.2%; Score 335; DB 9; Length 482;  
 Best Local Similarity 30.6%; Pred. No. 1.3e-12;  
 RESULT 1027  
 ID ADP31119 standard; protein: 8973 AA.  
 DE Human secreted protein SEQ ID #3117.  
 PN WO2004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 14.2%; Score 335; DB 8; Length 8973;  
 Best Local Similarity 29.9%; Pred. No. 2.1e-11;  
 RESULT 1028  
 ID AAW79137 standard; protein: 261 AA.  
 DE FlCA Gly-ala insert present in chimeric IkappaB construct.  
 PN WO9822577-A1.

PD	28-MAY-1998.
PA	(MASU/) MASUCCI M G.
Query Match	14.2%; Score 334.5; DB 2; Length 261;
Best Local Similarity	29.1%; Pred. No. 7.6e-13;
RESULT 1029	
ID	AAB36927 standard; protein; 440 AA.
DE	Nephila clavipes minor ampullate spidroin 1 consensus protein #2.
PN	WO2003020916-A2.
PD	13-MAR-2003.
PA	(UYWY-) UNIV. WYOMING.
Query Match	14.1%; Score 334; DB 6; Length 440;
Best Local Similarity	27.9%; Pred. No. 1.3e-12;
RESULT 1030	
ID	ABP72662 standard; protein; 498 AA.
DE	Rv181c gene product of Mycobacterium tuberculosis.
PN	WO2003018754-A2.
PD	06-MAR-2003.
PA	(NEUR-) NEURONZ LTD.
PA	(NEUR-) NEURONZ BIOSCIENCES INC.
Query Match	14.1%; Score 334; DB 6; Length 498;
Best Local Similarity	29.3%; Pred. No. 1.5e-12;
RESULT 1031	
ID	AB36666 standard; protein; 498 AA.
DE	Protein encoded by Prokaryotic essential gene #2213.
PN	WO2002717183-A2.
PD	03-OCT-2002.
PA	(ELITR-) ELITRA PHARM INC.
Query Match	14.1%; Score 334; DB 6; Length 498;
Best Local Similarity	29.3%; Pred. No. 1.5e-12;
RESULT 1032	
ID	ADZ7999 standard; protein; 498 AA.
DE	Mycobacterium tuberculosis NRP-related Rv1818c protein.
PN	WO2005042561-A2.
PD	12-MAY-2005.
PA	(NEUR-) NEUREN PHARM LTD.
PA	(NEUR-) NEUREN PHARM INC.
Query Match	14.1%; Score 334; DB 9; Length 498;
Best Local Similarity	29.3%; Pred. No. 1.5e-12;
RESULT 1033	
ID	ABB68951 standard; protein; 342 AA.
DE	Drosophila melanogaster polyprotein SEQ ID NO 33645.
PN	WO200171042-A2.
PD	27-SEP-2001.
PA	(PEKE-) PE CORP NV.
Query Match	14.1%; Score 332.5; DB 4; Length 342;
Best Local Similarity	29.5%; Pred. No. 1.3e-12;
RESULT 1034	
ID	AAM50043 standard; protein; 364 AA.
DE	N. clavipes spidroin synthetic homologue SMI2 protein.
PN	DE10113781-A1.
PD	13-DEC-2001.
PA	(IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match	14.0%; Score 331.5; DB 5; Length 364;
Best Local Similarity	29.3%; Pred. No. 1.6e-12;
RESULT 1035	
ID	AEI17599 standard; protein; 159 AA.
DE	Glyser peptide linker (159-mer).
PN	WO2006108590-A1.
PD	19-OCT-2006.
PA	(ZLBB-) ZLB BEHRING GMBH.
Query Match	14.0%; Score 331; DB 10; Length 159;
Best Local Similarity	39.2%; Pred. No. 7.7e-13;
RESULT 1036	
ID	AEI57457 standard; protein; 1029 AA.
DE	Thale cress polypeptide, SEQ ID NO: 1924.
PN	US2006143729-A1.
PD	29-JUN-2006.
PA	(CERE-) CERES INC.
Query Match	14.0%; Score 331; DB 10; Length 1029;
Best Local Similarity	31.4%; Pred. No. 4.6e-12;
RESULT 1037	
ID	AAB36668 standard; protein; 447 AA.
DE	Argiope aurantia major ampullate spidroin 1 (Maspl) protein.

  

PN	WO2003020916-A2.
PD	13-MAR-2003.
PA	(UYWY-) UNIV. WYOMING.
Query Match	14.0%; Score 330; DB 6; Length 447;
Best Local Similarity	29.5%; Pred. No. 2.4e-12;
RESULT 1038	
ID	ADP60979 standard; protein; 293 AA.
DE	Plant polypeptide, SEQ ID 11056.
PN	US2004216190-A1.
PD	28-OCT-2004.
PA	(KOVA/) KOVALIC D K.
Query Match	13.9%; Score 329.5; DB 8; Length 293;
Best Local Similarity	33.1%; Pred. No. 1.7e-12;
RESULT 1039	
ID	AEI57139 standard; protein; 1191 AA.
DE	Thale cress polypeptide, SEQ ID NO: 1606.
PN	US2006143729-A1.
PD	29-JUN-2006.
PA	(CERE-) CERES INC.
Query Match	13.9%; Score 329.5; DB 10; Length 1191;
Best Local Similarity	27.7%; Pred. No. 6.6e-12;
RESULT 1040	
ID	ADK51951 standard; protein; 780 AA.
DE	Repeat protein polymer repeat sequence, SEQ ID 19.
PN	WO2003039465-A1.
PD	04-DEC-2003.
PA	(DOWC) DOW CORNING CORP.
PA	(GEMV) GENENCOR INT INC.
Query Match	13.9%; Score 329; DB 8; Length 780;
Best Local Similarity	25.7%; Pred. No. 4.7e-12;
RESULT 1041	
ID	ADR70468 standard; protein; 780 AA.
DE	Silk-elastin polymer SELP47K.
PN	US2004180027-A1.
PD	16-SEP-2004.
PA	(KUMA/) KUMAR M.
PA	(CUKV/) CUEVAS W A.
Query Match	13.9%; Score 329; DB 8; Length 780;
Best Local Similarity	25.7%; Pred. No. 4.7e-12;
RESULT 1042	
ID	ADU98730 standard; protein; 780 AA.
DE	Active agent release control system-related SELP47K protein SeqID19
PN	US2004228913-A1.
PD	18-NOV-2004.
PA	(KUMA/) KUMAR M.
PA	(MAZE/) MAZEAUD I.
PA	(CHRI/) CHRISTIANO S P.
Query Match	13.9%; Score 329; DB 9; Length 780;
Best Local Similarity	25.7%; Pred. No. 4.7e-12;
RESULT 1043	
ID	ADU81661 standard; protein; 780 AA.
DE	Silk-elastin polymer SELP47K, SEQ ID NO:19.
PN	US2004234609-A1.
PD	25-NOV-2004.
PA	(COLL/) COLLIER K D.
PA	(CUEV/) CUEVAS W A.
PA	(KUMA/) KUMAR M.
Query Match	13.9%; Score 329; DB 9; Length 780;
Best Local Similarity	25.7%; Pred. No. 4.7e-12;
RESULT 1044	
ID	ABB57376 standard; protein; 780 AA.
DE	SELP 47K amino acid sequence SEQ ID NO:19.
PN	US2005142094-A1.
PD	30-JUN-2005.
PA	(KUMA/) KUMAR M.
Query Match	13.9%; Score 329; DB 9; Length 780;
Best Local Similarity	25.7%; Pred. No. 4.7e-12;
RESULT	

PA (CUEV/) CUEVAS W A.  
 PA (KUMA/) KUMAR M.  
 Query Match 13.9%; Score 329; DB 10; Length 780;  
 Best Local Similarity 25.7%; Pred. No. 4.7e-12;  
 RESULT 1046  
 ID ADV78699 standard; protein; 386 AA.  
 DE Human-derived cell attachment protein - SEQ ID 163.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 13.9%; Score 328; DB 9; Length 386;  
 Best Local Similarity 28.8%; Pred. No. 2.8e-12;  
 RESULT 1047  
 ID ADO08759 standard; protein; 302 AA.  
 DE Novel surgical dressing-related protein SegID46.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 13.8%; Score 326.5; DB 8; Length 302;  
 Best Local Similarity 29.6%; Pred. No. 2.7e-12;  
 RESULT 1048  
 ID ADV78653 standard; protein; 302 AA.  
 DE Human-derived cell attachment protein - SEQ ID 117.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 13.8%; Score 326.5; DB 9; Length 302;  
 Best Local Similarity 29.6%; Pred. No. 2.7e-12;  
 RESULT 1049  
 ID ABB81230 standard; protein; 334 AA.  
 DE Mycobacterium bovis BCG strain Pasteur PE-PGRS protein sequence.  
 PN WO954487-A2.  
 PD 28-OCT-1999.  
 PA (INSP) INSTR PASTEUR.  
 Query Match 13.8%; Score 326.5; DB 3; Length 334;  
 Best Local Similarity 30.0%; Pred. No. 3e-12;  
 RESULT 1050  
 ID ABU36981 standard; protein; 439 AA.  
 DE Protein encoded by Prokaryotic essential gene #22508.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 13.8%; Score 325.5; DB 6; Length 439;  
 Best Local Similarity 29.0%; Pred. No. 4.4e-12;  
 RESULT 1051  
 ID ADO08784 standard; protein; 471 AA.  
 DE Novel surgical dressing-related protein SegID71.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 13.7%; Score 324.5; DB 8; Length 471;  
 Best Local Similarity 28.1%; Pred. No. 5.5e-12;  
 RESULT 1052  
 ID ADV78677 standard; protein; 471 AA.  
 DE Human-derived cell attachment protein - SEQ ID 141.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 13.7%; Score 324.5; DB 9; Length 471;  
 Best Local Similarity 28.1%; Pred. No. 5.5e-12;  
 RESULT 1053  
 ID ADO08764 standard; protein; 482 AA.  
 DE Novel surgical dressing-related protein SegID51.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 13.7%; Score 324; DB 8; Length 482;  
 Best Local Similarity 29.3%; Pred. No. 6e-12;  
 RESULT 1054  
 ID ADV78658 standard; protein; 482 AA.

DE Human-derived cell attachment protein - SEQ ID 122.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 13.7%; Score 324; DB 9; Length 482;  
 Best Local Similarity 29.3%; Pred. No. 6e-12;  
 RESULT 1055  
 ID ADR70478 standard; protein; 1038 AA.  
 DE Silk-elastin polymer SLP 67K.  
 PN US2004180027-A1.  
 PD 16-SEP-2004.  
 PA (KUMA/) KUMAR M.  
 PA (CUEV/) CUEVAS W A.  
 Query Match 13.7%; Score 324; DB 8; Length 1038;  
 Best Local Similarity 25.0%; Pred. No. 1.3e-11;  
 RESULT 1056  
 ID ADU98740 standard; protein; 1038 AA.  
 DE Active agent release control system-related protein SegID30.  
 PN US2004228913-A1.  
 PD 18-NOV-2004.  
 PA (KUMA/) KUMAR M.  
 PA (MAZE/) MAZEAD I.  
 PA (CHRI/) CHRISTIANO S P.  
 Query Match 13.7%; Score 324; DB 9; Length 1038;  
 Best Local Similarity 25.0%; Pred. No. 1.3e-11;  
 RESULT 1057  
 ID ADU81671 standard; protein; 1038 AA.  
 DE Silk/elastin peptide repeat sequence, SEQ ID NO:30.  
 PN US2004234609-A1.  
 PD 25-NOV-2004.  
 PA (COLL/) COLLIER K D.  
 PA (CUEV/) CUEVAS W A.  
 PA (KUMA/) KUMAR M.  
 Query Match 13.7%; Score 324; DB 9; Length 1038;  
 Best Local Similarity 25.0%; Pred. No. 1.3e-11;  
 RESULT 1058  
 ID AEB57386 standard; protein; 1038 AA.  
 DE SLP 67K repeat sequence protein polymer SEQ ID NO:30.  
 PN US2005142094-A1.  
 PD 30-JUN-2005.  
 PA (KUMA/) KUMAR M.  
 Query Match 13.7%; Score 324; DB 9; Length 1038;  
 Best Local Similarity 25.0%; Pred. No. 1.3e-11;  
 RESULT 1059  
 ID AEB12100 standard; protein; 1038 AA.  
 DE Repeat sequence used in biomolecular conjugates.  
 PN US2006153791-A1.  
 PD 13-JUL-2006.  
 PA (COLL/) COLLIER K D.  
 PA (CUEV/) CUEVAS W A.  
 PA (KUMA/) KUMAR M.  
 Query Match 13.7%; Score 324; DB 8; Length 1038;  
 Best Local Similarity 25.0%; Pred. No. 1.3e-11;  
 RESULT 1060  
 ID ADR60977 standard; protein; 295 AA.  
 DE Plant polypeptide, SEQ ID 11054.  
 PN US2004216190-A1.  
 PD 28-OCT-2004.  
 PA (KOVA/) KOVALIC D K.  
 Query Match 13.6%; Score 322.5; DB 8; Length 295;  
 Best Local Similarity 32.6%; Pred. No. 4.6e-12;  
 RESULT 1061  
 ID AAR80255 standard; peptide; 972 AA.  
 DE Polymer SLP4.  
 PN WO9524478-A1.  
 PD 14-SEP-1995.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 13.6%; Score 322.5; DB 2; Length 972;  
 Best Local Similarity 24.8%; Pred. No. 1.5e-11;  
 RESULT 1062  
 ID ABR53476 standard; protein; 972 AA.  
 DE Protein polymer SLP4 polymer block amino acid sequence.  
 PN US2002045567-A1.



PA 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match  
RESULT 1063  
ID AAB70185 standard; peptide; 504 AA.  
DE Peptide dendrimer carrier #10.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match  
Best Local Similarity 13.6%; Score 321.5; DB 4; Length 504;  
RESULT 1064  
ID AAB70186 standard; peptide; 1016 AA.  
DE Peptide dendrimer carrier #11.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match  
Best Local Similarity 13.6%; Score 321.5; DB 4; Length 1016;  
RESULT 1065  
ID AAB70187 standard; peptide; 2040 AA.  
DE Peptide dendrimer carrier #12.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match  
Best Local Similarity 13.6%; Score 321.5; DB 4; Length 2040;  
RESULT 1066  
ID ADX80594 standard; protein; 263 AA.  
DE Plant full length insert polypeptide seqid 49960.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABR/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 13.6%; Score 320.5; DB 8; Length 263;  
RESULT 1067  
ID AB116242 standard; protein; 273 AA.  
DE Cell adhesion polypeptide P3-1.  
PN JP2006150072-A.  
PD 15-JUN-2006.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match  
Best Local Similarity 13.6%; Score 320.5; DB 10; Length 273;  
RESULT 1068  
ID AB036473 standard; protein; 594 AA.  
DE Protein encoded by Prokaryotic essential gene #22000.  
PN WO2002717183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 13.5%; Score 320; DB 6; Length 594;  
RESULT 1069  
ID ABB70834 standard; protein; 620 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39294.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 13.5%; Score 320; DB 4; Length 620;  
RESULT 1070  
ID ADV42109 standard; protein; 620 AA.  
DE Fruitfly resilin exon 1 protein.  
PN WO2004104043-A1.  
PD 02-DEC-2004.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match  
13.5%; Score 320; DB 9; Length 620;

Best Local Similarity 26.7%; Pred. No. 1.3e-11;  
RESULT 1071  
ID ADV44206 standard; protein; 620 AA.  
DE Drosophila resilin polypeptide #1.  
PN WO2004104042-A1.  
PD 02-DEC-2004.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match  
Best Local Similarity 13.5%; Score 320; DB 9; Length 620;  
RESULT 1072  
ID AAB36861 standard; protein; 1953 AA.  
DE Nephila madagascariensis major ampullate spidroin 2 (MasP2)-like protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match  
Best Local Similarity 13.5%; Score 320; DB 6; Length 1953;  
RESULT 1073  
ID AED28263 standard; protein; 2476 AA.  
DE Chinese oak silkworm heavy chain fibroin, repetitive sequence.  
PN WO2005094911-A2.  
PD 13-OCT-2005.  
PA (OXFO-) OXFORD BIOMATERIALS LTD.  
Query Match  
Best Local Similarity 13.5%; Score 320; DB 9; Length 2476;  
RESULT 1074  
ID ADP31118 standard; protein; 5820 AA.  
DE Human secreted protein SEQ ID #3116.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 13.5%; Score 318.5; DB 8; Length 5820;  
RESULT 1075  
ID ABB81229 standard; protein; 318 AA.  
DE Mycobacterium tuberculosis strain H37Rv PE-PGRS protein sequence.  
PN WO9954487-A2.  
PD 28-OCT-1999.  
PA (INSP) INST PASTEUR.  
Query Match  
Best Local Similarity 13.5%; Score 318; DB 3; Length 318;  
RESULT 1076  
ID ADR70473 standard; protein; 884 AA.  
DE Silk-elastin polymer SEIP 47-E13.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KUMA/) KUMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match  
Best Local Similarity 13.5%; Score 318; DB 8; Length 884;  
RESULT 1077  
ID ADU98735 standard; protein; 884 AA.  
DE Active agent release control system-related protein seqid25.  
PN US2004228913-A1.  
PD 18-NOV-2004.  
PA (KUMA/) KUMAR M.  
PA (MAZE/) MAZERUD I.  
PA (CHRI/) CHRISTIANO S P.  
Query Match  
Best Local Similarity 13.5%; Score 318; DB 9; Length 884;  
RESULT 1078  
ID ADU81666 standard; protein; 884 AA.  
DE Silk/elastin peptide repeat sequence, SEQ ID NO:25.  
PN US2004234609-A1.  
PD 25-NOV-2004.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match  
Best Local Similarity 13.5%; Score 318; DB 9; Length 884;  
RESULT 1079  
ID ABB57381 standard; protein; 884 AA.  
DE SEIP 47E-13 repeat sequence protein polymer SEQ ID NO:25.

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PN US2005142094-A1.
PD 30-JUN-2005.
PA (KUMA/) KUMAR M.
Query Match
Best Local Similarity 13.5%; Score 318; DB 9; Length 884;
RESULT 1080
ID AEJ12095 standard; protein; 884 AA.
DE Glycine-rich peptide repeat sequence, SEQ ID: 25.
PN US2006153791-A1.
PD 13-JUL-2006.
PA (COLL/) COLLIER K D.
PA (CUEV/) CUEVAS W A.
PA (KUMA/) KUMAR M.
Query Match
Best Local Similarity 13.5%; Score 318; DB 10; Length 884;
RESULT 1081
ID AAR80253 standard; peptide; 988 AA.
DE Polymer SLP7.
PN WO9524478-A1.
PD 14-SEP-1995.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match
Best Local Similarity 13.4%; Score 317.5; DB 2; Length 988;
RESULT 1082
ID ABP53474 standard; protein; 988 AA.
DE Protein polymer SLP7 polymer block amino acid sequence.
PN US2002045567-A1.
PD 18-APR-2002.
PA (CAPP/) CAPPELLO J.
PA (STED/) STEDRONSKY E R.
Query Match
Best Local Similarity 13.4%; Score 317.5; DB 5; Length 988;
RESULT 1083
ID AD059401 standard; protein; 2655 AA.
DE Antheraea yamamai fibroin.
PN KR2002094304-A.
PD 18-DEC-2002.
PA (RURA-) RURAL DEV ADMINISTRATION.
Query Match
Best Local Similarity 13.4%; Score 317; DB 7; Length 2655;
RESULT 1084
ID AD008778 standard; protein; 506 AA.
DE Novel surgical dressing-related protein SeqID55.
PN JP2004049821-A.
PD 19-FEB-2004.
PA (SANN) SANYO CHEM IND LTD.
PA (ALCA-) ALCARE KK.
Query Match
Best Local Similarity 13.4%; Score 316; DB 8; Length 506;
RESULT 1085
ID ADV78671 standard; protein; 506 AA.
DE Human-derived cell attachment protein - SEQ ID 135.
PN JP2005002106-A.
PD 06-JAN-2005.
PA (SANN) SANYO CHEM IND LTD.
Query Match
Best Local Similarity 13.4%; Score 316; DB 9; Length 506;
RESULT 1086
ID ADR70479 standard; protein; 965 AA.
DE Silk-elastin polymer SLP 58.
PN US2004180027-A1.
PD 16-SEP-2004.
PA (KUMA/) KUMAR M.
PA (CUEV/) CUEVAS W A.
Query Match
Best Local Similarity 13.4%; Score 315.5; DB 8; Length 965;
RESULT 1087
ID ADU98741 standard; protein; 965 AA.
DE Active agent release control system-related protein SeqID31.
PN US2004228913-A1.
PD 18-NOV-2004.
PA (KUMA/) KUMAR M.
PA (MAZE/) MAZEAUD I.

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PA (CHRI/) CHRISTIANO S P.
Query Match
Best Local Similarity 13.4%; Score 315.5; DB 9; Length 965;
RESULT 1088
ID ADU81672 standard; protein; 965 AA.
DE Silk/elastin peptide repeat sequence, SEQ ID NO:31.
PN US2004234609-A1.
PD 25-NOV-2004.
PA (COLL/) COLLIER K D.
PA (CUEV/) CUEVAS W A.
PA (KUMA/) KUMAR M.
Query Match
Best Local Similarity 13.4%; Score 315.5; DB 9; Length 965;
RESULT 1089
ID AAB57387 standard; protein; 965 AA.
DE SLP 58 repeat sequence protein polymer SEQ ID NO:31.
PN US2005142094-A1.
PD 30-JUN-2005.
PA (KUMA/) KUMAR M.
Query Match
Best Local Similarity 13.4%; Score 315.5; DB 9; Length 965;
RESULT 1090
ID AEJ12101 standard; protein; 965 AA.
DE Silk and elastin protein.
PN US2006153791-A1.
PD 13-JUL-2006.
PA (COLL/) COLLIER K D.
PA (CUEV/) CUEVAS W A.
PA (KUMA/) KUMAR M.
Query Match
Best Local Similarity 13.4%; Score 315.5; DB 10; Length 965;
RESULT 1091
ID AEB91452 standard; protein; 543 AA.
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:162.
PN WO2005076010-A2.
PD 18-AUG-2005.
PA (COLL) COUNCIL SCI & IND RES SOUTH AFRICA.
Query Match
Best Local Similarity 13.3%; Score 314.5; DB 9; Length 543;
RESULT 1092
ID AAM94219 standard; protein; 116 AA.
DE Human reproductive system related antigen SEQ ID NO: 2877.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 13.3%; Score 314; DB 4; Length 116;
RESULT 1093
ID ADY05705 standard; protein; 242 AA.
DE Plant full length insert polypeptide seqid 61520.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match
Best Local Similarity 13.2%; Score 312; DB 8; Length 242;
RESULT 1094
ID AAB70180 standard; peptide; 1488 AA.
DE Peptide dendrimer carrier #5.
PN WO200107469-A2.
PD 01-FEB-2001.
PA (VERD/) VERDINI A.
Query Match
Best Local Similarity 13.2%; Score 312; DB 4; Length 1488;
RESULT 1095
ID ADG88556 standard; protein; 200 AA.
DE Poly Gly flexible linker.
PN US2003176333-A1.
PD 18-SEP-2003.

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PA (RIGEL-) RIGEL PHARM INC.  
 Query Match 13.1%; Score 309.5; DB 7; Length 200;  
 Best Local Similarity 32.3%; Pred. No. 2e-11;  
 RESULT 1096  
 ID AD984541 standard; protein: 200 AA.  
 DE T2R G-protein coupled receptor related linker seq id 94.  
 PN US2004038312-A1.  
 PD 26-FEB-2004.  
 PA (ZUKER/) ZUKER C S.  
 PA (ADLER/) ADLER J E.  
 PA (HOON/) HOON M.  
 PA (RYBA/) RYBA N.  
 PA (MOEL/) MOELER K.  
 Query Match 13.1%; Score 309.5; DB 8; Length 200;  
 Best Local Similarity 32.3%; Pred. No. 2e-11;  
 RESULT 1097  
 ID ADM96215 standard; protein: 200 AA.  
 DE Poly Gly flexible linker.  
 PN US2004071708-A1.  
 PD 15-APR-2004.  
 PA (IMMU-) IMMUSOL INC.  
 Query Match 13.1%; Score 309.5; DB 8; Length 200;  
 Best Local Similarity 32.3%; Pred. No. 2e-11;  
 RESULT 1098  
 ID ADV94806 standard; protein: 200 AA.  
 DE Poly-Gly flexible linker SEQ ID NO:7.  
 PN US2005009033-A1.  
 PD 13-JAN-2005.  
 PA (REGC-) UNIV CALIFORNIA.  
 Query Match 13.1%; Score 309.5; DB 9; Length 200;  
 Best Local Similarity 32.3%; Pred. No. 2e-11;  
 RESULT 1099  
 ID AED67728 standard; protein: 200 AA.  
 DE Poly Gly flexible linker.  
 PN US2005250113-A1.  
 PD 10-NOV-2005.  
 PA (REGC-) UNIV CALIFORNIA.  
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 13.1%; Score 309.5; DB 9; Length 200;  
 Best Local Similarity 32.3%; Pred. No. 2e-11;  
 RESULT 1100  
 ID AET01658 standard; protein: 200 AA.  
 DE Poly-Gly flexible linker.  
 PN US7056685-B1.  
 PD 06-JUN-2006.  
 PA (AMGE-) AMGEN INC.  
 Query Match 13.1%; Score 309.5; DB 10; Length 200;  
 Best Local Similarity 32.3%; Pred. No. 2e-11;  
 RESULT 1101  
 ID AET16223 standard; protein: 200 AA.  
 DE HEAT stabilizing (Gly)1 maximal repeat auxiliary polypeptide.  
 PN JP2006150072-A.  
 PD 15-JUN-2006.  
 PA (SANN-) SANYO CHEM IND LTD.  
 Query Match 13.1%; Score 309.5; DB 10; Length 200;  
 Best Local Similarity 32.3%; Pred. No. 2e-11;  
 RESULT 1102  
 ID ADO08771 standard; protein: 296 AA.  
 DE Novel surgical dressing-related protein SeqIDS8.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN-) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 13.1%; Score 309.5; DB 8; Length 296;  
 Best Local Similarity 27.5%; Pred. No. 2.9e-11;  
 RESULT 1103  
 ID ADV78664 standard; protein: 296 AA.  
 DE Human-derived cell attachment protein - SEQ ID 128.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANN-) SANYO CHEM IND LTD.  
 Query Match 13.1%; Score 309.5; DB 9; Length 296;  
 Best Local Similarity 27.5%; Pred. No. 2.9e-11;

RESULT 1104  
 ID ABG71303 standard; protein: 201 AA.  
 DE PINPOINT poly-Gly linker protein.  
 PN US6444421-B1.  
 PD 03-SEP-2002.  
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 13.1%; Score 309; DB 5; Length 201;  
 Best Local Similarity 31.9%; Pred. No. 2.2e-11;  
 RESULT 1105  
 ID AAW05704 standard; peptide: 235 AA.  
 DE Glycine-rich repeat sequence of EBV nuclear antigen.  
 PN WO9632483-A1.  
 PD 17-OCT-1996.  
 PA (MASU/) MASUCCI M.  
 Query Match 13.0%; Score 308; DB 2; Length 235;  
 Best Local Similarity 29.6%; Pred. No. 2.9e-11;  
 RESULT 1106  
 ID AAW79126 standard; protein: 235 AA.  
 DE Epstein Barr Virus EBNA1 protein gly-ala repeat region.  
 PN WO9822577-A1.  
 PD 28-MAY-1998.  
 PA (MASU/) MASUCCI M G.  
 Query Match 13.0%; Score 308; DB 2; Length 235;  
 Best Local Similarity 29.6%; Pred. No. 2.9e-11;  
 RESULT 1107  
 ID AAB70188 standard; peptide: 465 AA.  
 DE Peptide dendrimer carrier #13.  
 PN WO200107469-A2.  
 PD 01-FEB-2001.  
 PA (VERDI/) VERDINI A.  
 Query Match 12.9%; Score 305.5; DB 4; Length 465;  
 Best Local Similarity 27.9%; Pred. No. 8e-11;  
 RESULT 1108  
 ID ABB61734 standard; protein: 1039 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 11994.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PERE-) PE CORP NY.  
 Query Match 12.9%; Score 305.5; DB 4; Length 1039;  
 Best Local Similarity 27.5%; Pred. No. 1.7e-10;  
 RESULT 1109  
 ID ADV09008 standard; protein: 242 AA.  
 DE Silk fibroin SEQ ID NO:1.  
 PN WO200272937-A1.  
 PD 19-SEP-2002.  
 PA (UNIV-) UNIV JAPAN TOKYO AGR.  
 Query Match 12.9%; Score 305; DB 5; Length 242;  
 Best Local Similarity 31.4%; Pred. No. 4.6e-11;  
 RESULT 1110  
 ID AEP40066 standard; protein: 242 AA.  
 DE Domestic silkworm silk-like protein (SLP) monomer protein SEQ ID: 18.  
 PN US2006019348-A1.  
 PD 26-JAN-2006.  
 PA (ASAK/) ASAKURA T.  
 Query Match 12.9%; Score 305; DB 10; Length 242;  
 Best Local Similarity 31.4%; Pred. No. 4.6e-11;  
 RESULT 1111  
 ID AEL17598 standard; protein: 140 AA.  
 DE Glycer peptide linker (140-mer).  
 PN WO2006108590-A1.  
 PD 19-OCT-2006.  
 PA (ZUBB-) ZUB BEHRING GMBH.  
 Query Match 12.9%; Score 304.5; DB 10; Length 140;  
 Best Local Similarity 40.4%; Pred. No. 2.9e-11;  
 RESULT 1112  
 ID ADP1138 standard; protein: 1350 AA.  
 DE Human secreted protein SEQ ID #1136.  
 PN WO2004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 12.9%; Score 304.5; DB 8; Length 1350;  
 Best Local Similarity 26.0%; Pred. No. 2.5e-10;  
 RESULT 1113

ID ADP31137 standard; protein; 1719 AA.  
DE Human secreted protein SEQ ID #3135.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.9%; Score 304.5; DB 8; Length 1719;  
Best Local Similarity 26.0%; Pred. No. 3.2e-10;  
RESULT 1114  
ID ADO08774 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SegID61.  
PN JF2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANTO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.8%; Score 303.5; DB 8; Length 322;  
Best Local Similarity 31.6%; Pred. No. 7.4e-11;  
RESULT 1115  
ID ADV78667 standard; protein; 322 AA.  
DE Human-derived cell attachment protein - SEQ ID 131.  
PN JP2005002106-A.  
PD 06-JUN-2005.  
PA (SANN) SANTO CHEM IND LTD.  
Query Match 12.8%; Score 303.5; DB 9; Length 322;  
Best Local Similarity 31.6%; Pred. No. 7.4e-11;  
RESULT 1116  
ID AEI5653 standard; protein; 1670 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1006.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.8%; Score 303.5; DB 10; Length 1670;  
Best Local Similarity 27.1%; Pred. No. 3.6e-10;  
RESULT 1117  
ID ADS28501 standard; protein; 592 AA.  
DE Bacterial polypeptide #17534.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.8%; Score 302; DB 8; Length 592;  
Best Local Similarity 27.7%; Pred. No. 1.6e-10;  
RESULT 1118  
ID AAR99059 standard; protein; 714 AA.  
DE Spider dragline variant, DP-2A polymer.  
PN W09429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 12.8%; Score 302; DB 2; Length 714;  
Best Local Similarity 28.4%; Pred. No. 2e-10;  
RESULT 1119  
ID AAY41013 standard; protein; 714 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 2.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'ORREAL SA.  
Query Match 12.8%; Score 302; DB 2; Length 714;  
Best Local Similarity 28.4%; Pred. No. 2e-10;  
RESULT 1120  
ID ADO08790 standard; protein; 506 AA.  
DE Novel surgical dressing-related protein SegID77.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANTO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.7%; Score 301; DB 8; Length 506;  
Best Local Similarity 26.6%; Pred. No. 1.6e-10;  
RESULT 1121  
ID ADV78683 standard; protein; 506 AA.  
DE Human-derived cell attachment protein - SEQ ID 147.  
PN JF2005002106-A.  
PD 06-JUN-2005.  
PA (SANN) SANTO CHEM IND LTD.  
Query Match 12.7%; Score 301; DB 9; Length 506;  
Best Local Similarity 26.6%; Pred. No. 1.6e-10;  
RESULT 1122  
ID ADS88365 standard; protein; 622 AA.  
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 220.  
PN W02004035783-A2.  
PD 29-APR-2004.  
PA (CELL-) CELLZOME AG.  
Query Match 12.7%; Score 300.5; DB 8; Length 622;  
Best Local Similarity 26.2%; Pred. No. 2.1e-10;  
RESULT 1123  
ID AEA15476 standard; protein; 622 AA.  
DE Human polypeptide #95.  
PN W02005047534-A2.  
PD 26-MAY-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 12.7%; Score 300.5; DB 9; Length 622;  
Best Local Similarity 26.2%; Pred. No. 2.1e-10;  
RESULT 1124  
ID AEB13340 standard; protein; 622 AA.  
DE Mutant keratin-9 SEQ ID NO 5.  
PN W02005061537-A2.  
PD 07-JUL-2005.  
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.  
PA (VABC-) VABCEGENE BIOTECH GMBH.  
Query Match 12.7%; Score 300.5; DB 9; Length 622;  
Best Local Similarity 26.2%; Pred. No. 2.1e-10;  
RESULT 1125  
ID ABR53481 standard; protein; 768 AA.  
DE Protein polymer SELP8K polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAP/) CAPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.7%; Score 300.5; DB 5; Length 768;  
Best Local Similarity 26.8%; Pred. No. 2.6e-10;  
RESULT 1126  
ID AAR80341 standard; protein; 884 AA.  
DE Protein polymer adhesive substrate SELP8K.  
PN W09523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1127  
ID AAM09213 standard; protein; 884 AA.  
DE SELP8K polymer.  
PN W09634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1128  
ID AAM53541 standard; protein; 884 AA.  
DE Expected amino acid sequence of pPT0345 encoding SELP8K polymer.  
PN W09810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1129  
ID AAM49728 standard; protein; 884 AA.  
DE SELP8K polymer.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1130  
ID AAY51882 standard; protein; 884 AA.  
DE Plasmid pPT0345 protein fragment containing SELP8K polymer units.

PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 3; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1131  
ID ABG31412 standard; protein; 884 AA.  
DE SELP8K polymer encoded by plasmid pPT0345.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 5; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1132  
ID ABW01628 standard; protein; 884 AA.  
DE Plasmid pPT0345 SELP8K polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 7; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1133  
ID AEF52497 standard; protein; 884 AA.  
DE Polymer SELP8K.  
PN US2006029638-A1.  
PD 09-FEB-2006.  
PA (STED/) STEDRONSKY E R.  
PA (CAP/) CAPPELLO J.  
Query Match 12.7%; Score 300.5; DB 10; Length 884;  
Best Local Similarity 26.8%; Pred. No. 3e-10;  
RESULT 1134  
ID ADU81678 standard; protein; 983 AA.  
DE Cotton binding peptide/silk-elastin polymer SELK47K-CBP, SEQ ID NO:37.  
PN US2004234609-A1.  
PD 25-NOV-2004.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 9; Length 983;  
Best Local Similarity 26.8%; Pred. No. 3.3e-10;  
RESULT 1135  
ID AEG12107 standard; protein; 983 AA.  
DE SELP47K-cellulose binding peptide (CBP) fusion protein.  
PN US2006153791-A1.  
PD 13-JUL-2006.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 10; Length 983;  
Best Local Similarity 26.8%; Pred. No. 3.3e-10;  
RESULT 1136  
ID ADU81673 standard; protein; 1027 AA.  
DE Ceeroplin A-Melittin/silk-elastin polymer CAM-SELK47K, SEQ ID NO:32.  
PN US2004234609-A1.  
PD 25-NOV-2004.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 9; Length 1027;  
Best Local Similarity 26.8%; Pred. No. 3.4e-10;  
RESULT 1137  
ID AEG12102 standard; protein; 1027 AA.  
DE Ceeroplin A-Melittin (CAM)-SELP47K fusion protein repeat sequence.  
PN US2006153791-A1.  
PD 13-JUL-2006.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 10; Length 1027;  
Best Local Similarity 26.8%; Pred. No. 3.4e-10;  
RESULT 1138  
ID ADU81674 standard; protein; 1105 AA.  
DE Antimicrobial peptide MB1-28/silk-elastin polymer MB1-SELK47K, SEQ ID:33.

PN US2004234609-A1.  
PD 25-NOV-2004.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 9; Length 1105;  
Best Local Similarity 26.8%; Pred. No. 3.7e-10;  
RESULT 1139  
ID AEG12103 standard; protein; 1105 AA.  
DE MB1-SELP47K fusion protein repeat sequence.  
PN US2006153791-A1.  
PD 13-JUL-2006.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 10; Length 1105;  
Best Local Similarity 26.8%; Pred. No. 3.7e-10;  
RESULT 1140  
ID ADU81675 standard; protein; 1125 AA.  
DE Green fluorescent protein/silk-elastin polymer SELK47-GFP, SEQ ID NO:34.  
PN US2004234609-A1.  
PD 25-NOV-2004.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 9; Length 1125;  
Best Local Similarity 26.8%; Pred. No. 3.8e-10;  
RESULT 1141  
ID AEG12104 standard; protein; 1125 AA.  
DE Green fluorescent protein (GFP)-SELP47K fusion protein.  
PN US2006153791-A1.  
PD 13-JUL-2006.  
PA (COLL/) COLLIER K D.  
PA (CUEV/) CUEVAS W A.  
PA (KUMA/) KUMAR M.  
Query Match 12.7%; Score 300.5; DB 10; Length 1125;  
Best Local Similarity 26.8%; Pred. No. 3.8e-10;  
RESULT 1142  
ID AAM6163 standard; protein; 738 AA.  
DE New DNA sequence isolated from Pinctada fucata.  
PN JF10080285-A.  
PD 31-MAR-1998.  
PA (MIKI-) MIKIMOTO SEIYAKU KK.  
Query Match 12.7%; Score 300; DB 2; Length 738;  
Best Local Similarity 24.4%; Pred. No. 2.7e-10;  
RESULT 1143  
ID AAE36879 standard; protein; 373 AA.  
DE Latrodectus geometricus major ampullate spidroin 2 (Masp2) protein #1.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UTWY-) UNIV WYOMING.  
Query Match 12.7%; Score 299; DB 6; Length 373;  
Best Local Similarity 28.0%; Pred. No. 1.6e-10;  
RESULT 1144  
ID AED28264 standard; protein; 2361 AA.  
DE Japanese oak silkmoch heavy chain fibroin, repetitive sequence.  
PN WO2005094911-A2.  
PD 13-OCT-2005.  
PA (OXFO-) OXFORD BIOMATERIALS LTD.  
Query Match 12.6%; Score 297.5; DB 9; Length 2361;  
Best Local Similarity 25.5%; Pred. No. 1.2e-09;  
RESULT 1145  
ID AAR80256 standard; peptide; 1024 AA.  
DE Polymer SELP5.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.5%; Score 296.5; DB 2; Length 1024;  
Best Local Similarity 21.8%; Pred. No. 6e-10;  
RESULT 1146  
ID ABP53477 standard; protein; 1024 AA.  
DE Protein polymer SELP5 polymer block amino acid sequence.  
PN US2002045567-A1.

PD 18-APR-2002.  
 PA (CAPP/) CAPPELLO J. R.  
 (STED/) STEDRONSKY E. R.  
 Query Match 12.5%; Score 296.5; DB 5; Length 1024;  
 Best Local Similarity 21.8%; Pred. No. 6e-10;  
 RESULT 1147  
 ID AAY40098 standard; protein; 531 AA.  
 DE Spider silk protein spidroine major 2.  
 PN FR2774588-A1.  
 PD 13-AUG-1999.  
 PA (OREA ) L'OREAL SA.  
 Query Match 12.5%; Score 296; DB 2; Length 531;  
 Best Local Similarity 27.7%; Pred. No. 3.5e-10;  
 RESULT 1148  
 ID ARI4309 standard; protein; 595 AA.  
 DE N.clavipes dragline silk protein-2.  
 PN EP452925-A.  
 PD 23-OCT-1991.  
 PA (UYWY-) UNIV OF WYOMING.  
 Query Match 12.5%; Score 296; DB 2; Length 595;  
 Best Local Similarity 27.7%; Pred. No. 3.9e-10;  
 RESULT 1149  
 ID AAW5347 standard; protein; 595 AA.  
 DE Nephila clavipes spider silk protein.  
 PN US5728810-A.  
 PD 17-MAR-1998.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 12.5%; Score 296; DB 2; Length 595;  
 Best Local Similarity 27.7%; Pred. No. 3.9e-10;  
 RESULT 1150  
 ID AAY59071 standard; protein; 595 AA.  
 DE N.clavipes spider silk protein 2.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 12.5%; Score 296; DB 3; Length 595;  
 Best Local Similarity 27.7%; Pred. No. 3.9e-10;  
 RESULT 1151  
 ID AAO1648 standard; protein; 624 AA.  
 DE Nephila clavipes dragline silk fibronin protein.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 12.5%; Score 296; DB 6; Length 624;  
 Best Local Similarity 27.7%; Pred. No. 4e-10;  
 RESULT 1152  
 ID ADC35241 standard; protein; 627 AA.  
 DE Maspin silk protein, SEQ ID 2.  
 PN WO2003057727-A1.  
 PD 17-JUL-2003.  
 PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 12.5%; Score 296; DB 7; Length 627;  
 Best Local Similarity 27.7%; Pred. No. 4.1e-10;  
 RESULT 1153  
 ID AAR80252 standard; peptide; 832 AA.  
 DE Polymer SLP8.  
 PN WO9524478-A1.  
 PD 14-SEP-1995.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 12.5%; Score 294.5; DB 2; Length 832;  
 Best Local Similarity 27.1%; Pred. No. 6.6e-10;  
 RESULT 1154  
 ID APP53473 standard; protein; 832 AA.  
 DE Protein polymer SLP8 polymer block amino acid sequence.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPP/) CAPPELLO J. R.  
 (STED/) STEDRONSKY E. R.  
 Query Match 12.5%; Score 294.5; DB 5; Length 832;  
 Best Local Similarity 27.1%; Pred. No. 6.6e-10;  
 RESULT 1155  
 ID AEC31442 standard; protein; 636 AA.  
 DE Argiope amoena major ampullate gland silk protein, fusion protein #2.

PN CN1563085-A.  
 PD 12-JAN-2005.  
 PA (UYNA-) UNIV NANJING.  
 Query Match 12.4%; Score 294; DB 9; Length 636;  
 Best Local Similarity 26.6%; Pred. No. 5.5e-10;  
 RESULT 1156  
 ID AAB23358 standard; protein; 674 AA.  
 DE Human tropinin protein from residue 69 to 749.  
 PN US611089-A.  
 PD 29-AUG-2000.  
 PA (BURN-) BURNHAM INST.  
 Query Match 12.4%; Score 294; DB 3; Length 674;  
 Best Local Similarity 28.7%; Pred. No. 5.8e-10;  
 RESULT 1157  
 ID ADC68317 standard; protein; 821 AA.  
 DE Human GPCR protein SEQ ID NO:1370.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Query Match 12.4%; Score 294; DB 7; Length 821;  
 Best Local Similarity 31.1%; Pred. No. 7e-10;  
 RESULT 1158  
 ID ABB67074 standard; protein; 586 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 28014.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 12.4%; Score 293.5; DB 4; Length 586;  
 Best Local Similarity 26.6%; Pred. No. 5.4e-10;  
 RESULT 1159  
 ID ABB62822 standard; protein; 586 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 15258.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 12.4%; Score 293.5; DB 4; Length 586;  
 Best Local Similarity 26.6%; Pred. No. 5.4e-10;  
 RESULT 1160  
 ID ADS96696 standard; protein; 586 AA.  
 DE Drosophila melanogaster protein, SEQ ID 317.  
 PN WO2004039999-A2.  
 PD 13-MAY-2004.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 12.4%; Score 293.5; DB 8; Length 586;  
 Best Local Similarity 26.6%; Pred. No. 5.4e-10;  
 RESULT 1161  
 ID ADA07852 standard; protein; 611 AA.  
 DE Pinctada margaritifera nacrein.  
 PN US2003027258-A1.  
 PD 06-FEB-2003.  
 PA (CHAN/) CHANG F F.  
 (LIHH/) LI H.  
 (HSIEH/) HSIEH-LI H M.  
 Query Match 12.4%; Score 293.5; DB 6; Length 611;  
 Best Local Similarity 26.5%; Pred. No. 5.6e-10;  
 RESULT 1162  
 ID ABE67442 standard; protein; 611 AA.  
 DE Pinctada margaritifera nacrein protein SEQ ID NO:4.  
 PN US2005282183-A1.  
 PD 22-DEC-2005.  
 PA (CHAN-) CHANGENE INC.  
 Query Match 12.4%; Score 293.5; DB 10; Length 611;  
 Best Local Similarity 26.5%; Pred. No. 5.6e-10;  
 RESULT 1163  
 ID ABO23517 standard; protein; 256 AA.  
 DE Mycobacterium tuberculosis outlier protein #1.  
 PN US2003039963-A1.  
 PD 27-FEB-2003.  
 PA (BRAH/) BRAHACHARI S K.  
 (RAMA/) RAMACHANDRAN S.  
 (NAND/) NANDI T.  
 (BHIM/) BHIMARAO C.

Query Match  
Best Local Similarity 12.4%; Score 293; DB 7; Length 256;  
REST 1164  
ID AD008786 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SegID73.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match  
Best Local Similarity 12.4%; Score 292.5; DB 8; Length 322;  
REST 1165  
ID ADV78679 standard; protein; 322 AA.  
DE Human-derived cell attachment protein - SEQ ID 143.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match  
Best Local Similarity 12.4%; Score 292.5; DB 9; Length 322;  
REST 1166  
ID AAE36889 standard; protein; 912 AA.  
DE Plecteurys cristic fibroin 1 protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYW-) UNIV WYOMING.  
Query Match  
Best Local Similarity 12.4%; Score 292; DB 6; Length 912;  
REST 1167  
ID ADP58455 standard; protein; 257 AA.  
DE Plant polypeptide, SEQ ID 8532.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA-) KOVALIC D K.  
Query Match  
Best Local Similarity 12.3%; Score 291.5; DB 8; Length 257;  
REST 1168  
ID AAR94895 standard; protein; 749 AA.  
DE Human trophinin.  
PN WO9610414-A1.  
PD 11-APR-1996.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Query Match  
Best Local Similarity 12.3%; Score 290.5; DB 2; Length 749;  
REST 1169  
ID AAB23357 standard; protein; 749 AA.  
DE Human trophinin protein.  
PN US6111089-A.  
PD 29-AUG-2000.  
PA (BURN-) BURNHAM INST.  
Query Match  
Best Local Similarity 12.3%; Score 290.5; DB 3; Length 749;  
REST 1170  
ID ABO60408 standard; protein; 805 AA.  
DE Human genome derived single exon protein #6642.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match  
Best Local Similarity 12.3%; Score 290.5; DB 8; Length 805;  
REST 1171  
ID AAB94744 standard; protein; 814 AA.  
DE Human protein sequence SEQ ID NO:15790.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 12.3%; Score 290.5; DB 4; Length 814;  
REST 1172  
ID AAM94034 standard; protein; 814 AA.  
DE Human stomach cancer expressed polypeptide SEQ ID NO 139.  
PN WO200109317-A1.

PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 12.3%; Score 290.5; DB 4; Length 814;  
REST 1173  
ID AAU32728 standard; protein; 1406 AA.  
DE Novel human secreted protein #3219.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 12.3%; Score 290.5; DB 4; Length 1406;  
REST 1174  
ID AEA09004 standard; protein; 543 AA.  
DE A. thaliana oleosin-type protein.  
PN WO2005046704-A1.  
PD 26-MAY-2005.  
PA (UYRI-) UNIV FEDERAL RIO DE JANEIRO UFRJ.  
PA (FIOC-) FIOCRUZ FUNDACAO CRUZ OSMALDO.  
Query Match  
Best Local Similarity 12.3%; Score 290; DB 9; Length 543;  
REST 1175  
ID ADY80732 standard; protein; 703 AA.  
DE Cobweb protein #2.  
PN CN1552854-A.  
PD 08-DEC-2004.  
PA (UYOI-) UNIV QINGHUA.  
Query Match  
Best Local Similarity 12.3%; Score 290; DB 9; Length 703;  
REST 1176  
ID AEI58727 standard; protein; 1055 AA.  
DE Soybean polypeptide, SEQ ID NO: 3194.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match  
Best Local Similarity 12.3%; Score 290; DB 10; Length 1055;  
REST 1177  
ID ADU17242 standard; protein; 295 AA.  
DE M. tuberculosis exported polypeptides #643.  
PN US2004214165-A1.  
PD 28-OCT-2004.  
PA (GICO/) GICOUEL B.  
PA (PORT/) PORTNOI D.  
PA (LIME/) LIME E.  
PA (BELI/) PELICIC V.  
PA (GUGI/) GUGIEMO A.  
PA (GOGU/) GOGUER D L S Y.  
Query Match  
Best Local Similarity 12.2%; Score 289; DB 8; Length 295;  
REST 1178  
ID AAY04999 standard; protein; 388 AA.  
DE Mycobacterium species protein sequence 50C.  
PN WO9909186-A2.  
PD 25-FEB-1999.  
PA (INSP-) INST PASTEUR.  
Query Match  
Best Local Similarity 12.2%; Score 289; DB 2; Length 388;  
REST 1179  
ID ADB61322 standard; protein; 627 AA.  
DE Spider silk related Maspin protein.  
PN WO2003060099-A2.  
PD 24-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
PA (ALWA/) ALMATTARI A.  
Query Match  
Best Local Similarity 12.2%; Score 289; DB 7; Length 627;  
REST 1180  
ID ADM46150 standard; protein; 627 AA.  
DE Nephtila clavipes spidroin 2 (Maspin) protein.  
PN WO2003057720-A2.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.

Query Match 12.2%; Score 289; DB 7; Length 627;  
Best Local Similarity 28.2%; Pred. No. 1.1e-09;  
RESULT 1181  
ID ADP93271 standard; protein; 627 AA.  
DE Nephila clavipes (spider) MaspIT protein - SEQ ID 28.  
PN WO2004090205-A2.  
PD 21-OCT-2004.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 12.2%; Score 289; DB 8; Length 627;  
Best Local Similarity 28.2%; Pred. No. 1.1e-09;  
RESULT 1182  
ID ABP53466 standard; protein; 768 AA.  
DE SLP8 related amino acid sequence #2.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPF/) CAPPELLO J. R.  
Query Match 12.2%; Score 288.5; DB 5; Length 768;  
Best Local Similarity 26.6%; Pred. No. 1.4e-09;  
RESULT 1183  
ID AAR80335 standard; protein; 877 AA.  
DE Protein polymeric adhesion substrate 1-G.  
PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.2%; Score 288.5; DB 2; Length 877;  
Best Local Similarity 26.6%; Pred. No. 1.6e-09;  
RESULT 1184  
ID AAM49724 standard; protein; 877 AA.  
DE Protein polymer adhesive substrate PPAS1-G.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.2%; Score 288.5; DB 2; Length 877;  
Best Local Similarity 26.6%; Pred. No. 1.6e-09;  
RESULT 1185  
ID AE157127 standard; protein; 1255 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1594.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.2%; Score 288.5; DB 10; Length 1255;  
Best Local Similarity 24.8%; Pred. No. 2.3e-09;  
RESULT 1186  
ID AE156481 standard; protein; 916 AA.  
DE Zea mays polypeptide, SEQ ID NO: 948.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.2%; Score 287.5; DB 10; Length 916;  
Best Local Similarity 25.4%; Pred. No. 1.9e-09;  
RESULT 1187  
ID ADO08763 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SegID50.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 12.1%; Score 286; DB 8; Length 322;  
Best Local Similarity 29.8%; Pred. No. 8.8e-10;  
RESULT 1188  
ID ADV78657 standard; protein; 322 AA.  
DE Human-derived cell attachment protein - SEQ ID 121.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 12.1%; Score 286; DB 9; Length 322;  
Best Local Similarity 29.8%; Pred. No. 8.8e-10;  
RESULT 1189  
ID ABE05673 standard; protein; 322 AA.  
DE Cell adhesive amino acid sequence SEQ ID NO: 87.  
PN JP2005263631-A.  
PD 29-SEP-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 12.1%; Score 286; DB 9; Length 322;  
Best Local Similarity 29.8%; Pred. No. 8.8e-10;  
RESULT 1190  
ID AAB36882 standard; protein; 563 AA.  
DE Nephila madagascariensis major ampullate spidroin 2 (Masp2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UWVY-) UNIV WYOMING.  
Query Match 12.1%; Score 286; DB 6; Length 563;  
Best Local Similarity 26.3%; Pred. No. 1.5e-09;  
RESULT 1191  
ID AE157435 standard; protein; 876 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1902.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.1%; Score 286; DB 10; Length 876;  
Best Local Similarity 27.1%; Pred. No. 2.3e-09;  
RESULT 1192  
ID AE158051 standard; protein; 1246 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2518.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.1%; Score 286; DB 10; Length 1246;  
Best Local Similarity 24.2%; Pred. No. 3.2e-09;  
RESULT 1193  
ID AE155991 standard; protein; 1248 AA.  
DE Thale cress polypeptide, SEQ ID NO: 458.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.1%; Score 286; DB 10; Length 1248;  
Best Local Similarity 24.2%; Pred. No. 3.2e-09;  
RESULT 1194  
ID AAB60403 standard; protein; 2112 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 286; DB 4; Length 2112;  
Best Local Similarity 24.3%; Pred. No. 5.3e-09;  
RESULT 1195  
ID AAM78356 standard; protein; 536 AA.  
DE Human protein SEQ ID NO 1018.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 285; DB 4; Length 536;  
Best Local Similarity 29.6%; Pred. No. 1.7e-09;  
RESULT 1196  
ID AAM50044 standard; protein; 271 AA.  
DE N. clavipes spidroin synthetic homologue SFI protein.  
PN DE10133781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 12.0%; Score 283.5; DB 5; Length 271;  
Best Local Similarity 29.7%; Pred. No. 1.1e-09;  
RESULT 1197  
ID AAB06023 standard; protein; 401 AA.  
DE Polar gelatin P tetramer, P4.  
PN EP101476-A2.  
PD 28-JUN-2000.  
PA (FUUF) FUJII PHOTO FILM BV.  
Query Match 12.0%; Score 283.5; DB 3; Length 401;  
Best Local Similarity 33.9%; Pred. No. 1.6e-09;  
RESULT 1198  
ID AAY72375 standard; protein; 599 AA.  
DE Amphiphilic recombinant collagen-like polymer, NIN2P4.  
PN EP1063565-A1.  
PD 27-DEC-2000.  
PA (FUUF) FUJII PHOTO FILM BV.



Query Match 12.0%; Score 283.5; DB 4; Length 599;  
Best Local Similarity 33.9%; Pred. No. 2.3e-09;  
RESULT 1199  
ID AAY72374 standard; protein: 599 AA.  
DE Amphibolic recombinant collagen-like polymer, N1N1P4.  
PN EP1063565-A1.  
PD 27-DEC-2000.  
PA (FUJI) FUJI PHOTO FILM BV.  
Query Match 12.0%; Score 283.5; DB 4; Length 599;  
Best Local Similarity 33.9%; Pred. No. 2.3e-09;  
RESULT 1200  
ID AEF90054 standard; protein: 464 AA.  
DE Rice RNA binding protein SEQ ID NO: 29.  
PN WO2006018432-A2.  
PD 23-FEB-2006.  
PA (CROP-) CROPOSEIGN NV.  
Query Match 12.0%; Score 283; DB 10; Length 464;  
Best Local Similarity 28.0%; Pred. No. 1.9e-09;  
RESULT 1201  
ID AE157507 standard; protein: 831 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1974.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.0%; Score 283; DB 10; Length 831;  
Best Local Similarity 27.0%; Pred. No. 3.3e-09;  
RESULT 1202  
ID AE157427 standard; protein: 1061 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1894.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 12.0%; Score 283; DB 10; Length 1061;  
Best Local Similarity 27.0%; Pred. No. 4.2e-09;  
RESULT 1203  
ID AAB23367 standard; protein: 1160 AA.  
DE Mouse trophinin protein.  
PN US6111089-A.  
PD 29-AUG-2000.  
PA (BURN-) BURNHAM INST.  
Query Match 12.0%; Score 283; DB 3; Length 1160;  
Best Local Similarity 29.6%; Pred. No. 4.6e-09;  
RESULT 1204  
ID AEA55062 standard; protein: 1987 AA.  
DE Mouse trophinin isoform 2 precursor protein, SEQ ID NO: 38.  
PN WO2005052182-A2.  
PD 09-JUN-2005.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Query Match 12.0%; Score 283; DB 9; Length 1987;  
Best Local Similarity 29.6%; Pred. No. 7.7e-09;  
RESULT 1205  
ID ADV42111 standard; protein: 310 AA.  
DE Recombinant resilin.  
PN WO2004104043-A1.  
PD 02-DEC-2004.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 12.0%; Score 282.5; DB 9; Length 310;  
Best Local Similarity 31.6%; Pred. No. 1.4e-09;  
RESULT 1206  
ID ADV44208 standard; protein: 310 AA.  
DE Drosophila proresilin polypeptide.  
PN WO2004104042-A1.  
PD 02-DEC-2004.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 12.0%; Score 282.5; DB 9; Length 310;  
Best Local Similarity 31.6%; Pred. No. 1.4e-09;  
RESULT 1207  
ID AAO08783 standard; protein: 316 AA.  
DE Novel surgical dressing-related protein SegID70.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.

Query Match 12.0%; Score 282.5; DB 8; Length 316;  
Best Local Similarity 26.9%; Pred. No. 1.4e-09;  
RESULT 1208  
ID ADV78676 standard; protein: 316 AA.  
DE Human-derived cell attachment protein - SEQ ID 140.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 12.0%; Score 282.5; DB 9; Length 316;  
Best Local Similarity 26.9%; Pred. No. 1.4e-09;  
RESULT 1209  
ID ADY60951 standard; protein: 185 AA.  
DE Abiotic stress tolerance-related rice protein SegID76.  
PN WO2005021723-A2.  
PD 10-MAR-2005.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA (UMOR) UNIV MISSOURI SYSTEM.  
PA (TEXA) UNIV TEXAS TECH SYSTEM.  
Query Match 11.9%; Score 281.5; DB 9; Length 185;  
Best Local Similarity 38.6%; Pred. No. 9.8e-10;  
RESULT 1210  
ID ADV42114 standard; protein: 314 AA.  
DE Honey bee resilin homolog SEQ ID NO: 6.  
PN WO2004104043-A1.  
PD 02-DEC-2004.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 11.9%; Score 281; DB 9; Length 314;  
Best Local Similarity 29.1%; Pred. No. 1.7e-09;  
RESULT 1211  
ID ADV44211 standard; protein: 314 AA.  
DE Honey bee resilin polypeptide #2.  
PN WO2004104042-A1.  
PD 02-DEC-2004.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 11.9%; Score 281; DB 9; Length 314;  
Best Local Similarity 29.1%; Pred. No. 1.7e-09;  
RESULT 1212  
ID ADH58964 standard; protein: 258 AA.  
DE Silk protein related protein #SEQ ID 33.  
PN WO2003100065-A1.  
PD 04-DEC-2003.  
PA (UUNI-) UNIV JAPAN TOKYO AGR.  
Query Match 11.9%; Score 280.5; DB 8; Length 258;  
Best Local Similarity 29.4%; Pred. No. 1.6e-09;  
RESULT 1213  
ID AEF40081 standard; protein: 258 AA.  
DE Silk and elastin-like protein (SELP) SEQ ID: 33.  
PN US2006019348-A1.  
PD 26-JAN-2006.  
PA (ASAK) ASAKURA T.  
Query Match 11.9%; Score 280.5; DB 10; Length 258;  
Best Local Similarity 29.4%; Pred. No. 1.6e-09;  
RESULT 1214  
ID AE157025 standard; protein: 906 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1492.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.9%; Score 280.5; DB 10; Length 906;  
Best Local Similarity 26.1%; Pred. No. 5.2e-09;  
RESULT 1215  
ID AE157455 standard; protein: 954 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1922.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.9%; Score 280.5; DB 10; Length 954;  
Best Local Similarity 26.1%; Pred. No. 5.4e-09;  
RESULT 1216  
ID AAB36876 standard; protein: 444 AA.  
DE Argiops trifasciata major ampullate spidroin 2 (Masp2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.

PA (UYWY-) UNIV WYOMING.  
 Query Match 11.8%; Score 280; DB 6; Length 444;  
 Best Local Similarity 27.1%; Pred. No. 2.8e-09;  
 RESULT 1217  
 ID ADN35278 standard; protein; 1028 AA.  
 DE Helical domain of type III collagen #2.  
 PN WO2004028404-A2.  
 PD 08-APR-2004.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.8%; Score 280; DB 8; Length 1028;  
 Best Local Similarity 27.4%; Pred. No. 6.3e-09;  
 RESULT 1218  
 ID ADN35277 standard; protein; 1313 AA.  
 DE Helical domain of type III collagen.  
 PN WO2004028404-A2.  
 PD 08-APR-2004.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.8%; Score 280; DB 8; Length 1313;  
 Best Local Similarity 27.4%; Pred. No. 7.9e-09;  
 RESULT 1219  
 ID ADE61480 standard; protein; 1380 AA.  
 DE Rat Protein A/COS725, SEQ ID NO 7400.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GENO-) GEN HOSPITAL CORP.  
 PA (FARB-) BAYER AG.  
 Query Match 11.8%; Score 280; DB 7; Length 1380;  
 Best Local Similarity 31.9%; Pred. No. 8.3e-09;  
 RESULT 1220  
 ID ABB50291 standard; protein; 1466 AA.  
 DE Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72.  
 PN WO2001751177-A2.  
 PD 11-OCT-2001.  
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 11.8%; Score 280; DB 4; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1221  
 ID ABB90747 standard; protein; 1466 AA.  
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 226.  
 PN WO200210211-A2.  
 PD 07-FEB-2002.  
 PA (UYJO-) UNIV JOHNS HOPKINS.  
 Query Match 11.8%; Score 280; DB 5; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1222  
 ID ABUS4454 standard; protein; 1466 AA.  
 DE Human tumour endothelial marker TEM 15.  
 PN WO200283874-A2.  
 PD 24-OCT-2002.  
 PA (UYJO-) UNIV JOHNS HOPKINS.  
 Query Match 11.8%; Score 280; DB 6; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1223  
 ID ABR47418 standard; protein; 1466 AA.  
 DE Breast cancer associated protein sequence SEQ ID NO:68.  
 PN WO2003004989-A2.  
 PD 16-JAN-2003.  
 PA (MILL-) MILLENIUM PHARM INC.  
 Query Match 11.8%; Score 280; DB 6; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1224  
 ID ADP65248 standard; protein; 1466 AA.  
 DE Human alpha 1 type III collagen preproprotein.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 11.8%; Score 280; DB 7; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1225  
 ID ADP65210 standard; protein; 1466 AA.  
 DE Human alpha 1 type III collagen preproprotein.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 11.8%; Score 280; DB 7; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1226  
 ID ADQ26091 standard; protein; 1466 AA.  
 DE Type III, alpha 1 collagen.  
 PN WO2004056386-A2.  
 PD 08-JUL-2004.  
 PA (UYLF-) RIJKSUNIV LEIDEN.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1227  
 ID ADQ29677 standard; protein; 1466 AA.  
 DE Human colorectal cancer-associated protein #32.  
 PN EP1439393-A2.  
 PD 21-JUL-2004.  
 PA (FARB-) BAYER HEALTHCARE LLC.  
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1228  
 ID ADRI6802 standard; protein; 1466 AA.  
 DE Human collagen III alpha2 (III) fragment protein.  
 PN US2004151731-A1.  
 PD 05-AUG-2004.  
 PA (JICHA/) JICHA D. L.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1229  
 ID ADRI6427 standard; protein; 1466 AA.  
 DE Human collagen I alpha2 (III) fragment protein.  
 PN US2004151732-A1.  
 PD 05-AUG-2004.  
 PA (JICHA/) JICHA D. L.  
 PA (PELU/) PELUSE S.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1230  
 ID AEM80366 standard; protein; 1466 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO2665, SEQ:922.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GERTH-) GENENTECH INC.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1231  
 ID ADR67267 standard; protein; 1466 AA.  
 DE Human bladder cancer associated amino acid sequence.  
 PN WO2004076613-A2.  
 PD 10-SEP-2004.  
 PA (HERR/) HERR A.  
 PA (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (STAU/) STAUB E.  
 PA (PIIA/) PIARSKY C.  
 PA (SPEC/) SPECHT T.  
 Query Match 11.8%; Score 280; DB 8; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1232  
 ID ADV70235 standard; protein; 1466 AA.  
 DE Tumour-associated antigenic target polypeptide TAT474.  
 PN WO2004112829-A2.  
 PD 29-DEC-2004.  
 PA (GERTH-) GENENTECH INC.  
 Query Match 11.8%; Score 280; DB 9; Length 1466;  
 Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
 RESULT 1233  
 ID ADZ09673 standard; protein; 1466 AA.  
 DE Human breast cancer marker COL3A1 protein.  
 PN EP1522594-A2.  
 PD 13-APR-2005.  
 PA (FARB-) BAYER HEALTHCARE AG.  
 Query Match 11.8%; Score 280; DB 9; Length 1466;

Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
RESULT 1234  
ID AER04495 standard; protein; 1466 AA.  
DE Human protein from gene overexpressed in cancer, COL3A1.  
PN WO2005044990-A2.  
PD 19-MAY-2005.  
PA (FARB ) BAYER HEALTHCARE LLC.  
Query Match  
Best Local Similarity 11.8%; Score 280; DB 9; Length 1466;  
RESULT 1235  
ID AER6966 standard; protein; 1466 AA.  
DE Microsatellite instability colorectal tumor marker protein SEQ ID NO:44.  
PN WO2006015047-A2.  
PD 09-FEB-2006.  
PA (FARB ) BAYER HEALTHCARE LLC.  
Query Match  
Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
RESULT 1236  
ID AER6989 standard; protein; 1466 AA.  
DE Colorectal cancer-associated marker protein SEQ ID NO:167.  
PN WO2006015047-A2.  
PD 09-FEB-2006.  
PA (FARB ) BAYER HEALTHCARE LLC.  
Query Match  
Best Local Similarity 11.8%; Score 280; DB 10; Length 1466;  
RESULT 1237  
ID AER2425 standard; protein; 1466 AA.  
DE Human type III collagen protein - SEQ ID 1.  
PN US2006100138-A1.  
PD 11-MAY-2006.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
PA (YANG/) YANG C.  
Query Match  
Best Local Similarity 27.4%; Pred. No. 8.8e-09;  
RESULT 1238  
ID ABG15191 standard; protein; 1469 AA.  
DE Novel human diagnostic protein #15182.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 11.8%; Score 280; DB 4; Length 1469;  
RESULT 1239  
ID ABE09399 standard; protein; 1470 AA.  
DE Novel protein-related config polypeptide sequence #465.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 11.8%; Score 280; DB 7; Length 1470;  
RESULT 1240  
ID ADU04510 standard; protein; 1572 AA.  
DE SUIP1-collagen III amino acid sequence, seq id 27.  
PN GB2400852-A.  
PD 27-OCT-2004.  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
Query Match  
Best Local Similarity 11.8%; Score 280; DB 8; Length 1572;  
RESULT 1241  
ID ADU04497 standard; protein; 1604 AA.  
DE Modified pro-alpha chain amino acid, seq id 14.  
PN GB2400852-A.  
PD 27-OCT-2004.  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
Query Match  
Best Local Similarity 11.8%; Score 280; DB 8; Length 1604;  
RESULT 1242  
ID ABR42661 standard; protein; 1726 AA.  
DE Decorin-modified pro-alpha chain.  
PN WO2003035692-A2.  
PD 01-MAY-2003.  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
Query Match  
Best Local Similarity 11.8%; Score 280; DB 6; Length 1726;  
RESULT 1243  
ID ADU04493 standard; protein; 1950 AA.  
DE Modified pro-alpha chain amino acid sequence, seq id 10.  
PN GB2400852-A.  
PD 27-OCT-2004.  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
Query Match  
Best Local Similarity 27.4%; Pred. No. 1.2e-08;  
RESULT 1244  
ID AEL17597 standard; protein; 118 AA.  
DE Glycer peptide linker (118-mer).  
PN WO2006108590-A1.  
PD 19-OCT-2006.  
PA (ZLBB-) ZLB BEHRING GMBH.  
Query Match  
Best Local Similarity 11.8%; Score 279.5; DB 10; Length 118;  
RESULT 1245  
ID AD008777 standard; protein; 338 AA.  
DE Novel surgical dressing-related protein SeqID64.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match  
Best Local Similarity 29.2%; Pred. No. 2.5e-09;  
RESULT 1246  
ID ADV78670 standard; protein; 338 AA.  
DE Human-derived cell attachment protein - SEQ ID 134.  
PN JP2005002106-A.  
PD 06-JAN-2005.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match  
Best Local Similarity 11.8%; Score 279; DB 9; Length 338;  
RESULT 1247  
ID ADP99004 standard; protein; 1096 AA.  
DE C. albicans specific gene, CayR047C, protein sequence.  
PN WO2004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match  
Best Local Similarity 11.8%; Score 279; DB 8; Length 1096;  
RESULT 1248  
ID AAM78355 standard; protein; 526 AA.  
DE Human protein SEQ ID NO 1017.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 11.8%; Score 278.5; DB 4; Length 526;  
RESULT 1249  
ID ABG5081 standard; protein; 526 AA.  
DE Human translocation (12; 16)(q13; p11) protein #2.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 11.8%; Score 278.5; DB 5; Length 526;  
RESULT 1250  
ID ADI26117 standard; protein; 526 AA.  
DE Human protein that promotes STAT6 activation #41.  
PN WO2003104277-A2.  
PD 18-DEC-2003.  
PA (ASAH) ASAHI KASEI KK.  
Query Match  
Best Local Similarity 11.8%; Score 278.5; DB 8; Length 526;  
RESULT 1251  
ID ABM61732 standard; protein; 526 AA.

DE Tumour-associated antigenic target (TAT) polypeptide PRO82568, SEQ:4466.  
PN W02004030615-A2.  
PD 15-APR-2004.  
PA (GENTH ) GENTECH INC.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 4.1e-09;  
RESULT 1252  
ID ADS88302 standard; protein; 526 AA.  
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 157.  
PN W02004035783-A2.  
PD 29-APR-2004.  
PA (CELL-) CELLZOME AG.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 4.1e-09;  
RESULT 1253  
ID AE158251 standard; protein; 1067 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2718.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.8%; Score 278.5; DB 10; Length 1067;  
Best Local Similarity 25.3%; Pred. No. 8e-09;  
RESULT 1254  
ID ABB61650 standard; protein; 2280 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 11742.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 11.8%; Score 278.5; DB 4; Length 2280;  
Best Local Similarity 26.3%; Pred. No. 1.7e-08;  
RESULT 1255  
ID AEL95732 standard; protein; 2280 AA.  
DE Drosophila melanogaster survival essential protein, SEQ:624.  
PN US713558-B1.  
PD 14-NOV-2006.  
PA (APPL-) APPLERA CORP.  
Query Match 11.8%; Score 278.5; DB 11; Length 2280;  
Best Local Similarity 26.3%; Pred. No. 1.7e-08;  
RESULT 1256  
ID AAR71704 standard; protein; 1078 AA.  
DE Collagen alpha 1 (III) chain precursor.  
PN W09508115-A1.  
PD 23-MAR-1995.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.8%; Score 278; DB 2; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.7e-09;  
RESULT 1257  
ID ABU40120 standard; protein; 237 AA.  
DE Protein encoded by Prokaryotic essential gene #25647.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.7%; Score 277; DB 6; Length 237;  
Best Local Similarity 30.7%; Pred. No. 2.4e-09;  
RESULT 1258  
ID AE158169 standard; protein; 1707 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2636.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.7%; Score 277; DB 10; Length 1707;  
Best Local Similarity 26.0%; Pred. No. 1.6e-08;  
RESULT 1259  
ID AE157609 standard; protein; 1708 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2076.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.7%; Score 277; DB 10; Length 1708;  
Best Local Similarity 26.0%; Pred. No. 1.6e-08;  
RESULT 1260  
ID ABP53461 standard; protein; 768 AA.  
DE SRP5 related amino acid sequence #3.  
PA

PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAP/) CAPPELO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 11.7%; Score 276.5; DB 5; Length 768;  
Best Local Similarity 23.1%; Pred. No. 7.8e-09;  
RESULT 1261  
ID ADE59683 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 5579.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1.4e-08;  
RESULT 1262  
ID ADD45148 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 10581.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1.4e-08;  
RESULT 1263  
ID ADD45604 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 11270.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1.4e-08;  
RESULT 1264  
ID ADE59687 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 5583.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1.4e-08;  
RESULT 1265  
ID ADD47529 standard; protein; 1372 AA.  
DE Rat Protein ADD4775, SEQ ID NO 13225.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1.4e-08;  
RESULT 1266  
ID AA84548 standard; protein; 1040 AA.  
DE A human collagen 1 (alpha2) protein helical region.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USSU ) US SURGICAL CORP.  
Query Match 11.7%; Score 276; DB 3; Length 1040;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1267  
ID AA84547 standard; protein; 1040 AA.  
DE A human collagen 1 (alpha2) protein helical region.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USSU ) US SURGICAL CORP.  
Query Match 11.7%; Score 276; DB 3; Length 1040;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1268  
ID AA976125 standard; peptide; 1078 AA.  
DE Collagen type III alpha-1.  
PN US6110689-A.  
PD 29-AUG-2000.  
PA (OSTE-) OSTEOMETER AS.

Query Match 11.7%; Score 276; DB 3; Length 1078;  
 Best Local Similarity 27.4%; Pred. No. 1.2e-08;  
 RESULT 1269  
 ID AAB16478 standard; protein; 1078 AA.  
 DE Human collagen alpha1 (III) protein.  
 PN US6323314-B1.  
 PD 27-NOV-2001.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 11.7%; Score 276; DB 5; Length 1078;  
 Best Local Similarity 27.4%; Pred. No. 1.2e-08;  
 RESULT 1270  
 ID ABB80736 standard; protein; 1078 AA.  
 DE Collagen type III-alpha1 protein.  
 PN US6355442-B1.  
 PD 12-MAR-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 11.7%; Score 276; DB 5; Length 1078;  
 Best Local Similarity 27.4%; Pred. No. 1.2e-08;  
 RESULT 1271  
 ID ABB09628 standard; peptide; 1078 AA.  
 DE Amino acid sequence of human collagen type III alpha1.  
 PN US6342361-B1.  
 PD 29-JAN-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 11.7%; Score 276; DB 5; Length 1078;  
 Best Local Similarity 27.4%; Pred. No. 1.2e-08;  
 RESULT 1272  
 ID ADF13078 standard; protein; 1078 AA.  
 DE Human collagen alpha1 (III) chain precursor.  
 PN US2003119058-A1.  
 PD 26-JUN-2003.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 11.7%; Score 276; DB 7; Length 1078;  
 Best Local Similarity 27.4%; Pred. No. 1.2e-08;  
 RESULT 1273  
 ID AAY56801 standard; protein; 1366 AA.  
 DE Human preproalpha 2 (I) collagen.  
 PN EP967226-A2.  
 PD 29-DEC-1999.  
 PA (COHE-) COHESION TECHNOLOGIES INC.  
 Query Match 11.7%; Score 276; DB 3; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1274  
 ID ABB90751 standard; protein; 1366 AA.  
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 234.  
 PN WO200210217-A2.  
 PD 07-FEB-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Query Match 11.7%; Score 276; DB 5; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1275  
 ID ABB90766 standard; protein; 1366 AA.  
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 265.  
 PN WO200210217-A2.  
 PD 07-FEB-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Query Match 11.7%; Score 276; DB 5; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1276  
 ID ABB90741 standard; protein; 1366 AA.  
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 214.  
 PN WO200210217-A2.  
 PD 07-FEB-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Query Match 11.7%; Score 276; DB 5; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1277  
 ID ABB54448 standard; protein; 1366 AA.  
 DE Human tumour endothelial marker TEM 10.  
 PN WO200283874-A2.  
 PD 24-OCT-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Query Match 11.7%; Score 276; DB 6; Length 1366;

Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1278  
 ID ABB54473 standard; protein; 1366 AA.  
 DE Human tumour endothelial marker TEM 40.  
 PN WO200283874-A2.  
 PD 24-OCT-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Query Match 11.7%; Score 276; DB 6; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1279  
 ID ABB54458 standard; protein; 1366 AA.  
 DE Human tumour endothelial marker TEM 20.  
 PN WO200283874-A2.  
 PD 24-OCT-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Query Match 11.7%; Score 276; DB 6; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1280  
 ID ABR92065 standard; protein; 1366 AA.  
 DE Human cervical cancer cell marker protein SEQ ID NO:38.  
 PN WO2002101075-A2.  
 PD 19-DEC-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 11.7%; Score 276; DB 6; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1281  
 ID ADK70437 standard; protein; 1366 AA.  
 DE Respiratory disease differentially expressed protein #3.  
 PN WO2003101283-A2.  
 PD 11-DEC-2003.  
 PA (INCY-) INCYTE CORP.  
 Query Match 11.7%; Score 276; DB 8; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1282  
 ID ADQ29669 standard; protein; 1366 AA.  
 DE Human colorectal cancer-associated protein #24.  
 PN EP1439393-A2.  
 PD 21-JUL-2004.  
 PA (FARB) BAYER HEALTHCARE LLC.  
 Query Match 11.7%; Score 276; DB 8; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1283  
 ID ADV87001 standard; protein; 1366 AA.  
 DE Collagen type I precursor chain COL1A2.  
 PN WO2004110470-A2.  
 PD 23-DEC-2004.  
 PA (UYBR-) UNIV BRISTOL.  
 Query Match 11.7%; Score 276; DB 9; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1284  
 ID AEA04491 standard; protein; 1366 AA.  
 DE Human protein from gene overexpressed in cancer, COL1A2.  
 PN WO2005044990-A2.  
 PD 19-MAY-2005.  
 PA (FARB) BAYER HEALTHCARE LLC.  
 Query Match 11.7%; Score 276; DB 9; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1285  
 ID AED74603 standard; protein; 1366 AA.  
 DE Human placental protein SEQ ID NO:1431.  
 PN US2005255114-A1.  
 PD 17-NOV-2005.  
 PA (NUVE-) NUVELO INC.  
 Query Match 11.7%; Score 276; DB 9; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1286  
 ID AEF69981 standard; protein; 1366 AA.  
 DE Colorectal cancer-associated marker protein SEQ ID NO:159.  
 PN WO2006015047-A2.  
 PD 09-FEB-2006.  
 PA (FARB) BAYER HEALTHCARE LLC.

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 Query Match 11.7%; Score 276; DB 10; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.4e-08;  
 RESULT 1287  
 ID ABO59421 standard; protein; 208 AA.  
 DE Human genome derived single exon protein #5655.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HAWZ/) HANZEL D K.  
 Query Match 11.6%; Score 275; DB 8; Length 208;  
 Best Local Similarity 32.1%; Pred. No. 2.8e-09;  
 RESULT 1288  
 ID ABM95509 standard; protein; 482 AA.  
 DE M. xanthus protein sequence, seq id 14708.  
 PN US6833447-B1.  
 PD 21-DEC-2004.  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 Query Match 11.6%; Score 275; DB 9; Length 482;  
 Best Local Similarity 31.2%; Pred. No. 6.2e-09;  
 RESULT 1289  
 ID ABG95084 standard; protein; 525 AA.  
 DE Human translocation (12; 16) (q13; p11) protein #5.  
 PN WO200269900-A2.  
 PD 12-SEP-2002.  
 PA (CONF-) CONFORMA THERAPEUTICS CORP.  
 Query Match 11.6%; Score 275; DB 5; Length 525;  
 Best Local Similarity 27.5%; Pred. No. 6.7e-09;  
 RESULT 1290  
 ID ADRI14649 standard; protein; 525 AA.  
 DE Human NF-kappaB pathway-associated protein SeqID550.  
 PN WO200406557-A2.  
 PD 05-AUG-2004.  
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
 Query Match 11.6%; Score 275; DB 8; Length 525;  
 Best Local Similarity 27.5%; Pred. No. 6.7e-09;  
 RESULT 1291  
 ID ABB61800 standard; protein; 944 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 12192.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 11.6%; Score 275; DB 4; Length 944;  
 Best Local Similarity 24.4%; Pred. No. 1.2e-08;  
 RESULT 1292  
 ID AEI56939 standard; protein; 1566 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 1406.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.6%; Score 274.5; DB 10; Length 1566;  
 Best Local Similarity 26.0%; Pred. No. 2e-08;  
 RESULT 1293  
 ID AEC31440 standard; protein; 457 AA.  
 DE Argiope amoena major ampullate gland silk protein, fusion protein #1.  
 PN CN1563085-A.  
 PD 12-JAN-2005.  
 PA (UYNA-) UNIV NANJING.  
 Query Match 11.6%; Score 274; DB 9; Length 457;  
 Best Local Similarity 28.2%; Pred. No. 6.7e-09;  
 RESULT 1294  
 ID ADH13201 standard; protein; 593 AA.  
 DE Human malignant neoplasia-related protein SeqID50.  
 PN EP1365034-A2.  
 PD 26-NOV-2003.  
 PA (FARB) BAYER AG.  
 Query Match 11.6%; Score 274; DB 8; Length 593;  
 Best Local Similarity 36.9%; Pred. No. 8.6e-09;  
 RESULT 1295  
 ID ABA15088 standard; protein; 593 AA.  
 DE Human polypeptide #24.  
 PN WO2005047534-A2.

PD 26-MAY-2005.  
 PA (FARB) BAYER HEALTHCARE AG.  
 Query Match 11.6%; Score 274; DB 9; Length 593;  
 Best Local Similarity 36.9%; Pred. No. 8.6e-09;  
 RESULT 1296  
 ID AD55631 standard; protein; 600 AA.  
 DE Protein (SEQ ID 1) related to oyster pearl keratin protein.  
 PN JP2003012696-A.  
 PD 15-JAN-2003.  
 PA (MATS/) MATSUSHIRO A.  
 Query Match 11.6%; Score 274; DB 7; Length 600;  
 Best Local Similarity 24.5%; Pred. No. 8.7e-09;  
 RESULT 1297  
 ID AAG29582 standard; protein; 730 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 35222.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 11.6%; Score 274; DB 3; Length 730;  
 Best Local Similarity 28.9%; Pred. No. 1.1e-08;  
 RESULT 1298  
 ID AAG29581 standard; protein; 752 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 35221.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 11.6%; Score 274; DB 3; Length 752;  
 Best Local Similarity 28.9%; Pred. No. 1.1e-08;  
 RESULT 1299  
 ID ADN35279 standard; protein; 1313 AA.  
 DE Synthetic collagen used as sealant tissue protein.  
 PN WO2004028404-A2.  
 PD 08-APR-2004.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.6%; Score 274; DB 8; Length 1313;  
 Best Local Similarity 27.2%; Pred. No. 1.8e-08;  
 RESULT 1300  
 ID AD70510 standard; protein; 1366 AA.  
 DE Human protein from lung cancer marker gene COL1A2, SEQ ID 195.  
 PN WO2005032495-A2.  
 PD 14-APR-2005.  
 PA (FARB) BAYER PHARM CORP.  
 Query Match 11.6%; Score 274; DB 9; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.9e-08;  
 RESULT 1301  
 ID AD70624 standard; protein; 1366 AA.  
 DE Human protein from lung cancer marker gene COL1A2, SEQ ID 309.  
 PN WO2005032495-A2.  
 PD 14-APR-2005.  
 PA (FARB) BAYER PHARM CORP.  
 Query Match 11.6%; Score 274; DB 9; Length 1366;  
 Best Local Similarity 29.8%; Pred. No. 1.9e-08;  
 RESULT 1302  
 ID AED01240 standard; protein; 160 AA.  
 DE Unbound dressing auxiliary peptide, SEQ ID 27.  
 PN US2005202069-A1.  
 PD 15-SEP-2005.  
 PA (KURO/) KUROKAWA M.  
 PA (NAKA/) NAKAMURA H.  
 Query Match 11.6%; Score 273.5; DB 9; Length 160;  
 Best Local Similarity 27.9%; Pred. No. 2.6e-09;  
 RESULT 1303  
 ID AER05646 standard; protein; 160 AA.  
 DE Auxiliary amino acid sequence SEQ ID NO:60.  
 PN JP2005263631-A.  
 PD 29-SEP-2005.  
 PA (SANN) SANYO CHEM IND LTD.  
 Query Match 11.6%; Score 273.5; DB 9; Length 160;  
 Best Local Similarity 27.9%; Pred. No. 2.6e-09;  
 RESULT 1304  
 ID AEB01612 standard; peptide; 160 AA.  
 DE Auxiliary peptide related to virus culture system, SEQ ID NO:33.  
 PN WO2005103235-A1.  
 PD 03-NOV-2005.  
 PA (DENK-) DENKA SEIKEN KK.

PA (SANN) SANYO CHEM IND LTD.  
Query Match 11.6%; Score 273.5; DB 9; Length 160;  
Best Local Similarity 27.9%; Pred. No. 2.6e-09;  
RESULT 1305  
ID ABB82114 standard; protein: 160 AA.  
DE Cell culture resin bead-related auxiliary protein - SEQ ID 33.  
PN JP2006042794-A.  
PD 16-FEB-2006.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 11.6%; Score 273.5; DB 10; Length 160;  
Best Local Similarity 27.9%; Pred. No. 2.6e-09;  
RESULT 1306  
ID AEL16164 standard; protein: 160 AA.  
DE Heat stabilizing (gly)1 repeat auxiliary polypeptide, SEQ:32.  
PN JP2006150072-A.  
PD 15-JUN-2006.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 11.6%; Score 273.5; DB 10; Length 160;  
Best Local Similarity 27.9%; Pred. No. 2.6e-09;  
RESULT 1307  
ID AEL167376 standard; protein: 160 AA.  
DE Heat stable auxiliary peptide, SEQ ID 32.  
PN JP2006174826-A.  
PD 06-JUL-2006.  
PA (SANN) SANYO CHEM IND LTD.  
Query Match 11.6%; Score 273.5; DB 10; Length 160;  
Best Local Similarity 27.9%; Pred. No. 2.6e-09;  
RESULT 1308  
ID ABB73577 standard; protein: 1389 AA.  
DE T101 protease aleurain signal sequence/collagen alpha 2 fusion protein.  
PN WO2006035442-A2.  
PD 06-APR-2006.  
PA (COLL-) COLPLANT LTD.  
Query Match 11.6%; Score 273; DB 10; Length 1389;  
Best Local Similarity 29.7%; Pred. No. 2.2e-08;  
RESULT 1309  
ID AAU31850 standard; protein: 2367 AA.  
DE Novel human secreted protein #2341.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.6%; Score 273; DB 4; Length 2367;  
Best Local Similarity 27.0%; Pred. No. 3.7e-08;  
RESULT 1310  
ID AAM49739 standard; protein: 479 AA.  
DE Protein polymer adhesive substrate PPA52-F.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 272.5; DB 2; Length 479;  
Best Local Similarity 26.2%; Pred. No. 8.7e-09;  
RESULT 1311  
ID ABO77606 standard; protein: 619 AA.  
DE Pseudomonas aeruginosa polypeptide #9781.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 11.5%; Score 272.5; DB 7; Length 619;  
Best Local Similarity 25.2%; Pred. No. 1.1e-08;  
RESULT 1312  
ID ADK51953 standard; protein: 696 AA.  
DE Repeat protein polymer repeat sequence, SEQ ID 21.  
PN WO200309465-A1.  
PD 04-DEC-2003.  
PA (DOMO) DOW CORNING CORP.  
Query Match 11.5%; Score 272.5; DB 8; Length 696;  
Best Local Similarity 28.6%; Pred. No. 1.2e-08;  
RESULT 1313  
ID AE156851 standard; protein: 972 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1318.  
PN US2006143729-A1.  
PD 23-JUN-2006.

PA (CERE-) CERES INC.  
Query Match 11.5%; Score 272.5; DB 10; Length 972;  
Best Local Similarity 23.4%; Pred. No. 1.7e-08;  
RESULT 1314  
ID AAM9214 standard; protein: 1065 AA.  
DE CLPE polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 272.5; DB 2; Length 1065;  
Best Local Similarity 27.7%; Pred. No. 1.9e-08;  
RESULT 1315  
ID ABB57364 standard; protein: 1373 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1029.  
PN WO20018188-A2.  
PD 22-NOV-2001.  
PA (UNIV-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 11.5%; Score 272.5; DB 5; Length 1373;  
Best Local Similarity 30.3%; Pred. No. 2.4e-08;  
RESULT 1316  
ID ADM44460 standard; protein: 1373 AA.  
DE Murine procollagen type I alpha-2 Col1a2.  
PN WO2005001090-A1.  
PD 06-JAN-2005.  
PA (NMAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 11.5%; Score 272.5; DB 9; Length 1373;  
Best Local Similarity 30.3%; Pred. No. 2.4e-08;  
RESULT 1317  
ID AEP19250 standard; protein: 1373 AA.  
DE Mus musculus procollagen, type I, alpha 2 (Col1a2).  
PN WO2006001396-A1.  
PD 05-JAN-2006.  
PA (NMAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 11.5%; Score 272.5; DB 10; Length 1373;  
Best Local Similarity 30.3%; Pred. No. 2.4e-08;  
RESULT 1318  
ID AAB82608 standard; protein: 291 AA.  
DE Spider recombinant silk protein PQE(ep1)7.  
PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MEL/) MELO C M.  
PA (ARCI/) ARCIDIACONO S.  
PA (BUTL/) BUTLER M M.  
PA (USSA) US SEC OF ARMY.  
Query Match 11.5%; Score 272; DB 4; Length 291;  
Best Local Similarity 28.1%; Pred. No. 5.8e-09;  
RESULT 1319  
ID ABB20586 standard; protein: 671 AA.  
DE Novel human diagnostic protein #20577.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.5%; Score 272; DB 4; Length 671;  
Best Local Similarity 30.2%; Pred. No. 1.3e-08;  
RESULT 1320  
ID ABB53470 standard; peptide: 696 AA.  
DE SELP9K related amino acid sequence #1.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 11.5%; Score 272; DB 5; Length 696;  
Best Local Similarity 27.9%; Pred. No. 1.3e-08;  
RESULT 1321  
ID ABB53482 standard; protein: 696 AA.  
DE Protein polymer SELP9K polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 11.5%; Score 272; DB 5; Length 696;  
Best Local Similarity 27.9%; Pred. No. 1.3e-08;  
RESULT 1322

ID ADK51955 standard; protein, 696 AA.  
DE Repeat protein polymer repeat sequence, SEQ ID 23.  
PN W02003099465-A1.  
PD 04-DEC-2003.  
PA (DOMO) DOM CORNING CORP.  
PA (GEMV) GENENCOR INT INC.  
Query Match 11.5%; Score 272; DB 8; Length 696;  
Best Local Similarity 27.9%; Pred. No. 1.3e-08;  
RESULT 1333  
ID A0U36642 standard; protein, 370 AA.  
DE Protein encoded by prokaryotic essential gene #22169.  
PN W020027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.5%; Score 271.5; DB 6; Length 370;  
Best Local Similarity 29.0%; Pred. No. 7.8e-09;  
RESULT 1324  
ID AAM79339 standard; protein, 569 AA.  
DE Human protein SEQ ID NO 2985.  
PN W0200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.5%; Score 271.5; DB 4; Length 569;  
Best Local Similarity 27.0%; Pred. No. 1.2e-08;  
RESULT 1325  
ID AAM79340 standard; protein, 569 AA.  
DE Human protein SEQ ID NO 2986.  
PN W0200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.5%; Score 271.5; DB 4; Length 569;  
Best Local Similarity 27.0%; Pred. No. 1.2e-08;  
RESULT 1326  
ID AAR80324 standard; protein, 762 AA.  
DE Protein polymeric adhesion substrate 1-A.  
PN W09523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.7e-08;  
RESULT 1327  
ID AAM57666 standard; peptide, 762 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.7e-08;  
RESULT 1328  
ID AAM53535 standard; protein, 762 AA.  
DE Amino acid sequence of the plasmid encoding fibrin gamma PPS1-A.  
PN W09810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.7e-08;  
RESULT 1329  
ID AAM49713 standard; protein, 762 AA.  
DE Protein polymer adhesive substrate PPS1-A.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.7e-08;  
RESULT 1330  
ID AE156801 standard; protein, 1037 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1268.  
PN US2006143729-A1.  
PD 28-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.5%; Score 271; DB 10; Length 1037;  
Best Local Similarity 26.5%; Pred. No. 2.3e-08;  
RESULT 1331

ID ABO58348 standard; protein, 2338 AA.  
DE Human genome derived single exon protein #4582.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENNY) PENN S G.  
PA (RANK) RANK D R.  
PA (HANZ) HANZEL D K.  
Query Match 11.5%; Score 271; DB 8; Length 2338;  
Best Local Similarity 27.6%; Pred. No. 4.9e-08;  
RESULT 1332  
ID ADRI6801 standard; protein, 1366 AA.  
DE Human collagen I alpha2 (I) chain protein.  
PN US200451731-A1.  
PD 05-AUG-2004.  
PA (JICH) JICHA D L.  
Query Match 11.4%; Score 270.5; DB 8; Length 1366;  
Best Local Similarity 30.0%; Pred. No. 3.1e-08;  
RESULT 1333  
ID ADRI6426 standard; protein, 1366 AA.  
DE Human collagen I alpha2 (I) chain protein.  
PN US200451732-A1.  
PD 05-AUG-2004.  
PA (JICH) JICHA D L.  
PA (PELU) PELUSE S.  
Query Match 11.4%; Score 270.5; DB 8; Length 1366;  
Best Local Similarity 30.0%; Pred. No. 3.1e-08;  
RESULT 1334  
ID ADR99147 standard; protein, 1366 AA.  
DE Collagen, type 1, alpha 2, COL1A2, SEQ ID 153.  
PN W02004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 11.4%; Score 270.5; DB 8; Length 1366;  
Best Local Similarity 30.0%; Pred. No. 3.1e-08;  
RESULT 1335  
ID ADC87061 standard; protein, 920 AA.  
DE Human GPCR protein SEQ ID NO:1514.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 11.4%; Score 270; DB 7; Length 920;  
Best Local Similarity 33.5%; Pred. No. 2.3e-08;  
RESULT 1336  
ID AAR28916 standard; protein, 1196 AA.  
DE Type III procollagen (prior art).  
PN W09219754-A1.  
PD 12-NOV-1992.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Query Match 11.4%; Score 270; DB 2; Length 1196;  
Best Local Similarity 27.2%; Pred. No. 3e-08;  
RESULT 1337  
ID AE157031 standard; protein, 1407 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1498.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.4%; Score 270; DB 10; Length 1407;  
Best Local Similarity 27.0%; Pred. No. 3.5e-08;  
RESULT 1338  
ID AAE02537 standard; protein, 1466 AA.  
DE Porcine alpha1(III) collagen.  
PN W0200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 11.4%; Score 270; DB 4; Length 1466;  
Best Local Similarity 23.5%; Pred. No. 3.6e-08;  
RESULT 1339  
ID AAE36870 standard; protein, 360 AA.  
DE Latrodectus geometricus major ampullate spidroin 1 (Maspl) protein.  
PN W02003020916-A2.  
PD 13-MAR-2003.  
PA (UTWY-) UNIV WYOMING.



Query Match 11.4%; Score 269.5; DB 6; Length 360;  
Best Local Similarity 25.1%; Pred. No. 1e-08;  
RESULT 1340  
ID AE157551 standard; protein; 845 AA.  
DE Zea mays polypeptide, SEQ ID NO: 1232.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.4%; Score 269.5; DB 10; Length 845;  
Best Local Similarity 28.0%; Pred. No. 2.3e-08;  
RESULT 1341  
ID ADP31413 standard; protein; 951 AA.  
DE Human secreted protein SEQ ID #3411.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 11.4%; Score 269.5; DB 8; Length 951;  
Best Local Similarity 25.8%; Pred. No. 2.6e-08;  
RESULT 1342  
ID ABG31413 standard; protein; 1065 AA.  
DE CLP6 polymer encoded by plasmid pPT0246.  
PN US642333-B1.  
PD 23-JUN-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.4%; Score 269.5; DB 5; Length 1065;  
Best Local Similarity 26.7%; Pred. No. 2.9e-08;  
RESULT 1343  
ID ABB70198 standard; protein; 272 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37386.  
PN WO20011042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 11.4%; Score 269; DB 4; Length 272;  
Best Local Similarity 29.9%; Pred. No. 8.3e-09;  
RESULT 1344  
ID AEB91459 standard; protein; 361 AA.  
DE Microbial pathogen adhesin protein sequence, SEQ ID NO:169.  
PN WO2005076010-A2.  
PD 18-AUG-2005.  
PA (COUNCIL) COUNCIL SCI & IND RES SOUTH AFRICA.  
Query Match 11.4%; Score 269; DB 9; Length 361;  
Best Local Similarity 28.8%; Pred. No. 1.1e-08;  
RESULT 1345  
ID ADC35284 standard; protein; 410 AA.  
DE ADF-4 silk protein.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXIA) NEXIA BIOTECHNOLOGIES INC.  
Query Match 11.4%; Score 269; DB 7; Length 410;  
Best Local Similarity 27.1%; Pred. No. 1.2e-08;  
RESULT 1346  
ID AEB48114 standard; protein; 410 AA.  
DE Spider dragline silk protein wild-type ADF-4 protein SEQ ID NO:4.  
PN EP1069801-A1.  
PD 28-DEC-2005.  
PA (UYMU-) UNIV TECH MUENCHEN.  
Query Match 11.4%; Score 269; DB 10; Length 410;  
Best Local Similarity 27.1%; Pred. No. 1.2e-08;  
RESULT 1347  
ID AEF65785 standard; protein; 410 AA.  
DE Spider dragline silk protein ADF-4 wild-type sequence.  
PN WO2006008163-A2.  
PD 26-JAN-2006.  
PA (UYMU-) UNIV TECH MUENCHEN.  
Query Match 11.4%; Score 269; DB 10; Length 410;  
Best Local Similarity 27.1%; Pred. No. 1.2e-08;  
RESULT 1348  
ID ADP31157 standard; protein; 474 AA.  
DE Human secreted protein SEQ ID #3155.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 11.4%; Score 269; DB 8; Length 474;

Best Local Similarity 28.9%; Pred. No. 1.4e-08;  
RESULT 1349  
ID AE157551 standard; protein; 945 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2018.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.4%; Score 269; DB 10; Length 945;  
Best Local Similarity 25.2%; Pred. No. 2.7e-08;  
RESULT 1350  
ID AAB70184 standard; peptide; 248 AA.  
DE Peptide dendrimer carrier #9.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERDIN) VERDIN A.  
Query Match 11.4%; Score 268.5; DB 4; Length 248;  
Best Local Similarity 31.2%; Pred. No. 8.2e-09;  
RESULT 1351  
ID ADX91858 standard; protein; 278 AA.  
DE Plant full length insert polypeptide seqid 54522.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LITU/) LITU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAR/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 11.4%; Score 268.5; DB 8; Length 278;  
Best Local Similarity 30.7%; Pred. No. 9.1e-09;  
RESULT 1352  
ID ADL92144 standard; protein; 1027 AA.  
DE Collagen protein sequence.  
PN WO200309862-A1.  
PD 04-DEC-2003.  
PA (NANO-) APPLIED NANOSYSTEMS BV.  
Query Match 11.4%; Score 268.5; DB 8; Length 1027;  
Best Local Similarity 27.7%; Pred. No. 3.2e-08;  
RESULT 1353  
ID AE155629 standard; protein; 2430 AA.  
DE Thale cress polypeptide, SEQ ID NO: 96.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 11.4%; Score 268.5; DB 10; Length 2430;  
Best Local Similarity 24.3%; Pred. No. 7.2e-08;  
RESULT 1354  
ID AE116225 standard; protein; 198 AA.  
DE Heat stabilizing (Gly-Gly-Ala)k maximal repeat auxiliary polypeptide.  
PN JP2006150072-A.  
PD 15-JUN-2006.  
PA (SANN) SANNY CHEM IND LTD.  
Query Match 11.3%; Score 268; DB 10; Length 198;  
Best Local Similarity 29.6%; Pred. No. 7.1e-09;  
RESULT 1355  
ID AAR80327 standard; protein; 762 AA.  
DE Protein polymeric adhesion substrate 1-B.  
PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2.6e-08;  
RESULT 1356  
ID AAM57668 standard; peptide; 762 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2.6e-08;  
RESULT 1357  
ID AAM49715 standard; protein; 762 AA.  
DE Protein polymer adhesive substrate PPA51-B.

PN US5773577-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.3%; Score 268; DB 2; Length 762;  
 Best Local Similarity 27.9%; Pred. No. 2.6e-08;  
 RESULT 1358  
 ID AAR71702 standard; protein, 1366 AA.  
 DE Collagen alpha 2 (I) chain precursor.  
 PN W09508115-A1.  
 PD 23-MAR-1995.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 11.3%; Score 267.5; DB 2; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1359  
 ID AAY96123 standard; peptide, 1366 AA.  
 DE Collagen type I alpha-2.  
 PN US6110689-A.  
 PD 29-AUG-2000.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 11.3%; Score 267.5; DB 3; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1360  
 ID ABB50293 standard; protein, 1366 AA.  
 DE Collagen type I alpha-2 ovarian tumour marker protein, SEQ ID NO:76.  
 PN W0200175177-A2.  
 PD 11-OCT-2001.  
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 11.3%; Score 267.5; DB 4; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1361  
 ID AAE16476 standard; protein, 1366 AA.  
 DE Human collagen alpha 2-type I protein.  
 PN US6323314-B1.  
 PD 27-NOV-2001.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1362  
 ID ABB80734 standard; protein, 1366 AA.  
 DE Protein sequence related to human collagen.  
 PN US6355442-B1.  
 PD 12-MAR-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1363  
 ID ABB09626 standard; peptide, 1366 AA.  
 DE Amino acid sequence of human collagen type I alpha2.  
 PN US6342361-B1.  
 PD 28-JUN-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1364  
 ID ADF13076 standard; protein, 1366 AA.  
 DE Human procollagen alpha2(I) chain precursor.  
 PN US2003119058-A1.  
 PD 26-JUN-2003.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 11.3%; Score 267.5; DB 7; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1365  
 ID ADV70234 standard; protein, 1366 AA.  
 DE Tumor-associated antigenic target polypeptide TAR473.  
 PN W02004112829-A2.  
 PD 29-DEC-2004.  
 PA (GENE) GENENTECH INC.  
 Query Match 11.3%; Score 267.5; DB 9; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1366  
 ID AEH24257 standard; protein, 1366 AA.  
 DE Human type I collagen protein - SEQ ID 3.  
 PN US2006100136-A1.

PD 11-MAY-2006.  
 PA (OLSE/) OLSEN D R.  
 PA (POLA/) POLAREK J W.  
 PA (YANG/) YANG C.  
 Query Match 11.3%; Score 267.5; DB 10; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 4.8e-08;  
 RESULT 1367  
 ID ADV78695 standard; protein, 192 AA.  
 DE Human-derived cell attachment protein - SEQ ID 159.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANY) SANYO CHEM IND LTD.  
 Query Match 11.3%; Score 267; DB 9; Length 192;  
 Best Local Similarity 31.9%; Pred. No. 7.9e-09;  
 RESULT 1368  
 ID ADP31438 standard; protein, 675 AA.  
 DE Human secreted protein SEQ ID #3436.  
 PN W02004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 11.3%; Score 266.5; DB 8; Length 675;  
 Best Local Similarity 26.6%; Pred. No. 2.8e-08;  
 RESULT 1369  
 ID AEL73846 standard; protein, 888 AA.  
 DE Lawsonia intracellularis immunological protein, SEQ ID NO:194.  
 PN W02006116763-A2.  
 PD 02-NOV-2006.  
 PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA INC.  
 Query Match 11.3%; Score 266.5; DB 10; Length 888;  
 Best Local Similarity 25.0%; Pred. No. 3.7e-08;  
 RESULT 1370  
 ID ABB64222 standard; protein, 317 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 19458.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 11.3%; Score 266; DB 4; Length 317;  
 Best Local Similarity 32.0%; Pred. No. 1.5e-08;  
 RESULT 1371  
 ID AE158065 standard; protein, 1169 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 2532.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.3%; Score 266; DB 10; Length 1169;  
 Best Local Similarity 26.0%; Pred. No. 5.1e-08;  
 RESULT 1372  
 ID AE157117 standard; protein, 1545 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 1584.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.3%; Score 266; DB 10; Length 1545;  
 Best Local Similarity 24.3%; Pred. No. 6.7e-08;  
 RESULT 1373  
 ID ADV78689 standard; protein, 471 AA.  
 DE Human-derived cell attachment protein - SEQ ID 153.  
 PN JP2005002106-A.  
 PD 06-JAN-2005.  
 PA (SANY) SANYO CHEM IND LTD.  
 Query Match 11.2%; Score 265.5; DB 9; Length 471;  
 Best Local Similarity 24.5%; Pred. No. 2.3e-08;  
 RESULT 1374  
 ID ADA07853 standard; protein, 568 AA.  
 DE Pinctada maxima naclrein.  
 PN US2003027258-A1.  
 PD 06-FEB-2003.  
 PA (CHAN/) CHANG F F.  
 PA (LIH/) LI H.  
 PA (HSIE/) HSIEH-LI H M.  
 Query Match 11.2%; Score 265.5; DB 6; Length 568;  
 Best Local Similarity 29.0%; Pred. No. 2.8e-08;  
 RESULT 1375

ID ABE67443 standard; protein; 568 AA.  
 DE Pinctada maxima nacrein protein SEQ ID NO:5.  
 PN US2005282183-A1.  
 PD 22-DEC-2005.  
 PA (CHAN-) CHANGENE INC.  
 Query Match 11.2%; Score 265.5; DB 10; Length 568;  
 Best Local Similarity 29.0%; Pred. No. 2.8e-08;  
 RESULT 1376  
 ID AEI60617 standard; protein; 1058 AA.  
 DE Bread wheat polypeptide, SEQ ID NO: 5084.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.2%; Score 265.5; DB 10; Length 1058;  
 Best Local Similarity 26.4%; Pred. No. 5e-08;  
 RESULT 1377  
 ID AAE02536 standard; protein; 1366 AA.  
 DE Porcine alpha2(I) collagen.  
 PN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.2%; Score 265.5; DB 4; Length 1366;  
 Best Local Similarity 29.0%; Pred. No. 6.4e-08;  
 RESULT 1378  
 ID AAU79907 standard; protein; 343 AA.  
 DE Fragment for resistance against dehydration stress, protein #5.  
 PN WO200226800-A1.  
 PD 04-APR-2002.  
 PA (SEIR-) SEIREN CO LTD.  
 Query Match 11.2%; Score 265; DB 5; Length 343;  
 Best Local Similarity 29.4%; Pred. No. 1.8e-08;  
 RESULT 1379  
 ID ABG28641 standard; protein; 399 AA.  
 DE Novel human diagnostic protein #28632.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 11.2%; Score 264.5; DB 4; Length 399;  
 Best Local Similarity 33.5%; Pred. No. 2.3e-08;  
 RESULT 1380  
 ID AAW79272 standard; protein; 536 AA.  
 DE Phenolic acid esterase amino acid sequence.  
 PN GB2324302-A.  
 PD 21-OCT-1998.  
 PA (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 536;  
 Best Local Similarity 29.8%; Pred. No. 3e-08;  
 RESULT 1381  
 ID ADK51954 standard; protein; 1008 AA.  
 DE Repeat protein polymer repeat sequence, SEQ ID 22.  
 PN WO200309465-A1.  
 PD 04-DEC-2003.  
 PA (DOMO-) DOW CORNING CORP.  
 Query Match 11.2%; Score 264.5; DB 8; Length 1008;  
 Best Local Similarity 27.5%; Pred. No. 5.5e-08;  
 RESULT 1382  
 ID ADR70477 standard; protein; 1063 AA.  
 DE Collagen-like protein.  
 PN US2004180027-A1.  
 PD 16-SEP-2004.  
 PA (KUMA/) KUMAR M.  
 Query Match 11.2%; Score 264.5; DB 8; Length 1063;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1383  
 ID ADU98739 standard; protein; 1063 AA.  
 DE Active agent release control system-related protein SeqID29.  
 PN US2004228913-A1.  
 PD 18-NOV-2004.  
 PA (KUMA/) KUMAR M.  
 Query Match 11.2%; Score 264.5; DB 3; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1392  
 ID ABW01629 standard; protein; 1065 AA.  
 PA (MAZE/) MAZEBAUD I.

PA (CHRI/) CHRISTIANO S P.  
 Query Match 11.2%; Score 264.5; DB 9; Length 1063;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1384  
 ID ADU91670 standard; protein; 1063 AA.  
 DE Artificial repeat sequence, SEQ ID NO:29.  
 PN US2004234609-A1.  
 PD 25-NOV-2004.  
 PA (COLL/) COLLIER K D.  
 Query Match 11.2%; Score 264.5; DB 9; Length 1063;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1385  
 ID ABE57385 standard; protein; 1063 AA.  
 DE Synthetic collagen-like protein SEQ ID NO:29.  
 PN US2005142094-A1.  
 PD 30-JUN-2005.  
 PA (KUMA/) KUMAR M.  
 Query Match 11.2%; Score 264.5; DB 9; Length 1063;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1386  
 ID ABE57390 standard; protein; 1063 AA.  
 DE Silk elastin repeat sequence protein copolymer SEQ ID NO:34.  
 PN US2005142094-A1.  
 PD 30-JUN-2005.  
 PA (KUMA/) KUMAR M.  
 Query Match 11.2%; Score 264.5; DB 9; Length 1063;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1387  
 ID AEJ12099 standard; protein; 1063 AA.  
 DE Silk and elastin peptide repeat sequence, SEQ ID: 29.  
 PN US2006153791-A1.  
 PD 13-JUL-2006.  
 PA (COLL/) COLLIER K D.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1388  
 ID AAR37748 standard; protein; 1065 AA.  
 DE Collagen-like polymer DCP6 encoded by clone pPT 0246.  
 PN WO9310154-A1.  
 PD 27-MAY-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1389  
 ID AAR33259 standard; protein; 1065 AA.  
 DE Collagen-like polymer sequence D gene 6 polymer protein (pPT0246).  
 PN US496712-A.  
 PD 05-MAR-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1390  
 ID AAW57656 standard; peptide; 1065 AA.  
 DE Collagen-like polymer.  
 PN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1391  
 ID AAY51883 standard; protein; 1065 AA.  
 DE Plasmid pPT0246 protein fragment containing Clp6 polymer units.  
 PN US6033654-A.  
 PD 07-MAR-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 3; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1392  
 ID ABW01629 standard; protein; 1065 AA.

DE Plasmid pPT0246 CLP6 polymer protein.  
 PN US2003104589-A1.  
 PD 05-JUN-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 7; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1393  
 ID AEF52498 standard; protein; 1065 AA.  
 DE Polymer CLP6.  
 PN US2006029638-A1.  
 PD 09-FEB-2006.  
 PA (STED/) STEDRONSKY E R.  
 PA (CAP/) CAPELLLO J.  
 Query Match 11.2%; Score 264.5; DB 10; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 5.8e-08;  
 RESULT 1394  
 ID AED74136 standard; protein; 1166 AA.  
 DE Human placental protein SEQ ID NO:964.  
 PN US2005255114-A1.  
 PD 17-NOV-2005.  
 PA (NUVE-) NUVELO INC.  
 Query Match 11.2%; Score 264; DB 9; Length 1166;  
 Best Local Similarity 29.0%; Pred. No. 6.8e-08;  
 RESULT 1395  
 ID AAB02534 standard; protein; 1466 AA.  
 DE Bovine alpha(III) collagen #2.  
 PN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.1%; Score 262.5; DB 4; Length 1466;  
 Best Local Similarity 26.3%; Pred. No. 1e-07;  
 RESULT 1396  
 ID AAB02533 standard; protein; 1466 AA.  
 DE Bovine alpha(III) collagen #1.  
 PN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.1%; Score 262.5; DB 4; Length 1466;  
 Best Local Similarity 26.3%; Pred. No. 1e-07;  
 RESULT 1397  
 ID ADF69307 standard; protein; 553 AA.  
 DE Human lung specific protein sequence SEQ ID NO:64.  
 PN WO2003102137-A2.  
 PD 11-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 11.1%; Score 262; DB 8; Length 553;  
 Best Local Similarity 26.1%; Pred. No. 4.4e-08;  
 RESULT 1398  
 ID ABB58985 standard; protein; 1937 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 3747.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Query Match 11.1%; Score 261.5; DB 4; Length 1937;  
 Best Local Similarity 24.9%; Pred. No. 1.6e-07;  
 RESULT 1399  
 ID AOR86371 standard; protein; 1049 AA.  
 DE Aspergillus fumigatus essential gene protein #421.  
 PN WO2004067709-A2.  
 PD 12-AUG-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 PA (ELIT-) ELITRA CANADA LTD.  
 Query Match 11.0%; Score 261; DB 8; Length 1049;  
 Best Local Similarity 23.7%; Pred. No. 9.4e-08;  
 RESULT 1400  
 ID ABB63141 standard; protein; 828 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 16215.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Query Match 11.0%; Score 260.5; DB 4; Length 828;  
 Best Local Similarity 26.5%; Pred. No. 8e-08;  
 RESULT 1401

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ID ADQ08606 standard; protein; 1104 AA.  
 DE Ciona intestinalis nervous system associated protein SegID8.  
 PN JP2004057127-A.  
 PD 26-FEB-2004.  
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.  
 Query Match 11.0%; Score 260.5; DB 8; Length 1104;  
 Best Local Similarity 28.6%; Pred. No. 1.1e-07;  
 RESULT 1402  
 ID ARI56271 standard; protein; 1403 AA.  
 DE Zea mays polypeptide, SEQ ID NO: 738.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.0%; Score 260; DB 10; Length 1403;  
 Best Local Similarity 27.1%; Pred. No. 1.4e-07;  
 RESULT 1403  
 ID AAB36880 standard; protein; 399 AA.  
 DE Lactodectus geometricus major ampullate spidroin 2 (Masp2) protein #2.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 11.0%; Score 259.5; DB 6; Length 399;  
 Best Local Similarity 27.3%; Pred. No. 4.6e-08;  
 RESULT 1404  
 ID ADP31162 standard; protein; 537 AA.  
 DE Human secreted protein SEQ ID #3160.  
 PN WO2004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 11.0%; Score 259; DB 8; Length 537;  
 Best Local Similarity 25.9%; Pred. No. 6.6e-08;  
 RESULT 1405  
 ID AEB57393 standard; protein; 1080 AA.  
 DE Synthetic collagen-like protein SEQ ID NO:37.  
 PN US2005142094-A1.  
 PD 30-JUN-2005.  
 PA (KUMA/) KUMAR M.  
 Query Match 11.0%; Score 259; DB 9; Length 1080;  
 Best Local Similarity 28.0%; Pred. No. 1.3e-07;  
 RESULT 1406  
 ID ARI58627 standard; protein; 1212 AA.  
 DE Bread wheat polypeptide, SEQ ID NO: 3094.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.0%; Score 259; DB 10; Length 1212;  
 Best Local Similarity 26.3%; Pred. No. 1.4e-07;  
 RESULT 1407  
 ID ARI56965 standard; protein; 1553 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 1432.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.0%; Score 259; DB 10; Length 1553;  
 Best Local Similarity 26.2%; Pred. No. 1.8e-07;  
 RESULT 1408  
 ID ARI57503 standard; protein; 1780 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 1970.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.0%; Score 259; DB 10; Length 1780;  
 Best Local Similarity 26.2%; Pred. No. 2.1e-07;  
 RESULT 1409  
 ID ARI57349 standard; protein; 4659 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 1816.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 11.0%; Score 259; DB 10; Length 4659;  
 Best Local Similarity 26.9%; Pred. No. 5.2e-07;  
 RESULT 1410  
 ID ABG5083 standard; protein; 462 AA.

DE Human translocation (12; 16)(q13, p11) protein #4.  
PN W0200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match 10.9%; Score 258.5; DB 5; Length 462;  
Best Local Similarity 32.7%; Pred. No. 6.1e-08;  
RESULT 1411  
ID AED40565 standard; protein; 462 AA.  
DE Human CHOP-10 amino acid sequence.  
PN US2005221432-A1.  
PD 06-OCT-2005.  
PA (RXYC/) RYCYZYN M.  
PA (BANN/) BANNISH G.  
PA (GILE/) GILES-KOMAR J.  
Query Match 10.9%; Score 258.5; DB 9; Length 462;  
Best Local Similarity 32.7%; Pred. No. 6.1e-08;  
RESULT 1412  
ID ADX96248 standard; protein; 478 AA.  
DE Plant full length insert polypeptide seqid 58912.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 10.9%; Score 258.5; DB 8; Length 478;  
Best Local Similarity 28.5%; Pred. No. 6.3e-08;  
RESULT 1413  
ID ADY05207 standard; protein; 480 AA.  
DE Plant full length insert polypeptide seqid 61022.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 10.9%; Score 258.5; DB 8; Length 480;  
Best Local Similarity 28.5%; Pred. No. 6.3e-08;  
RESULT 1414  
ID ADP31163 standard; protein; 594 AA.  
DE Human secreted protein SEQ ID #3161.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.9%; Score 258; DB 8; Length 594;  
Best Local Similarity 26.2%; Pred. No. 8.3e-08;  
RESULT 1415  
ID AAR37751 standard; protein; 1077 AA.  
DE CLP 3.1 monomer containing peptide.  
PN W0310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.9%; Score 258; DB 2; Length 1077;  
Best Local Similarity 28.7%; Pred. No. 1.5e-07;  
RESULT 1416  
ID AEI57857 standard; protein; 1532 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2324.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 10.9%; Score 258; DB 10; Length 1532;  
Best Local Similarity 24.2%; Pred. No. 2.1e-07;  
RESULT 1417  
ID ADI26113 standard; protein; 518 AA.  
DE Human protein that promotes STAT6 activation #39.  
PN W02003104277-A2.  
PD 18-DEC-2003.  
PA (ASAH) ASAH KASEI KK.  
Query Match 10.9%; Score 257.5; DB 8; Length 518;

Best Local Similarity 26.2%; Pred. No. 7.8e-08;  
RESULT 1418  
ID AEI55841 standard; protein; 1081 AA.  
DE Thale cress polypeptide, SEQ ID NO: 308.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 10.9%; Score 257.5; DB 10; Length 1081;  
Best Local Similarity 26.2%; Pred. No. 1.6e-07;  
RESULT 1419  
ID ABB71788 standard; protein; 385 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42156.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 10.9%; Score 257; DB 4; Length 385;  
Best Local Similarity 35.4%; Pred. No. 6.3e-08;  
RESULT 1420  
ID ADP31164 standard; protein; 534 AA.  
DE Human secreted protein SEQ ID #3162.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.9%; Score 257; DB 8; Length 534;  
Best Local Similarity 26.0%; Pred. No. 8.7e-08;  
RESULT 1421  
ID AAR37746 standard; protein; 633 AA.  
DE Collagen-like polymer DCP5 encoded by clone pPT 0232.  
PN W09310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 1e-07;  
RESULT 1422  
ID AAR3257 standard; protein; 633 AA.  
DE Collagen-like polymer sequence D gene 5 polymer protein (pPT0232).  
PN US5496712-A.  
PD 05-MAR-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 1e-07;  
RESULT 1423  
ID AAM57655 standard; peptide; 633 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 1e-07;  
RESULT 1424  
ID ABU17075 standard; protein; 974 AA.  
DE Protein encoded by Prokaryotic essential gene #2602.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.9%; Score 257; DB 6; Length 974;  
Best Local Similarity 20.4%; Pred. No. 1.5e-07;  
RESULT 1425  
ID AAR37745 standard; protein; 1065 AA.  
DE Collagen-like polymer DCP4 encoded by clone pPT 0249.  
PN W09310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.9%; Score 257; DB 2; Length 1065;  
Best Local Similarity 28.0%; Pred. No. 1.7e-07;  
RESULT 1426  
ID AAR93256 standard; protein; 1065 AA.  
DE Collagen-like polymer sequence D gene 4 polymer protein (pPT0249).  
PN US5496712-A.  
PD 05-MAR-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.9%; Score 257; DB 2; Length 1065;  
Best Local Similarity 28.0%; Pred. No. 1.7e-07;

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RESULT 1427
ID AAM57654 standard; peptide; 1065 AA.
DE Collagen-like polymer.
PN US5773249-A.
PD 30-JUN-1998.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match
Best local Similarity 10.9%; Score 257; DB 2; Length 1065;
PD 29-JUN-2006.
RESULT 1428
ID AE157425 standard; protein; 894 AA.
DE Thale cress polypeptide, SEQ ID NO: 1892.
PN US2006143729-A1.
PD 29-JUN-2006.
PA (CERE-) CERES INC.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 10; Length 894;
PD 29-JUN-2006.
RESULT 1429
ID AE157509 standard; protein; 957 AA.
DE Thale cress polypeptide, SEQ ID NO: 1976.
PN US2006143729-A1.
PD 29-JUN-2006.
PA (CERE-) CERES INC.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 10; Length 957;
PD 29-JUN-2006.
RESULT 1430
ID ADU81677 standard; protein; 1016 AA.
DE Radioprotective peptide P4/silk-elastin polymer P4-SELK47K, SEQ ID NO:36.
PN US2004234609-A1.
PD 25-NOV-2004.
PA (COLL/) COLLIER K D.
PA (CUEV/) CUEVAS W A.
PA (KUMA/) KUMAR M.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 9; Length 1016;
PD 30-JUN-2005.
RESULT 1431
ID AEB57388 standard; protein; 1016 AA.
DE SELP47K-P4 repeat sequence protein polymer SEQ ID NO:32.
PN US2005142094-A1.
PD 30-JUN-2005.
PA (KUMA/) KUMAR M.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 9; Length 1016;
PD 30-JUN-2005.
RESULT 1432
ID AEU12106 standard; protein; 1016 AA.
DE SELP47K-radio protective P4 fusion protein.
PN US2006153791-A1.
PD 13-JUL-2006.
PA (COLL/) COLLIER K D.
PA (CUEV/) CUEVAS W A.
PA (KUMA/) KUMAR M.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 10; Length 1016;
PD 13-JUL-2006.
RESULT 1433
ID AE156889 standard; protein; 1094 AA.
DE Thale cress polypeptide, SEQ ID NO: 1356.
PN US2006143729-A1.
PD 29-JUN-2006.
PA (CERE-) CERES INC.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 10; Length 1094;
PD 29-JUN-2006.
RESULT 1434
ID AE156549 standard; protein; 1168 AA.
DE Thale cress polypeptide, SEQ ID NO: 1016.
PN US2006143729-A1.
PD 29-JUN-2006.
PA (CERE-) CERES INC.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 10; Length 1168;
PD 29-JUN-2006.
RESULT 1435
ID AE157459 standard; protein; 1572 AA.
DE Thale cress polypeptide, SEQ ID NO: 1926.
PN US2006143729-A1.
PD 29-JUN-2006.
PA (CERE-) CERES INC.
Query Match
Best local Similarity 10.9%; Score 256.5; DB 10; Length 1572;
PD 29-JUN-2006.
RESULT 1436
ID AED95261 standard; protein; 1067 AA.
DE Dog procollagen type IIA.
PN WO2005106495-A1.
PD 10-NOV-2005.
PA (PHAA) PHARMACIA & UPJOHN CO LLC.
Query Match
Best local Similarity 10.8%; Score 256; DB 9; Length 1067;
PD 10-NOV-2005.
RESULT 1437
ID AEG49841 standard; protein; 1487 AA.
DE Human variant type II collagen (COL2A1) amino acid sequence - SEQ ID 7.
PN US2006051794-A1.
PD 09-MAR-2006.
PA (LITV/) TSAI S.
PA (LITV/) LIU Y.
PA (CHEN/) CHEN W.
Query Match
Best local Similarity 10.8%; Score 256; DB 10; Length 1487;
PD 09-MAR-2006.
RESULT 1438
ID AAM50035 standard; protein; 230 AA.
DE N. clavipes spideroin synthetic homologue SE1 protein.
PN DE10113781-A1.
PD 13-DEC-2001.
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.
Query Match
Best local Similarity 10.8%; Score 255.5; DB 5; Length 230;
PD 13-DEC-2001.
RESULT 1439
ID ADI26207 standard; protein; 589 AA.
DE Human protein that promotes STAT6 activation #86.
PN WO2003104277-A2.
PD 18-DEC-2003.
PA (ASAH) ASAH KASEI KK.
Query Match
Best local Similarity 10.8%; Score 255.5; DB 8; Length 589;
PD 18-DEC-2003.
RESULT 1440
ID ABO53050 standard; protein; 592 AA.
DE Human putative spliceosome associated protein (SAP) #26.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match
Best local Similarity 10.8%; Score 255.5; DB 6; Length 592;
PD 10-APR-2003.
RESULT 1441
ID ADI26209 standard; protein; 592 AA.
DE Human protein that promotes STAT6 activation #87.
PN WO2003104277-A2.
PD 18-DEC-2003.
PA (ASAH) ASAH KASEI KK.
Query Match
Best local Similarity 10.8%; Score 255.5; DB 8; Length 592;
PD 18-DEC-2003.
RESULT 1442
ID ADU81676 standard; protein; 1043 AA.
DE Cotton binding peptide/silk-elastin polymer CBP-SELK47K-S2B1, SEQ ID:35.
PN US2004234609-A1.
PD 25-NOV-2004.
PA (COLL/) COLLIER K D.
PA (CUEV/) CUEVAS W A.
PA (KUMA/) KUMAR M.
Query Match
Best local Similarity 10.8%; Score 255.5; DB 9; Length 1043;
PD 25-NOV-2004.
RESULT 1443
ID AE12105 standard; protein; 1043 AA.
DE Cotton binding peptide (CBP)-SELP47K-S2B1 fusion protein.
PN US2006153791-A1.
PD 13-JUL-2006.
PA (COLL/) COLLIER K D.
PA (CUEV/) CUEVAS W A.
PA (KUMA/) KUMAR M.
Query Match
Best local Similarity 10.8%; Score 255.5; DB 10; Length 1043;
PD 13-JUL-2006.

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Best Local Similarity 24.0%; Pred. No. 2e-07;  
 RESULT 1444  
 ID AEI57167 standard; protein; 1474 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 1634.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 10.8%; Score 255.5; DB 10; Length 1474;  
 Best Local Similarity 26.0%; Pred. No. 2.8e-07;  
 RESULT 1445  
 ID ABB66654 standard; protein; 499 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 26754.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 10.8%; Score 254.5; DB 4; Length 499;  
 Best Local Similarity 26.5%; Pred. No. 1.2e-07;  
 RESULT 1446  
 ID ADN99871 standard; protein; 632 AA.  
 DE Novel human protein sequence #687.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 10.7%; Score 254; DB 8; Length 632;  
 Best Local Similarity 34.2%; Pred. No. 1.6e-07;  
 RESULT 1447  
 ID ABP53478 standard; protein; 1040 AA.  
 DE Protein polymer SEIP6 polymer block amino acid sequence.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPP/) CAPELLLO J.  
 (STED/) STERONSKY E R.  
 Query Match 10.7%; Score 254; DB 5; Length 1040;  
 Best Local Similarity 22.9%; Pred. No. 2.5e-07;  
 RESULT 1448  
 ID AEI58299 standard; protein; 1331 AA.  
 DE Thale cress polypeptide, SEQ ID NO: 2766.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 10.7%; Score 254; DB 10; Length 1331;  
 Best Local Similarity 23.8%; Pred. No. 3.2e-07;  
 RESULT 1449  
 ID ABM83560 standard; protein; 1417 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:3809.  
 PN WO2004023873-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 10.7%; Score 254; DB 8; Length 1417;  
 Best Local Similarity 27.4%; Pred. No. 3.4e-07;  
 RESULT 1450  
 ID ADE55694 standard; protein; 1419 AA.  
 DE Rat Protein AAA79780, SEQ ID NO 1513.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 (FARR ) BAYER AG.  
 Query Match 10.7%; Score 254; DB 7; Length 1419;  
 Best Local Similarity 26.4%; Pred. No. 3.4e-07;  
 RESULT 1451  
 ID AED95260 standard; protein; 1419 AA.  
 DE Immature rat collagen type II alpha 1.  
 PN WO2005106495-A1.  
 PD 10-NOV-2005.  
 PA (PHAA ) PHARMACIA & UPJOHN CO LLC.  
 Query Match 10.7%; Score 254; DB 9; Length 1419;  
 Best Local Similarity 26.4%; Pred. No. 3.4e-07;  
 RESULT 1452  
 ID ABG61861 standard; protein; 1487 AA.  
 DE Prostate cancer-associated protein #62.  
 PN WO200230268-A2.  
 PD 18-APR-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 10.7%; Score 254; DB 5; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 3.5e-07;  
 RESULT 1453  
 ID ABP56769 standard; protein; 1487 AA.  
 DE Collagen IIA protein.  
 PN WO2002100426-A1.  
 PD 19-DEC-2002.  
 PA (SMIN ) SMITH & NEPHEW PLC.  
 Query Match 10.7%; Score 254; DB 6; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 3.5e-07;  
 RESULT 1454  
 ID ADX15809 standard; protein; 1487 AA.  
 DE Human Col 2A1.  
 PN WO2005012512-A1.  
 PD 10-FEB-2005.  
 PA (NAKA/) NAKAMURA N.  
 Query Match 10.7%; Score 254; DB 9; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 3.5e-07;  
 RESULT 1455  
 ID AEG49837 standard; protein; 1487 AA.  
 DE Human type II collagen (COL2A1) amino acid sequence - SEQ ID 3.  
 PN US2006051794-A1.  
 PD 09-MAR-2006.  
 PA (TSAT/) TSAI S.  
 (LTUY/) LTU Y.  
 (CHEN/) CHEN W.  
 Query Match 10.7%; Score 254; DB 10; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 3.5e-07;  
 RESULT 1456  
 ID AEG49839 standard; protein; 1487 AA.  
 DE Human variant type II collagen (COL2A1) amino acid sequence - SEQ ID 5.  
 PN US2006051794-A1.  
 PD 09-MAR-2006.  
 PA (TSAT/) TSAI S.  
 (LTUY/) LTU Y.  
 (CHEN/) CHEN W.  
 Query Match 10.7%; Score 254; DB 10; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 3.5e-07;  
 RESULT 1457  
 ID AAG77793 standard; protein; 1745 AA.  
 DE Human pro-alpha-3(V) fibrillar procollagen polypeptide.  
 PN WO200164871-A2.  
 PD 07-SEP-2001.  
 PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
 Query Match 10.7%; Score 254; DB 4; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 4.1e-07;  
 RESULT 1458  
 ID ABB97234 standard; protein; 1745 AA.  
 DE Novel human protein SEQ ID NO: 502.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSE INC.  
 Query Match 10.7%; Score 254; DB 5; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 4.1e-07;  
 RESULT 1459  
 ID ADQ19841 standard; protein; 1745 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2660.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 10.7%; Score 254; DB 8; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 4.1e-07;  
 RESULT 1460  
 ID AEU58230 standard; protein; 1928 AA.  
 DE Hepatitis C treatment related human protein SEQ ID No 6.  
 PN US7094401-B1.  
 PD 22-AUG-2006.  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 Query Match 10.7%; Score 253.5; DB 10; Length 1928;  
 Best Local Similarity 23.5%; Pred. No. 4.8e-07;  
 RESULT 1461  
 ID AEL17596 standard; protein; 99 AA.  
 DE Glyser peptide linker (99-mer).

PN WO2006108590-A1.  
 PD 19-OCT-2006.  
 PA (ZLBB-) ZLB BEHRING GMBH.  
 Query Match 10.7%; Score 253; DB 10; Length 99;  
 RESULT 1462.  
 ID AAM50048 standard; protein; 264 AA.  
 DE N. clavipes spideroin synthetic homologue FA2 protein #2.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPK-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 10.7%; Score 253; DB 5; Length 264;  
 RESULT 1463.  
 ID ADK51957 standard; protein; 780 AA.  
 DE Repeat protein polymer repeat sequence, SEQ ID 25.  
 PN WO2003099465-A1.  
 PD 04-DEC-2003.  
 PA (DOMO) DOW CORNING CORP.  
 PA (GEWV) GENENCOR INT INC.  
 Query Match 10.7%; Score 253; DB 8; Length 780;  
 RESULT 1464.  
 ID ADC21544 standard; protein; 1014 AA.  
 DE Human type II collagen protein sequence.  
 PN WO2003006603-A2.  
 PD 23-JUN-2003.  
 PA (AREX-) AREXIS AB.  
 Query Match 10.7%; Score 253; DB 7; Length 1014;  
 RESULT 1465.  
 ID AED95251 standard; protein; 1014 AA.  
 DE Mature human collagen type II.  
 PN WO2005106495-A1.  
 PD 10-NOV-2005.  
 PA (PHAA) PHARMACIA & UPJOHN CO LLC.  
 Query Match 10.7%; Score 253; DB 9; Length 1014;  
 RESULT 1466.  
 ID AAE18321 standard; protein; 1020 AA.  
 DE Collagen like protein, CLP3.1.  
 PN WO200200016-A1.  
 PD 03-JAN-2002.  
 PA (LUMT-) LUMINIS PTY LTD.  
 Query Match 10.7%; Score 253; DB 5; Length 1020;  
 RESULT 1467.  
 ID AAR93261 standard; protein; 1077 AA.  
 DE CLP 3.1 polymer sequence (pPT0297).  
 PN US5436712-A.  
 PD 05-MAR-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.7%; Score 253; DB 2; Length 1077;  
 RESULT 1468.  
 ID AAM57657 standard; peptide; 1077 AA.  
 DE Collagen-like polymer.  
 PN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.7%; Score 253; DB 2; Length 1077;  
 RESULT 1469.  
 ID ABP60377 standard; peptide; 1217 AA.  
 DE Bombyx mori sericin SEQ ID NO 2.  
 PN WO200286133-A1.  
 PD 31-OCT-2002.  
 PA (SEIR-) SEIREN CO LTD.  
 Query Match 10.7%; Score 253; DB 6; Length 1217;  
 RESULT 1470.  
 ID AE156023 standard; protein; 1306 AA.

DE Thale cress polypeptide, SEQ ID NO: 490.  
 PN US2006143729-A1.  
 PD 29-JUN-2006.  
 PA (CERE-) CERES INC.  
 Query Match 10.7%; Score 253; DB 10; Length 1306;  
 RESULT 1471.  
 ID AAR59751 standard; protein; 1418 AA.  
 DE Type II collagen.  
 PN WO9414070-A1.  
 PD 23-JUN-1994.  
 PA (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.  
 Query Match 10.7%; Score 253; DB 2; Length 1418;  
 RESULT 1472.  
 ID AAR71703 standard; protein; 1418 AA.  
 DE Collagen alpha 1 (II) chain precursor.  
 PN WO9508115-A1.  
 PD 23-MAR-1995.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 10.7%; Score 253; DB 2; Length 1418;  
 RESULT 1473.  
 ID AAY96124 standard; peptide; 1418 AA.  
 DE Collagen type II alpha-1.  
 PN US6110689-A.  
 PD 29-AUG-2000.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 10.7%; Score 253; DB 3; Length 1418;  
 RESULT 1474.  
 ID AAB35624 standard; protein; 1418 AA.  
 DE Human type II collagen.  
 PN US6132976-A.  
 PD 17-OCT-2000.  
 PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.  
 Query Match 10.7%; Score 253; DB 4; Length 1418;  
 RESULT 1475.  
 ID AE16477 standard; protein; 1418 AA.  
 DE Human collagen alpha1 (II) protein.  
 PN US6323314-B1.  
 PD 27-NOV-2001.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 10.7%; Score 253; DB 5; Length 1418;  
 RESULT 1476.  
 ID ABB80735 standard; protein; 1418 AA.  
 DE Collagen type II-alpha1 protein.  
 PN US6355442-B1.  
 PD 12-MAR-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 10.7%; Score 253; DB 5; Length 1418;  
 RESULT 1477.  
 ID ABB93927 standard; protein; 1418 AA.  
 DE Human polypeptide orthologous to DACC-2.  
 PN WO200264625-A1.  
 PD 22-AUG-2002.  
 PA (ADPP-) ADP PHARM PTY LTD.  
 Query Match 10.7%; Score 253; DB 5; Length 1418;  
 RESULT 1478.  
 ID ABB09627 standard; peptide; 1418 AA.  
 DE Amino acid sequence of human collagen type II alpha1.  
 PN US6342361-B1.  
 PD 29-JAN-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 10.7%; Score 253; DB 5; Length 1418;  
 RESULT 1479.  
 ID ADP13077 standard; protein; 1418 AA.



DE Human collagen alpha1(II) chain precursor.  
PN US2003119058-A1.  
PD 26-JUN-2003.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 10.7%; Score 253; DB 7; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3.9e-07;  
RESULT 1480  
ID AEB25695 standard; protein; 1418 AA.  
DE Human collagen related amino acid sequence, seq id 1.  
PN FR2865034-A1.  
PD 15-JUN-2005.  
PA (SYNA-) SYNARC SAS.  
Query Match 10.7%; Score 253; DB 9; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3.9e-07;  
RESULT 1481  
ID AEP95247 standard; protein; 1418 AA.  
DE Immature human collagen type II.  
PN WO2005106495-A1.  
PD 10-NOV-2005.  
PA (PHAA-) PHARMACIA & UPJOHN CO LLC.  
Query Match 10.7%; Score 253; DB 9; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3.9e-07;  
RESULT 1482  
ID AE157891 standard; protein; 1516 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2358.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 10.7%; Score 253; DB 10; Length 1516;  
Best Local Similarity 24.6%; Pred. No. 4.1e-07;  
RESULT 1483  
ID AE157589 standard; protein; 1533 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2056.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 10.7%; Score 253; DB 10; Length 1533;  
Best Local Similarity 24.3%; Pred. No. 4.2e-07;  
RESULT 1484  
ID ADV44219 standard; protein; 197 AA.  
DE Buffalo fly resilin homolog SEQ ID NO 11.  
PN WO2004104043-A1.  
PD 02-DEC-2004.  
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
Query Match 10.7%; Score 252.5; DB 9; Length 197;  
Best Local Similarity 34.0%; Pred. No. 6.3e-08;  
RESULT 1485  
ID ADV44216 standard; protein; 197 AA.  
DE Buffalo fly resilin polypeptide #1.  
PN WO2004104042-A1.  
PD 02-DEC-2004.  
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
Query Match 10.7%; Score 252.5; DB 9; Length 197;  
Best Local Similarity 34.0%; Pred. No. 6.3e-08;  
RESULT 1486  
ID AFI16198 standard; protein; 198 AA.  
DE Heat stabilizing motif b maximal repeat auxiliary polypeptide.  
PN JP2006150072-A.  
PD 15-JUN-2006.  
PA (SANN-) SANYO CHEM IND LTD.  
Query Match 10.7%; Score 252.5; DB 10; Length 198;  
Best Local Similarity 34.8%; Pred. No. 6.3e-08;  
RESULT 1487  
ID ADV09319 standard; protein; 455 AA.  
DE Plant full length insert polypeptide seqid 65134.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ-) LIU J.  
PA (ZHOU-) ZHOU Y.  
PA (KOVA-) KOVALIC D K.  
PA (SCRE-) SCREEN S E.  
PA (TABA-) TABASKA J E.  
PA (CAOY-) CAO Y.

Query Match 10.7%; Score 252.5; DB 8; Length 455;  
Best Local Similarity 28.1%; Pred. No. 1.4e-07;  
RESULT 1488  
ID ADX80040 standard; protein; 529 AA.  
DE Plant full length insert polypeptide seqid 49406.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ-) LIU J.  
PA (ZHOU-) ZHOU Y.  
PA (KOVA-) KOVALIC D K.  
PA (SCRE-) SCREEN S E.  
PA (TABA-) TABASKA J E.  
PA (CAOY-) CAO Y.  
Query Match 10.7%; Score 252.5; DB 8; Length 529;  
Best Local Similarity 28.7%; Pred. No. 1.6e-07;  
RESULT 1489  
ID ADW99579 standard; protein; 1014 AA.  
DE Human gelatin protein - SEQ ID 12.  
PN WO2005012356-A2.  
PD 10-FEB-2005.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.7%; Score 252.5; DB 9; Length 1014;  
Best Local Similarity 27.9%; Pred. No. 3e-07;  
RESULT 1490  
ID AE157383 standard; protein; 1308 AA.  
DE Thale cress polypeptide, SEQ ID NO: 1850.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 10.7%; Score 252.5; DB 10; Length 1308;  
Best Local Similarity 26.2%; Pred. No. 3.9e-07;  
RESULT 1491  
ID AE157753 standard; protein; 1474 AA.  
DE Thale cress polypeptide, SEQ ID NO: 2220.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Query Match 10.7%; Score 252.5; DB 10; Length 1474;  
Best Local Similarity 26.2%; Pred. No. 4.3e-07;  
RESULT 1492  
ID ADP11446 standard; protein; 1755 AA.  
DE Human secreted protein SEQ ID #3444.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.7%; Score 252.5; DB 8; Length 1755;  
Best Local Similarity 24.2%; Pred. No. 5.1e-07;  
RESULT 1493  
ID AAO16498 standard; protein; 227 AA.  
DE Argiope trifasciata spider silk protein #2.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 10.7%; Score 252; DB 6; Length 227;  
Best Local Similarity 29.2%; Pred. No. 7.7e-08;  
RESULT 1494  
ID AAP90064 standard; protein; 429 AA.  
DE Antigenic protein for malaria vaccination.  
PN USN7238746-N.  
PD 21-MAR-1989.  
PA (USSH-) NAT INST OF HEALTH.  
Query Match 10.7%; Score 252; DB 1; Length 429;  
Best Local Similarity 19.9%; Pred. No. 1.4e-07;  
RESULT 1495  
ID AAW61562 standard; protein; 1487 AA.  
DE Human type II collagen alpha-chain protein.  
PN WO9835235-A1.  
PD 13-AUG-1998.  
PA (UYSH-) UNIV SHEFFIELD.  
Query Match 10.7%; Score 252; DB 2; Length 1487;  
Best Local Similarity 27.1%; Pred. No. 4.7e-07;  
RESULT 1496  
ID ABG93945 standard; protein; 1497 AA.

DE Mouse polypeptide orthologous to DACC-10.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADBP-) ADP PHARM PTY LTD.  
PA (UNST) UNIV SYDNEY.  
Query Match 10.7%; Score 252; DB 5; Length 1497;  
Best Local Similarity 26.0%; Pred. No. 4.7e-07;  
RESULT 1497  
ID ADE77159 standard; protein; 462 AA.  
DE Human protein expressed in a liver disorder #83.  
PN US200310871-A1.  
PD 12-JUN-2003.  
PA (KASE/) KASER M R.  
Query Match 10.6%; Score 251.5; DB 8; Length 462;  
Best Local Similarity 29.9%; Pred. No. 1.6e-07;  
RESULT 1498  
ID ADP31648 standard; protein; 889 AA.  
DE Human secreted protein SEQ ID #3646.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.6%; Score 251.5; DB 8; Length 889;  
Best Local Similarity 26.6%; Pred. No. 3.1e-07;  
RESULT 1499  
ID AAP70709 standard; protein; 402 AA.  
DE Plasmodium cynomolgi sporozoite circumsporozoite protein.  
PN WO8700533-A.  
PD 29-JAN-1987.  
PA (UYNV) UNIV NEW YORK STATE.  
PA (ARNO/) ARNOT D E.  
Query Match 10.6%; Score 251; DB 1; Length 402;  
Best Local Similarity 25.5%; Pred. No. 1.5e-07;  
RESULT 1500  
ID ADD45053 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 10485.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 5.3e-07;

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OM protein - protein search, using sw model

Run on: March 28, 2007, 21:01:22 ; Search time 42 seconds  
(without alignments)  
1007.985 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 2363  
Sequence: 1 MKRQGPLACLLALCLGSGE.....KLGFINDAINKDQSSRIP 440

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450.5	19.1	1079	2 B70807	hypothetical glyci
2	439.5	18.6	1306	2 A70934	hypothetical glyci
3	423	17.9	366	2 T49109	glycine-rich prote
4	415.5	17.6	1381	2 E70806	hypothetical glyci
5	412.5	17.5	484	2 E70846	hypothetical glyci
6	406	17.2	1901	2 E70806	hypothetical glyci
7	404.5	17.1	532	2 F70580	hypothetical glyci
8	403	17.1	1489	2 D70807	hypothetical glyci
9	400.5	16.9	1538	2 H70846	hypothetical glyci
10	399.5	16.9	853	2 A70896	hypothetical glyci
11	395	16.7	714	2 A70807	hypothetical glyci
12	395	16.7	1660	2 A70869	hypothetical glyci
13	392.5	16.6	923	2 E70820	hypothetical glyci
14	392	16.6	731	2 C70974	hypothetical glyci
15	392	16.6	1329	2 E70917	hypothetical glyci
16	386	16.3	778	2 F70963	hypothetical glyci
17	383.5	16.2	767	2 E70895	hypothetical glyci
18	383	16.2	641	1 Q08E31	nuclear antigen EB
19	381.5	16.1	741	2 E70917	hypothetical glyci
20	380.5	16.1	837	2 E70835	hypothetical glyci
21	379	16.0	465	1 S01820	glycine-rich cell
22	378	16.0	588	2 F70971	hypothetical glyci
23	376.5	15.9	749	2 A70812	hypothetical glyci
24	375	15.9	914	2 H70967	hypothetical glyci
25	373.5	15.8	584	2 G70804	hypothetical glyci
26	373.5	15.8	667	2 A70893	hypothetical glyci
27	372	15.7	694	2 E70868	hypothetical glyci
28	371	15.7	615	2 H70589	hypothetical glyci
29	371	15.7	718	2 A36068	major ampullate fi

30	370.5	15.7	491	2 D70916	hypothetical glyci
31	369.5	15.6	1428	2 T08852	luerin A - Califo
32	366	15.5	408	2 S57483	glycine-rich protei
33	365.5	15.5	496	2 H70839	hypothetical glyci
34	365	15.4	576	2 A70900	hypothetical glyci
35	365	15.4	591	2 B70523	hypothetical glyci
36	364.5	15.4	801	2 F70824	hypothetical glyci
37	364	15.4	606	2 H70816	hypothetical glyci
38	363	15.4	481	2 A35628	hypothetical glyci
39	363	15.4	639	2 D70931	hypothetical glyci
40	360	15.2	562	2 B70953	hypothetical glyci
41	359.5	15.2	1011	2 F70620	hypothetical glyci
42	359	15.2	463	2 B70893	hypothetical glyci
43	358.5	15.2	338	1 KMMU	glycine-rich cell
44	355	15.0	291	1 S31415	glycine-rich prote
45	352.5	14.9	384	1 A26099	glycine-rich cell
46	352	14.9	274	2 T25404	hypothetical prote
47	352	14.9	603	2 A70770	hypothetical glyci
48	351	14.9	957	2 D70835	hypothetical glyci
49	350.5	14.8	461	2 F70571	hypothetical glyci
50	350	14.8	316	1 A38743	hypothetical glyci
51	349	14.8	618	2 A70989	hypothetical glyci
52	349	14.8	882	2 B70812	hypothetical glyci
53	345	14.6	713	1 UNMS	period clock prote
54	345	14.6	966	2 A33626	fibrogen alpha c
55	344	14.6	525	2 D70878	hypothetical glyci
56	344	14.6	783	2 E70824	hypothetical glyci
57	342	14.5	515	2 H70663	hypothetical glyci
58	339.5	14.4	487	2 E70983	hypothetical glyci
59	339	14.3	937	2 S58135	hyally regulated
60	335	14.2	434	2 E70768	hypothetical glyci
61	334	14.1	255	2 B84777	hypothetical prote
62	334	14.1	498	2 C70720	hypothetical glyci
63	329	13.9	549	2 D70720	hypothetical prote
64	325.5	13.8	439	2 D70954	hypothetical glyci
65	322	13.5	1207	2 T23754	hypothetical prote
66	320	13.5	594	2 G70545	hypothetical glyci
67	315	13.3	302	2 C64470	hypothetical prote
68	314.5	13.3	543	2 F70726	hypothetical glyci
69	312.5	13.2	252	1 S01821	hypothetical glyci
70	308.5	13.1	2639	2 T31328	glycine-rich prote
71	308	13.0	271	2 S34666	glycine-rich prote
72	306.5	12.9	419	1 OZZDM	circumsporozoite p
73	306	12.9	284	2 T23158	hypothetical prote
74	302	12.8	592	2 B82759	endo-1,4-beta-gluc
75	301	12.7	485	2 A60610	circumsporozoite p
76	300.5	12.7	622	2 I37984	keratin 9, type I,
77	299.5	12.7	3198	2 A43426	glycine-rich prote
78	298.5	12.6	210	2 J01060	hypothetical prote
79	298.5	12.6	2174	2 B55965	hypothetical glyci
80	296.5	12.5	1585	2 T31611	hypothetical prote
81	296	12.5	627	2 A44112	spidroin 2, dragl1
82	293.5	12.4	794	2 T10519	pre-pro-legumin -
83	293	12.4	256	2 A70514	hypothetical glyci
84	290.5	12.3	749	2 T38488	trypsinin - human
85	290	12.3	543	2 S19933	glycine-rich prote
86	290	12.3	751	2 B64741	cuticle collagen -
87	289	12.2	1414	1 S23809	collagen alpha 2(I
88	288.5	12.2	528	2 G02127	fus-1-like protein -
89	287	12.1	13288	2 T03099	musin, submaxillar
90	286	12.1	286	2 C61615	beticin MG-2 - gre
91	283	12.0	1051	2 A35763	collagen alpha 2 c
92	282	11.9	543	2 T49892	glycine-rich prote
93	280	11.8	1466	1 CGHUL	collagen alpha 1(I
94	278.5	11.8	526	1 S33799	RNA-binding protei
95	278	11.8	220	2 T14441	glycine-rich prote
96	278	11.8	270	2 A60830	keratin, 70k type
97	277	11.7	256	2 T03371	glycine-rich prote
98	276.5	11.7	682	2 T28899	hypothetical prote
99	275	11.6	1172	2 T32759	hypothetical prote
100	274	11.6	593	1 KRHUO	keratin 10, type I
101	274	11.6	730	2 E96559	hypothetical prote
102	274	11.6	3016	2 S77300	hypothetical prote

103	273.5	11.6	183	2	PN0109	keratin-like prote
104	272.5	11.5	1373	1	A43291	collagen alpha 2(I
105	272.5	11.5	1492	1	A40333	collagen alpha 1(I
106	272	11.5	375	2	TS0427	S-antigen precursor
107	272	11.5	1156	2	T43326	gemline RNA helic
108	271.5	11.5	370	2	G70872	hypothetical glyci
109	271	11.5	681	2	AB2155	hypothetical prote
110	270.5	11.4	1027	2	S28774	collagen alpha cha
111	270	11.4	1844	2	TS1890	related to Nup98-N
112	269	11.4	361	2	G70682	hypothetical glyci
113	269	11.4	1366	1	CGH025	collagen alpha 2(I
114	268.5	11.4	259	2	T15126	hypothetical prote
115	268	11.3	183	1	KNR262	glycine-rich cell
116	266	11.3	683	2	A82704	1,4-beta-cellulosa
117	265	11.2	568	2	JC7210	molluscan shell ma
118	265.5	11.2	615	2	E70663	probable PPE prote
119	263	11.1	435	2	T15143	hypothetical prote
120	263	11.1	1752	2	A45407	collagen alpha 3(I
121	262.5	11.1	645	2	F70825	probable PPE prote
122	262.5	11.1	1049	1	CGB078	collagen alpha 1(I
123	262.5	11.1	2038	2	A43742	female sterite hom
124	262	11.1	1349	2	T48103	type VII collagen
125	260	11.0	730	2	A36226	collagen alpha 1 c
126	260	11.0	1486	1	B40333	collagen alpha 1(I
127	258.5	10.9	462	4	S33798	FUS/CHOP mutant fu
128	257.5	10.9	386	1	S22315	SNRNP-associated p
129	257.5	10.9	581	1	KRMS2	keratin, type II c
130	257.5	10.9	1464	1	SS9856	collagen alpha 1(I
131	255.5	10.8	589	2	S71954	RNA/ssDNA-binding
132	255	10.8	632	2	S42731	collagen alpha 1 c
133	254	10.7	1747	2	A54121	collagen alpha-4 c
134	253.5	10.7	401	1	OZ20AC	circumsporozoite p
135	253.5	10.7	539	2	T28770	hypothetical prote
136	253	10.7	1217	2	SS2714	sericin1b - silkwo
137	253	10.7	1487	1	CGH06C	RNA-binding protei
138	252.5	10.7	404	2	SS4729	probable PPE prote
139	252	10.7	582	2	F70675	probable PPE prote
140	252	10.7	1497	2	T49607	procollagen type V
141	251.5	10.6	490	2	T05444	hypothetical prote
142	251.5	10.6	860	1	EAMS	elastin precursor
143	251	10.6	429	2	A54504	circumsporozoite p
144	251	10.6	671	1	CGRTS	collagen alpha 1(I
145	249.5	10.6	395	2	A41156	circumsporozoite p
146	249.5	10.6	940	2	JE0221	FB19 protein - hum
147	249	10.5	590	2	E70946	probable PPE prote
148	248.5	10.5	1032	2	G89427	protein T08D2.3 Ii
149	248	10.5	343	2	T05221	hypothetical prote
150	248	10.5	385	2	S40778	ribonucleoprotein
151	247.5	10.5	1418	2	T45467	collagen alpha 1(I
152	247.5	10.5	3300	2	D70575	probable PPE prote
153	246.5	10.4	1453	1	S21626	collagen alpha 1(I
154	246.5	10.4	1464	1	CGH05	collagen alpha 1(I
155	246.5	10.4	1958	2	B40505	hypothetical prote
156	245.5	10.4	354	2	B70663	probable PPE prote
157	245.5	10.4	636	2	S41067	collagen alpha 1(I
158	245.5	10.4	1419	2	A41182	collagen alpha 1(I
159	245.5	10.4	1487	2	B41182	collagen alpha 1(I
160	245	10.4	886	2	I50694	collagen alpha 1(I
161	245	10.4	1684	2	T02367	hypothetical prote
162	243	10.3	424	2	T08093	oleosin homolog ST
163	243	10.3	1226	2	T24045	hypothetical prote
164	242.5	10.3	205	2	T07959	probable cell wall
165	242.5	10.3	1496	1	CGH02V	collagen alpha 2(I
166	242.5	10.3	1775	2	A31893	collagen alpha 1(I
167	242	10.2	385	2	T20410	hypothetical prote
168	242	10.2	779	1	CGB01S	collagen alpha 1(I
169	241.5	10.2	608	2	T05442	glycine-rich prote
170	241.5	10.2	1042	1	CGCHIS	collagen alpha 1(I
171	241	10.2	380	2	A48295	collagen 1 - marin
172	241	10.2	964	1	CGCH2S	collagen alpha 2(I
173	241	10.2	1546	1	CGH02E	collagen alpha 2(I
174	241	10.2	1744	2	S40991	collagen alpha 1(I
175	240.5	10.2	673	1	CGB06C	collagen alpha 1(I
176	240	10.2	170	2	JC2213	hypothetical 14.7K
177	240	10.2	678	2	A70762	probable PPE prote
178	239.5	10.1	812	2	S31521	collagen COL1 - f
179	239.5	10.1	1669	1	CGMS4B	collagen alpha 1(I
180	239	10.1	1806	1	CGH01E	collagen alpha 1(I
181	238.5	10.1	212	2	A44994	eggshell protein I
182	238.5	10.1	387	2	C41156	circumsporozoite p
183	238.5	10.1	183	2	C41156	circumsporozoite p
184	237	10.0	570	2	S07330	keratin, epidermal
185	236.5	10.0	220	2	A44805	eggshell protein p
186	236.5	10.0	1733	1	B45344	probable nuclear p
187	236	10.0	888	2	S28791	collagen alpha 1X
188	235	9.9	839	2	F75518	hypothetical prote
189	234.5	9.9	207	2	B44994	eggshell protein 2
190	234.5	9.9	419	2	T14448	oleosin homolog pc
191	234.5	9.9	438	2	S53787	collagen alpha cha
192	234.5	9.9	2109	1	I50421	aggrecan precursor
193	234.5	9.9	2944	2	A54849	collagen alpha 1(V
194	234.5	9.9	3507	2	T34513	hypothetical prote
195	234	9.9	227	2	B41342	circumsporozoite p
196	234	9.9	1655	2	T13998	gene mastermind pr
197	233.5	9.9	165	1	KNR2G1	glycine-rich cell
198	233.5	9.9	171	1	H84709	probable glycine-r
199	233.5	9.9	180	2	T28938	hypothetical prote
200	233	9.9	783	2	T35389	probable serine-cha
201	233	9.9	864	1	EART	elastin precursor
202	232.5	9.8	290	2	T23416	hypothetical prote
203	232.5	9.8	643	1	KRH02	keratin 1, type II
204	231.5	9.8	244	2	T04592	glycine-rich prote
205	231	9.8	221	2	T49493	glycine-rich cell
206	231	9.8	413	2	E70661	probable PE protei
207	231	9.8	1758	2	T29350	hypothetical prote
208	230.5	9.8	1300	2	T03166	probable immediate
209	230.5	9.8	209	2	B70969	probable PPE prote
210	230	9.7	115	2	D61615	sericin Mg-1 - gre
211	230	9.7	1778	2	TS0074	probable nucleopor
212	229.5	9.7	569	1	KRMS1	keratin, 59K type
213	229	9.7	162	2	C95356	glycine-rich prote
214	229	9.7	391	2	T06224	COR39 protein - wh
215	228.5	9.7	190	2	B48571	circumsporozoite p
216	228.5	9.7	430	1	H8BYD8	heat shock protein
217	228.5	9.7	555	2	S70791	vesab protein - Myc
218	228.5	9.7	561	2	A31994	keratin 10, type I
219	228	9.6	373	2	S40777	heterogeneous ribo
220	228	9.6	920	2	B34493	collagen alpha 1(I
221	227.5	9.6	180	2	T49530	related to glycine
222	227	9.6	371	2	E88633	protein P56B3.1 Ii
223	227	9.6	402	1	CGB02S	ice nucleation pro
224	227	9.6	1210	2	A25547	collagen alpha 2(I
225	227	9.6	1759	2	T29351	collagen alpha 2(I
226	226.5	9.6	326	2	A41732	heterogeneous ribo
227	226.5	9.6	469	2	T06987	dehydrin homolog W
228	226.5	9.6	641	2	T30076	hypothetical prote
229	226.5	9.6	918	2	S23377	collagen alpha 2(V
230	226.5	9.6	1022	2	S04111	collagen alpha 2(V
231	226	9.6	1669	1	CGH04B	collagen alpha 1(I
232	225.5	9.5	1113	2	S28925	nuclear pore compl
233	224	9.5	167	2	S21359	keratin, type I, c
234	224	9.5	404	2	B84745	probable RNA-bind
235	224	9.5	447	2	T42987	hypothetical prote
236	224	9.5	1532	2	A61262	collagen alpha 1(X
237	223.5	9.5	572	2	T08509	trb1 protein - Ent
238	223	9.4	545	2	T15667	hypothetical prote
239	223	9.4	1200	1	SNPSO	ice nucleation pro
240	222.5	9.4	1063	1	D86731	hypothetical prote
241	222.5	9.4	1761	2	T13990	collagen type IV a
242	222.5	9.4	2523	2	A34840	probable PPE prote
243	222	9.4	365	2	D70604	heterogeneous ribo
244	222	9.4	552	2	D70604	probable PPE prote
245	222	9.4	1691	1	CGH06B	collagen alpha 6(I
246	221.5	9.4	173	2	JO1064	glycine-rich prote
247	221	9.4	310	2	I50696	collagen alpha 1(I
248	221	9.4	575	2	T52420	dehydrin 5 [import

249	221	9.4	575	2	S35327	protein kinase sgg	322	204.5	8.7	770	2	S59623	tropoelastin - she
250	220.5	9.3	316	2	T20497	hypothetical prote	323	204.5	8.7	1019	1	A32856	collagen alpha 1(V
251	220.5	9.3	618	2	H70552	probable PPE prote	324	204	8.6	177	2	A31204	eggshell protein p
252	220.5	9.3	645	2	A44861	keratin, 67K type	325	204	8.6	228	2	S19932	glycine-rich prote
253	220	9.3	917	2	S09646	collagen alpha 2(V	326	204	8.6	547	2	A36046	collagen alpha cha
254	220	9.3	1018	1	CGH02A	collagen alpha 2(V	327	204	8.6	1146	2	A38587	collagen, cornea-s
255	219.5	9.3	207	2	T07381	glycine-rich prote	328	203	8.6	223	2	B96506	hypothetical prote
256	219.5	9.3	2248	2	A35938	profiilagrin - hum	329	203	8.6	680	2	T08080	probable myosinas
257	218	9.2	287	2	A60643	antigen 5401 - Bim	330	203	8.6	825	2	JC4163	DNA-binding protei
258	217.5	9.2	1880	2	T18531	tractin - medicina	331	203	8.6	1034	2	JC2143	ice nucleation act
259	217	9.2	575	2	S27761	dehydrin Dhm5 - ba	332	203	8.6	2327	2	T42630	aggreacan - bovine
260	216.5	9.2	674	2	S13301	collagen alpha 1(X	333	202.5	8.6	351	2	B34840	heterogeneous ribo
261	216.5	9.2	2090	2	S26058	probable transform	334	202.5	8.6	677	2	S23296	collagen alpha 2(I
262	216	9.1	409	2	T20847	hypothetical prote	335	202.5	8.6	1028	1	CGH03A	collagen alpha 1(V
263	215.5	9.1	2132	1	A55182	aggreacan precursor	336	202.5	8.6	3176	2	CGH03A	collagen alpha 3(V
264	215	9.1	200	2	S10334	glycine-rich prote	337	202	8.5	430	2	S52700	NUP42 protein - ye
265	215	9.1	479	2	F70573	hypothetical prote	338	201.5	8.5	393	2	T20268	hypothetical prote
266	215	9.1	1029	1	S21369	collagen alpha 2(V	339	201	8.5	1712	1	CGH02B	hypothetical prote
267	215	9.1	1567	2	S11672	ice nucleation pro	340	200.5	8.5	312	2	T25048	hypothetical prote
268	215	9.1	1690	1	CGH01B	collagen alpha 4(I	341	200.5	8.5	353	3	B34504	heterogeneous nucl
269	215	9.1	1838	1	CGH01V	collagen alpha 1(V	342	200.5	8.5	623	1	S33167	gene pointed prote
270	215	9.1	1843	2	S18803	collagen alpha 1(V	343	200.5	8.5	675	2	S20819	collagen alpha 3(I
271	214.5	9.1	290	2	A32249	collagen - sea urc	344	200.5	8.5	2232	2	T34434	hypothetical prote
272	214.5	9.1	368	2	T29173	hypothetical prote	345	200	8.5	1096	2	H86237	protein F14N23.29
273	214.5	9.1	465	2	F75524	hypothetical prote	346	200	8.5	1258	2	E70969	ice nucleation pro
274	214.5	9.1	1018	2	H83135	probable adhesin P	347	200	8.5	3716	2	JC0188	probable PPE prote
275	214	9.1	1024	2	S18251	collagen alpha 1(X	348	199.5	8.4	214	1	KNNT2S	glycine-rich prote
276	214	9.1	1275	2	T33369	hypothetical prote	349	199.5	8.4	670	2	T49510	fibroin-3 related
277	213.5	9.0	245	2	F70787	hypothetical prote	350	199.5	8.4	1022	2	A48686	probable RNA helic
278	213.5	9.0	695	2	T24950	hypothetical glyci	351	199.5	8.4	707	2	T24663	hypothetical prote
279	213.5	9.0	959	2	B44402	nuclear pore compl	352	199	8.4	825	1	EDBEXD	immediate-early pr
280	213.5	9.0	1670	1	CGH03B	collagen alpha 3(I	353	198.5	8.4	191	3	A42844	abscisic acid-and
281	213.5	9.0	2415	1	A39086	aggreacan precursor	354	198.5	8.4	380	2	T14447	oleosin homolog pc
282	212.5	9.0	1804	2	H96597	hypothetical prote	355	198.5	8.4	921	3	S40495	collagen alpha 1(I
283	212.5	9.0	2351	2	B98047	hypothetical prote	356	198.5	8.4	1433	2	A46053	bullous pemphigoid
284	212	9.0	390	2	S27766	WC5120 protein - w	357	198.5	8.4	1691	1	S42075	collagen alpha 5(I
285	212	9.0	635	2	A57131	sporoziote surface	358	198	8.4	346	2	S40775	ribonucleoprotein
286	212	9.0	907	2	A45560	collagen alpha 1(I	359	198	8.4	541	2	S51799	nucleoporin NUP57
287	211.5	9.0	488	2	A27353	collagen alpha 1(I	360	198	8.4	1213	2	S16356	ovo protein - fru1
288	211	8.9	967	2	S66852	hypothetical prote	361	197.5	8.4	744	2	S15435	collagen alpha 1(V
289	210.5	8.9	471	2	T33997	hypothetical prote	362	197	8.3	361	2	T14460	oleosin homolog gb
290	210.5	8.9	3190	2	T13828	CRMB-binding prote	363	197	8.3	1142	2	JX0369	collagen alpha 1(X
291	209.5	8.9	688	2	A55330	collagen alpha 2(I	364	196.5	8.3	571	1	UMFP	period clock prote
292	209.5	8.9	920	2	A45748	collagen alpha 1(V	365	196.5	8.3	754	2	A55267	collagen alpha 5(I
293	209	8.8	680	2	S31216	collagen alpha 1(X	366	196	8.3	136	2	T29282	hypothetical prote
294	209	8.8	1707	2	A33526	collagen alpha 2(I	367	196	8.3	1147	1	MMAX1B	myosin heavy chain
295	209	8.8	3137	2	A37797	collagen alpha 3(V	368	195.5	8.3	314	2	T08675	hypothetical prote
296	208.5	8.8	377	2	T08095	oleosin homolog ST	369	195.5	8.3	633	3	B40983	collagen alpha 1(X
297	208	8.8	201	2	T00799	hypothetical prote	370	195.5	8.3	698	2	JU0163	No-on-transient A
298	208	8.8	307	2	T27609	hypothetical prote	371	195.5	8.3	700	2	JU0162	No-on-transient A
299	208	8.8	457	2	H70820	hypothetical glyci	372	195.5	8.3	921	2	S42617	collagen alpha 1(I
300	208	8.8	618	2	S32436	collagen alpha 2(I	373	195.5	8.3	1560	2	T02885	peroxisome prolif
301	207.5	8.8	365	2	A26459	helix-destabilizin	374	195	8.3	358	2	S40776	ribonucleoprotein
302	207	8.8	208	2	T46896	mezoziote surface	375	195	8.3	469	2	A24450	collagen alpha 2(V
303	207	8.8	313	2	T04776	hypothetical prote	376	195	8.3	1748	2	S42136	cnfB protein - Tet
304	207	8.8	405	2	T29167	hypothetical prote	377	194.5	8.2	383	3	A53053	dentin stalo protei
305	207	8.8	645	2	D90782	probable tail fibe	378	194.5	8.2	839	2	H90577	lipoprotein Vsa1 I
306	207	8.8	645	2	H85642	collagen tail fibe	379	194.5	8.2	959	2	S32605	collagen alpha 3(V
307	207	8.8	680	2	CGH01D	probable tail fibe	380	194	8.2	1028	2	T03516	hypothetical prote
308	206.5	8.7	2124	2	A28452	sericin - silkworm	381	194	8.2	1400	2	T31555	hypothetical prote
309	206.5	8.7	190	2	A24713	heterogeneous ribo	382	194	8.2	1436	2	B70520	probable PPE prote
310	206.5	8.7	342	2	S14432	collagen alpha 1(I	383	193.5	8.2	931	2	S13580	collagen alpha 1(I
311	206.5	8.7	615	2	A05269	collagen alpha 1(V	384	193.5	8.2	1096	2	T08619	collagen alpha c
312	206.5	8.7	1025	2	S34839	collagen alpha 1(V	385	192	8.1	526	1	KRBOVI	keratin, 54K type
313	206	8.7	447	2	G84687	probable disease r	386	191.5	8.1	644	1	FGHUA	fibritrogen alpha c
314	206	8.7	1322	2	S07053	ice nucleation pro	387	191.5	8.1	866	2	D44234	collagen alpha 1(X
315	205.5	8.7	406	2	G71404	probable ribonucle	388	191.5	8.1	1315	2	A56101	collagen alpha 1(X
316	205.5	8.7	518	2	A55840	macrophage bacteri	389	191.5	8.1	1774	2	B56101	collagen alpha 1(X
317	205	8.7	502	2	A48679	differentiated ker	390	191	8.1	323	2	T19142	hypothetical prote
318	205	8.7	775	2	A61228	collagen alpha 2(I	391	190.5	8.1	743	1	S23779	collagen alpha 1(V
319	205	8.7	1417	2	A83080	hypothetical prote	392	190.5	8.1	796	2	S57844	lethal(3)malignant
320	205	8.7	1603	2	S23810	collagen alpha 1(X	393	190.5	8.1	2329	2	T28125	hypothetical prote
321	204.5	8.7	382	2	S20375	collagen alpha 3(V	394	190	8.0	344	2	S41707	PopAI protein - Ps

395	190	8.0	963	2	B70524	probable PPE prote	468	178.5	7.6	335	2	T14449	oleosin homolog pc
396	189.5	8.0	289	2	P96770	protein RNA-bindin	469	178	7.5	300	2	T19929	hypothetical prote
397	189	8.0	301	2	B31219	collagen 2 - Caeno	470	178	7.5	393	2	S59499	cellulase egli - s
398	189	8.0	848	2	S02262	glutenin high mole	471	178	7.5	539	2	T50579	probable membrane
399	189	8.0	1176	2	C26427	period clock prote	472	178	7.5	688	2	T48796	probable ATP-depen
400	189	8.0	1215	2	A26588	period clock prote	473	177.5	7.5	314	2	T34269	hypothetical prote
401	189	8.0	1218	2	A26427	period clock prote	474	177.5	7.5	327	2	T34203	hypothetical prote
402	188.5	8.0	203	1	J01061	glycine-rich prote	475	177	7.5	176	2	S30147	glycine-rich RNA b
403	188.5	8.0	363	2	T51341	RNA helicase R19 l	476	177	7.5	255	2	AF1857	hypothetical prote
404	188.5	8.0	423	2	A41207	collagen 13, nonfi	477	177	7.5	304	2	T26185	hypothetical prote
405	188.5	8.0	632	2	T02627	hypothetical prote	478	177	7.5	304	2	T26184	hypothetical prote
406	188	8.0	487	2	C70830	probable PPE prote	479	177	7.5	495	2	B71360	hypothetical prote
407	188	8.0	1596	2	A33106	neurogenic locus m	480	177	7.5	908	2	A33280	sarcalumenin precu
408	187.5	7.9	752	2	T34355	hypothetical prote	481	177	7.5	1199	2	A40670	nuclear envelope p
409	187.5	7.9	956	2	T08144	myrosinase-binding	482	177	7.5	3759	2	A35085	retinorax proteoin
410	187.5	7.9	1076	2	C96620	protein T30E16.23	483	176.5	7.5	137	2	T04930	glycine-rich cell
411	187.5	7.9	1718	2	T14603	hypothetical prote	484	176.5	7.5	367	2	A32068	circumsporozoite p
412	187	7.9	586	2	T26667	hypothetical prote	485	176.5	7.5	638	2	I53169	cytokeratin 2 - hu
413	186.5	7.9	252	2	A55047	collagen alpha 1(V	486	176.5	7.5	798	2	T21369	hypothetical prote
414	186.5	7.9	356	2	S16907	collagen alpha 1(I	487	176.5	7.5	1241	2	S01827	period clock prote
415	186.5	7.9	378	1	OZ2QAB	circumsporozoite p	488	176.5	7.5	2554	2	AB3528	extracellular seri
416	186.5	7.9	398	1	OZ2QAS	circumsporozoite p	489	176	7.4	325	2	T18594	hypothetical prote
417	186	7.9	671	2	A35912	homeotic protein o	490	176	7.4	747	1	EABO	elastin precursor,
418	186	7.9	1763	2	S16366	collagen alpha 2(I	491	175.5	7.4	316	2	S08169	collagen col-12 pr
419	185.5	7.9	346	1	S35500	heterogeneous ribo	492	175.5	7.4	403	2	S08170	collagen col-13 pr
420	185.5	7.9	753	2	JC2099	glutinin, high mol	493	175.5	7.4	403	2	T08471	harpin - Erwina a
421	185.5	7.9	789	2	A30843	glutinin, high mol	494	175.5	7.4	775	1	EDBRI1	immediate-early pr
422	185.5	7.9	791	2	UN0690	glutinin, high-mol	495	175	7.4	201	2	F84596	glycine-rich prote
423	185	7.8	704	2	T34034	hypothetical prote	496	175	7.4	352	2	T24279	hypothetical prote
424	185	7.8	867	2	S57795	probable deoxyribo	497	175	7.4	358	2	T26281	hypothetical prote
425	185	7.8	1004	2	C82672	surface-exposed ou	498	175	7.4	363	2	T16831	hypothetical prote
426	184.5	7.8	330	2	T26004	hypothetical prote	499	175	7.4	464	2	S59513	collagen II A1 pro
427	184.5	7.8	388	2	JC6164	circumsporozoite p	500	175	7.4	528	2	D46449	hypothetical prote
428	184.5	7.8	798	2	T33022	hypothetical prote	501	175	7.4	588	2	T38403	probable nucleopor
429	184.5	7.8	1063	2	A40353	acidic nuclear pro	502	174.5	7.4	340	2	T20807	hypothetical prote
430	184	7.8	333	2	T23618	hypothetical prote	503	174.5	7.4	406	2	S38170	SBP40 protein - ye
431	184	7.8	625	2	A34615	proflaggrin - rat	504	174.5	7.4	460	2	T33110	hypothetical prote
432	184	7.8	813	2	S70795	vaa protein precu	505	174.5	7.4	629	2	A29666	keratin, 65K type
433	184	7.8	1102	2	A32247	virg protein - Shi	506	174.5	7.4	672	2	I40333	tracheal colonizat
434	183.5	7.8	445	2	A27263	50K spicule matrix	507	174	7.4	239	2	S49193	GCR 101 protein -
435	183.5	7.8	541	2	T15299	hypothetical prote	508	174	7.4	314	2	T32247	hypothetical prote
436	183.5	7.7	174	2	S18654	variant surface an	509	174	7.4	330	2	S46657	collagen alpha 1(X
437	182.5	7.7	306	2	S33538	embryogenic cell p	510	174	7.4	344	2	T40167	hypothetical prote
438	182.5	7.7	443	2	C70780	probable PPE prote	511	174	7.4	387	2	E95995	hypothetical calci
439	182.5	7.7	472	2	S28026	nuclear pore compl	512	174	7.4	448	2	T15188	hypothetical prote
440	182.5	7.7	1293	2	B40025	maleless protein,	513	174	7.4	475	2	T03170	hypothetical prote
441	182.5	7.7	2204	2	A70524	probable PPE prote	514	174	7.4	718	1	S33168	gene pointed prote
442	182	7.7	287	2	B39615	merozoite 45K surf	515	174	7.4	782	2	T32155	hypothetical prote
443	182	7.7	305	2	T20906	hypothetical prote	516	173.5	7.3	204	2	T09592	protein cora, cold
444	182	7.7	1053	2	B70987	probable PPE prote	517	173.5	7.3	424	1	Z3BPPI	coat protein A pre
445	181.5	7.7	154	2	B84468	probable glycine-r	518	173.5	7.3	424	1	Z3BPPI	coat protein A pre
446	181.5	7.7	1287	2	I46032	nuclear DNA helica	519	173.5	7.3	424	1	Z3BPPI	coat protein A pre
447	181	7.7	256	2	T11669	protein CPRD22, dr	520	173.5	7.3	542	2	T29707	hypothetical prote
448	181	7.7	356	2	T22827	hypothetical prote	521	173.5	7.3	558	2	E70756	hypothetical glyci
449	181	7.7	456	2	A32947	flaggrin precursor	522	173.5	7.3	779	2	A35006	cell surface glyco
450	181	7.7	569	2	S42886	collagen - silkwor	523	173.5	7.3	1912	2	T29088	vitellinogenin 1 pr
451	181	7.7	614	2	T33149	hypothetical prote	524	173	7.3	258	2	S71561	drought-induced pr
452	181	7.7	1388	2	A53317	collagen alpha 1(X	525	173	7.3	281	2	C90577	lipoprotein vaa l
453	181	7.7	1533	2	A46221	abdominal segment	526	173	7.3	347	2	B39112	merozoite 45K surf
454	180.5	7.6	196	2	S49194	GCR 17 protein - f	527	173	7.3	656	1	A49358	RNA-binding protei
455	180.5	7.6	605	2	T33913	hypothetical prote	528	173	7.3	1032	2	T34433	hypothetical prote
456	180.5	7.6	744	1	A34246	collagen alpha 1(V	529	173	7.3	1043	2	T13733	FTZ-F1 protein - f
457	180.5	7.6	744	1	S23298	collagen alpha 1(V	530	172.5	7.3	864	2	A48266	protein-tyrosine k
458	180	7.6	268	2	B61615	fibroin heavy chai	531	172	7.3	446	2	T45525	WCCA homolog limpo
459	180	7.6	434	1	Z3BPIK	coat protein A - p	532	172	7.3	1052	2	AF2959	conserved hypobet
460	180	7.6	674	2	S23297	collagen alpha 1(X	533	172	7.3	1341	2	H98323	hypothetical prote
461	180	7.6	792	1	EABU	elastin precursor,	534	171.5	7.3	655	1	A55726	RNA-binding protei
462	179.5	7.6	784	2	A26601	elastin precursor,	535	171.5	7.3	1127	2	A25018	circadian rhythm p
463	179.5	7.6	838	2	EEWTHW	glutinin, high mol	536	171	7.2	337	2	T23794	hypothetical prote
464	179	7.6	310	2	T29731	hypothetical prote	537	171	7.2	1176	2	T18042	ice nucleation pro
465	179	7.6	314	2	T32985	hypothetical prote	538	170.5	7.2	108	1	S01844	fibroin - silkworm
466	179	7.6	995	2	T22942	hypothetical prote	539	170.5	7.2	367	2	JC4831	adsorption protein
467	178.5	7.6	313	2	T22828	hypothetical prote	540	170.5	7.2	396	2	T29773	hypothetical prote

541	170.5	7.2	1589	2	T42233	614	163	6.9	418	2	T15142	hypothetical prote
542	170.5	7.2	4936	2	AH2515	615	163	6.9	490	2	T09084	phosphatidylinosit
543	170	7.2	434	2	S08091	616	163	6.9	633	2	F84564	probable protein k
544	170	7.2	615	2	T20839	617	162.5	6.9	262	1	T18PM1	tail fiber protein
545	170	7.2	1208	2	S17286	618	162.5	6.9	289	2	T20177	hypothetical prote
546	170	7.2	3498	2	T22330	619	162.5	6.9	658	2	T41309	hypothetical threo
547	169.5	7.2	183	2	S51773	620	162.5	6.9	925	2	JC2033	G protein-coupled
548	169.5	7.2	661	1	S59633	621	162.5	6.9	1168	1	MMAXIC	myosin heavy chain
549	169.5	7.2	849	2	A96592	622	162	6.9	166	1	KRB02B	keratin, 68k type
550	169.5	7.2	924	2	F87103	623	162	6.9	198	2	T49558	collagen alpha 1(I
551	169.5	7.2	988	2	T08102	624	162	6.9	323	2	T24582	hypothetical prote
552	169.5	7.2	1504	2	T49896	625	162	6.9	1067	2	S35423	protein kinase e9g
553	169	7.2	290	2	T24586	626	162	6.9	1888	2	S78476	collagen alpha 1(X
554	169	7.2	304	2	T22482	627	161.5	6.8	316	2	T19288	hypothetical prote
555	169	7.2	308	2	T37286	628	161.5	6.8	500	2	T20961	hypothetical prote
556	169	7.2	380	2	T28888	629	161.5	6.8	707	2	S52390	D-hordein precuro
557	168.5	7.1	640	2	A54502	630	161.5	6.8	800	2	I51653	dsRNA-binding prot
558	168	7.1	234	2	G95989	631	161.5	6.8	978	2	D81411	hypothetical prote
559	168	7.1	252	2	T03160	632	161.5	6.8	1441	2	B86807	hypothetical prote
560	168	7.1	633	2	A25473	633	161	6.8	284	2	T29528	hypothetical prote
561	168	7.1	673	2	T00328	634	161	6.8	290	2	T24590	hypothetical prote
562	168	7.1	684	2	A53019	635	161	6.8	591	2	A45135	hypothetical prote
563	167.5	7.1	183	2	S57772	636	161	6.8	650	2	G87572	prolactinagrin - hum
564	167.5	7.1	276	2	T33925	637	161	6.8	805	2	T25795	calcium-binding pr
565	167.5	7.1	286	2	B45632	638	161	6.8	925	2	T19361	hypothetical prote
566	167.5	7.1	629	2	S42629	639	161	6.8	1701	2	T43213	ENBP1 protein - ba
567	167.5	7.1	786	2	T16509	640	161	6.8	1852	1	V10CH2	vitellogenin II pr
568	167.5	7.1	1075	2	T48805	641	160.5	6.8	212	2	B86179	hypothetical prote
569	167.5	7.1	1366	2	T35985	642	160.5	6.8	281	2	C88638	protein F58F6.1 (I
570	167.5	7.1	1747	2	A45974	643	160.5	6.8	323	2	T27450	hypothetical prote
571	167.5	7.1	1857	2	S31212	644	160.5	6.8	327	2	S25421	nucleolar protein
572	167	7.1	106	2	F84797	645	160.5	6.8	1516	2	T01055	hypothetical prote
573	167	7.1	166	2	T10463	646	160.5	6.8	2020	2	C48399	ABC-type transport
574	167	7.1	303	2	T19289	647	160	6.8	169	2	T10463	glycine-rich prote
575	167	7.1	325	2	T12248	648	160	6.8	262	2	S00275	tail fiber protein
576	167	7.1	369	2	F96788	649	160	6.8	266	2	T22706	hypothetical prote
577	167	7.1	407	2	T21956	650	160	6.8	299	2	T22705	hypothetical prote
578	167	7.1	1221	2	T13283	651	160	6.8	320	1	DDRT	helix-deestabilizin
579	167	7.1	1237	2	D71850	652	160	6.8	320	1	A44485	heterogeneous ribo
580	167	7.1	1772	2	T36105	653	160	6.8	320	2	S04617	heterogeneous ribo
581	166.5	7.0	313	2	A28444	654	160	6.8	320	2	S02061	heterogeneous ribo
582	166.5	7.0	416	2	T32458	655	160	6.8	378	1	OZZOAL	circumsporozite p
583	166.5	7.0	556	2	T36501	656	160	6.8	582	2	S10099	transcription fact
584	166.5	7.0	556	2	AH1981	657	160	6.8	671	2	A38109	autolysin - Entero
585	166.5	7.0	634	2	T08145	658	160	6.8	987	2	E70808	probable PPE prote
586	166.5	7.0	738	2	E87627	659	160	6.8	1296	2	T13386	collar protein iso
587	166.5	7.0	1120	2	H88449	660	160	6.8	1325	2	T13386	hypothetical prote
588	166	7.0	291	2	T26576	661	160	6.8	1649	2	C86822	hypothetical prote
589	166	7.0	617	2	T49444	662	159.5	6.7	186	2	S28021	ribis protein - Ar
590	166	7.0	1122	2	B26427	663	159.5	6.7	260	2	S00276	tail fiber protein
591	166	7.0	1519	2	S41525	664	159.5	6.7	301	2	B84533	hypothetical prote
592	165.5	7.0	220	2	A02990	665	159.5	6.7	336	2	T20348	hypothetical prote
593	165.5	7.0	220	2	E98293	666	159.5	6.7	654	2	A34734	transcription fact
594	165.5	7.0	389	2	D26995	667	159.5	6.7	742	4	C34734	transcription fact
595	165	7.0	291	2	T20083	668	159.5	6.7	825	4	B34734	transcription fact
596	165	7.0	319	2	T32250	669	159.5	6.7	1534	2	A56734	ribosome receptor,
597	165	7.0	433	2	S20963	670	159	6.7	299	2	T19564	hypothetical prote
598	165	7.0	823	2	S14055	671	159	6.7	302	2	T32872	hypothetical prote
599	164.5	7.0	200	2	B86181	672	159	6.7	494	2	T15502	hypothetical prote
600	164.5	7.0	600	2	S07638	673	159	6.7	516	2	C44479	collagen alpha 1(X
601	164.5	7.0	819	2	T08745	674	159	6.7	1711	1	A47392	chromodomain-helic
602	164.5	7.0	1446	1	A45344	675	158.5	6.7	307	2	T16842	hypothetical prote
603	164	6.9	237	2	A88640	676	158.5	6.7	461	2	S17367	secreted 45k prote
604	164	6.9	368	2	H96990	677	158	6.7	231	2	T25407	ribisb protein - w
605	164	6.9	561	2	T16148	678	158	6.7	299	2	T35407	hypothetical prote
606	163.5	6.9	299	2	T00837	679	158	6.7	306	2	T21938	hypothetical prote
607	163.5	6.9	414	1	T38977	680	158	6.7	1460	2	S48457	nucleoporin RAT7 -
608	163.5	6.9	623	2	A45137	681	158	6.7	3124	2	A40020	collagen alpha 1(X
609	163.5	6.9	666	2	A42296	682	157.5	6.7	317	2	T19143	hypothetical prote
610	163.5	6.9	668	2	C71868	683	157.5	6.7	830	2	S15720	glutinin high mole
611	163.5	6.9	729	2	S35532	684	157	6.6	145	2	T08435	dehydrin 18 - Barl
612	163.5	6.9	928	2	C81265	685	157	6.6	225	2	S05546	
613	163	6.9	254	2	A31488	686	157	6.6	249	2	B33144	homeotic protein U

687	157	6.6	299	2	T24833	hypothetical prote	760	151.5	6.4	486	1	KRXL	keratin 3, type I,
688	157	6.6	363	1	OZQAK	cyclosporozoite p	761	151.5	6.4	797	2	A3681.1	hypothetical prote
689	157	6.6	366	1	S1449	collagen short cha	762	151.5	6.4	901	2	JC6093	dead ringer nuclea
690	157	6.6	623	2	A45571	surface antigen 2,	763	151.5	6.4	1076	1	A35632	nuclear pore prote
691	157	6.6	624	2	A55576	collagen alpha 2(X	764	151	6.4	161	2	S71453	glycine-rich RNA-b
692	157	6.6	806	2	T13690	hypothetical prote	765	151	6.4	333	2	E48423	homeotic protein e
693	157	6.6	829	2	E81086	iron-regulated pro	766	151	6.4	339	2	T22607	hypothetical prote
694	157	6.6	1829	2	AF0394	probable adhesin h	767	151	6.4	387	2	T34507	cutical collagen 6
695	156.5	6.6	1910	2	S53050	RNA binding protei	768	151	6.4	405	2	S19355	hypothetical prote
696	156.5	6.6	273	2	T40618	probable cell wall	769	151	6.4	537	2	B33485	spore coat protein
697	156.5	6.6	387	2	H86445	probable G-box bin	770	150.5	6.4	587	2	E95933	probable calcium-b
698	156.5	6.6	471	2	A39024	collagen alpha 3(I	771	150.5	6.4	461	2	T51044	related to spore c
699	156.5	6.6	758	2	T48813	mixed-linked glucan	772	150.5	6.4	524	2	A82580	polyvinylalcohol d
700	156.5	6.6	1217	2	T25894	hypothetical prote	773	150	6.3	234	2	T49448	hypothetical prote
701	156.5	6.6	1777	2	T34369	hypothetical prote	774	150	6.3	255	2	T06811	dehydrin 2 - garde
702	156.5	6.6	3295	2	AE0074	probable adhesin Y	775	150	6.3	283	2	T19732	hypothetical prote
703	156	6.6	169	2	S30148	glycine-rich prote	776	150	6.3	327	2	T29031	hypothetical prote
704	156	6.6	259	2	S46286	RNA-binding protei	777	150	6.3	359	2	T22774	hypothetical prote
705	156	6.6	291	2	T34494	hypothetical prote	778	150	6.3	423	2	A55797	collagen precursor
706	156	6.6	320	2	S30192	heterogeneous ribo	779	150	6.3	1072	2	G95851	probable hemolysin
707	156	6.6	431	1	MTM2G	homeotic protein H	780	150	6.3	1390	2	T18883	hypothetical prote
708	156	6.6	571	2	T43456	hypothetical prote	781	149.5	6.3	148	2	T09527	hypothetical prote
709	156	6.6	1665	2	T29008	hypothetical prote	782	149.5	6.3	287	2	T22637	hypothetical prote
710	155.5	6.6	163	2	T23076	hypothetical prote	783	149.5	6.3	317	2	T29960	hypothetical prote
711	155.5	6.6	169	1	S38331	glycine-rich RNA-b	784	149.5	6.3	325	2	S02170	collagen alpha 1(I
712	155.5	6.6	298	2	T32371	hypothetical prote	785	149.5	6.3	385	2	D41732	heterogeneous nucl
713	155	6.6	419	1	KRXI2B	keratin, 64K type	786	149.5	6.3	419	2	T04886	DAG protein homolo
714	155	6.6	1487	1	EDBE1	immediate-early pr	787	149.5	6.3	473	2	I50629	collagen - chicken
715	154.5	6.5	270	2	A36034	fibritrogen alpha c	788	149.5	6.3	573	2	C86266	EF19.21 protein -
716	154.5	6.5	304	2	T22602	hypothetical prote	789	149.5	6.3	1028	2	A56038	DNA-binding protei
717	154.5	6.5	343	2	T29547	hypothetical prote	790	149	6.3	264	2	S37137	priion protein - gr
718	154.5	6.5	433	1	QOBEV2	U44 protein - hum	791	149	6.3	318	2	S27977	cuticle collagen d
719	154.5	6.5	705	2	S18733	glutelin high mole	792	149	6.3	329	2	US0167	collagen col 6 - C
720	154.5	6.5	346	2	S55659	tegument protein 6	793	149	6.3	345	1	B41732	heterogeneous nucl
721	154	6.5	205	2	T05713	dehydrin - barley	794	149	6.3	371	1	JN0450	conglutinin precu
722	154	6.5	297	2	T27525	eyelid - fruit fly	795	149	6.3	371	2	I45878	conglutinin - bovi
723	154	6.5	2715	2	T13049	eyelid - fruit fly	796	149	6.3	966	2	T51891	hypothetical prote
724	153.5	6.5	135	2	T01322	aluminum-induced p	797	149	6.3	963	2	T48707	related to regulat
725	153.5	6.5	157	2	S18651	variant surface an	798	149	6.3	1112	2	H95964	probable outer mem
726	153.5	6.5	178	2	E88637	protein W09G12.6 [	799	148.5	6.3	107	2	H85356	glycine-rich prote
727	153.5	6.5	289	2	T34241	hypothetical prote	800	148.5	6.3	283	2	T29960	hypothetical prote
728	153.5	6.5	304	2	T23801	hypothetical prote	801	148.5	6.3	302	2	T21257	hypothetical prote
729	153.5	6.5	309	2	T19389	hypothetical prote	802	148.5	6.3	364	2	S43574	hypothetical prote
730	153.5	6.5	311	2	S08110	salivary protein 1	803	148.5	6.3	454	2	T35180	C05B5.3 protein (c
731	153.5	6.5	333	2	T20436	hypothetical prote	804	148.5	6.3	456	2	E86903	hypothetical prote
732	153.5	6.5	401	2	C88571	protein C05B5.3 [I	805	148.5	6.3	660	2	A24266	hypothetical prote
733	153.5	6.5	437	2	S15144	hypothetical prote	806	148	6.3	289	2	T27708	hypothetical prote
734	153.5	6.5	1791	2	T02345	hypothetical prote	807	148	6.3	298	2	E95286	hypothetical prote
735	153.5	6.5	1829	2	S35027	cytochrome P450	808	148	6.3	299	2	T20605	hypothetical prote
736	153	6.5	132	2	S14977	glycine-rich prote	809	148	6.3	306	2	T21939	hypothetical prote
737	153	6.5	164	2	S1846	radial protein - r	810	148	6.3	447	2	T18447	H1PM protein - Erw
738	153	6.5	232	2	S18139	dehydrin DHN3 - r	811	148	6.3	549	2	B86264	hypothetical prote
739	153	6.5	285	2	T29982	histone-specific t	812	148	6.3	661	2	A58768	ATP-dependent RNA
740	153	6.5	349	2	A41349	transcription fact	813	148	6.3	892	2	T27005	hypothetical prote
741	153	6.5	349	2	S77570	protein kinase (EC	814	148	6.3	1305	2	T00607	probable inositol
742	153	6.5	483	1	TVRTKA	probable dehydroge	815	147.5	6.2	235	2	G01226	leukoplysin - huma
743	153	6.5	629	2	T34726	155k transcritpion	816	147.5	6.2	300	2	T24482	hypothetical prote
744	153	6.5	1487	1	EDBER6	hypothetical prote	817	147.5	6.2	482	2	B31795	collagen alpha 1(X
745	152.5	6.5	257	2	C84533	hypothetical prote	818	147.5	6.2	589	2	T29299	hypothetical prote
746	152.5	6.5	279	2	T26125	hypothetical prote	819	147.5	6.2	1329	2	T29074	hypothetical prote
747	152.5	6.5	299	2	T29956	hypothetical prote	820	147.5	6.2	1584	2	T18276	protein-tyrosine k
748	152.5	6.5	316	2	T19221	hypothetical prote	821	147	6.2	226	2	S27759	maturation-associa
749	152.5	6.5	420	2	D83556	probable coat prot	822	147	6.2	264	2	A54330	major prion protei
750	152.5	6.5	584	2	E70825	hypothetical glyci	823	147	6.2	282	2	JS0168	collagen col-8 - C
751	152.5	6.5	1198	2	T49726	hypothetical prote	824	147	6.2	283	2	T19731	hypothetical prote
752	152	6.4	258	2	A29259	ubx protein - frui	825	147	6.2	374	1	A42046	surfactant protein
753	152	6.4	474	2	A26421	snuffion A - Bache	826	147	6.2	578	2	S55102	PSB2 protein - Yea
754	152	6.4	735	2	T35778	probable fusidic a	827	147	6.2	684	2	T36771	probable integral
755	152	6.4	815	2	B30843	glutelin high mole	828	147	6.2	760	2	A45174	eye cell developme
756	152	6.4	828	2	C88402	protein H05C05.1 [	829	147	6.2	762	2	S08207	siatolglycoprotein
757	151.5	6.4	182	2	A36686	ultra-high-sulfur	830	147	6.2	1317	2	A54831	nuclear pore compl
758	151.5	6.4	294	2	T21668	hypothetical prote	831	147	6.2	1594	2	T43072	hemolysin A - Edwa
759	151.5	6.4	367	2	JC6087	helix-loop-helix t	832	146.5	6.2	166	2	T18691	hypothetical prote



833	146.5	6.2	294	2	T22639	hypothetical prote
834	146.5	6.2	310	2	T22641	hypothetical prote
835	146.5	6.2	368	2	G84769	hypothetical prote
836	146.5	6.2	377	2	A47380	RING finger-contai
837	146.5	6.2	593	2	A48459	S antigen, heat st
838	146.5	6.2	704	2	S21911	Brocra-NS-Z3 prote
839	146	6.2	258	2	T13591	tail fiber adhesin
840	146	6.2	281	2	T32765	hypothetical prote
841	146	6.2	283	2	J50170	collagen col-19 -
842	146	6.2	295	2	T22833	hypothetical prote
843	146	6.2	412	2	A84455	hypothetical prote
844	146	6.2	467	2	I50476	keratin type I g
845	146	6.2	712	2	A45638	immunodominant mic
846	146	6.2	1215	2	T32734	myosin-1A - Acanth
847	146	6.2	1340	2	A39808	proteoglycan core
848	145.5	6.2	215	2	T17207	hypothetical prote
849	145.5	6.2	313	2	T26465	hypothetical prote
850	145.5	6.2	461	2	A43782	keratin, type II -
851	145.5	6.2	561	1	CDBCP3	clacacin DPL3 prote
852	145.5	6.2	643	2	T03518	hypothetical prote
853	145.5	6.2	658	2	A01010	probable surface p
854	145.5	6.2	815	2	JN0689	glutenin, high-mol
855	145.5	6.2	1467	2	A75564	conserved hypotet
856	145	6.1	150	2	C86224	hypothetical prote
857	145	6.1	154	2	S34637	glycine-rich prote
858	145	6.1	170	2	T03018	glycine-rich prote
859	145	6.1	375	1	A45225	pulmonary surfacta
860	145	6.1	380	1	GNVSMB	genome polyprotein
861	145	6.1	451	1	A40168	transcription fact
862	145	6.1	539	2	G95405	hypothetical prote
863	145	6.1	556	2	T36502	serine/threonine p
864	145	6.1	633	2	T02673	heterogeneous nucl
865	145	6.1	919	2	A39248	androgen receptor
866	145	6.1	3345	2	T33423	hypothetical prote
867	144.5	6.1	156	2	S52246	transposable retro
868	144.5	6.1	453	2	A41640	vestigial protein
869	144.5	6.1	512	2	S70644	annexin VII - Afri
870	144.5	6.1	937	2	A56517	nucleoporin Nup98
871	144.5	6.1	2761	2	T21064	hypothetical prote
872	144	6.1	208	2	T21689	hypothetical prote
873	144	6.1	283	2	T29837	hypothetical prote
874	144	6.1	294	2	T29839	hypothetical prote
875	144	6.1	381	2	T27806	hypothetical prote
876	144	6.1	492	2	A87471	hypothetical prote
877	144	6.1	1475	2	S42718	nuclear pore compl
878	143.5	6.1	168	1	S12332	glycine-rich RNA-b
879	143.5	6.1	228	1	A44962	collagen UCOL1 - p
880	143.5	6.1	341	2	B70700	conserved hypotet
881	143.5	6.1	527	2	B70700	hypothetical prote
882	143.5	6.1	608	2	T32923	hypothetical prote
883	143.5	6.1	660	1	QOBE3	BHLFI protein - hu
884	143.5	6.1	709	2	T28712	hypothetical prote
885	143.5	6.1	720	1	A55160	trig protein - frui
886	143.5	6.1	1268	1	B99789	hemagglutinin/hemo
887	143.5	6.1	1270	2	E85649	hypothetical prote
888	143.5	6.1	1665	2	T43169	hypothetical prote
889	143	6.1	182	2	A02947	keratin, 60K type
890	143	6.1	294	2	T29838	hypothetical prote
891	143	6.1	556	2	T42100	serine/threonine p
892	142.5	6.0	197	2	I46413	keratin KAP5.5 - s
893	142.5	6.0	329	2	T32783	hypothetical prote
894	142.5	6.0	590	2	A26638	homeotic protein D
895	142.5	6.0	648	2	A26638	glutennin high mole
896	142.5	6.0	693	2	T33251	hypothetical prote
897	142	6.0	159	2	C49773	ecdysone-dependent
898	142	6.0	164	2	S11847	rab16C protein - r
899	142	6.0	167	2	S71779	glycine-rich RNA-b
900	142	6.0	266	1	TIABPX	tail fiber protein
901	142	6.0	269	1	S48444	probable temperatu
902	142	6.0	272	2	C75548	hypothetical prote
903	142	6.0	324	2	T28032	hypothetical prote
904	142	6.0	351	1	OZ20KU	clitumsporozoite p
905	142	6.0	387	2	S00867	colicin N - Escher
906	142	6.0	449	1	S30205	transcription fact
907	142	6.0	475	2	C86863	N-acetylmutamoyl-L
908	142	6.0	1166	2	T13958	SYNGAP-b1 protein
909	142	6.0	1249	2	T14270	Ras-GTPase activat
910	142	6.0	1286	2	S28634	adhesin AIDA-1 pre
911	142	6.0	1293	2	T14259	ras GTPase-activa
912	142	6.0	1588	2	A86036	probable adhesin Z
913	142	6.0	2535	2	H91188	probable adhesin E
914	141.5	6.0	255	2	AC0304	probable hemolysin
915	141.5	6.0	474	2	A35026	flaggagin A - mous
916	141.5	6.0	788	2	T38240	transcription fact
917	141.5	6.0	1398	2	U80747	regulatory protein
918	141.5	6.0	1398	2	T13741	hypothetical prote
919	141.5	6.0	3355	2	E83641	probable hemagglut
920	141.5	6.0	3968	2	A44265	trithorax homolog
921	141	6.0	191	2	I46412	keratin KAP5.4 - s
922	141	6.0	253	2	A33144	homeotic protein U
923	141	6.0	511	2	S10527	endoglucanase B pr
924	141	6.0	684	2	A56154	Abi substrate ena
925	140.5	5.9	148	2	B71419	hypothetical prote
926	140.5	5.9	309	2	T28708	hypothetical prote
927	140.5	5.9	317	2	T39869	probable lysosomp
928	140.5	5.9	431	2	S09824	hypothetical prote
929	140.5	5.9	484	2	S66713	hypothetical prote
930	140.5	5.9	561	2	T22917	probable ATP-depen
931	140.5	5.9	579	2	T37248	probable matrix me
932	140.5	5.9	1690	2	T35694	ATP dependent DNA
933	140	5.9	111	2	T29295	hypothetical prote
934	140	5.9	296	2	T21070	hypothetical prote
935	140	5.9	327	2	S38342	fibritillatin - mous
936	140	5.9	360	2	T37285	collagen dpy-2 - C
937	140	5.9	425	1	KRXL2A	keratin, 64K type
938	140	5.9	669	2	A97443	hypothetical prote
939	140	5.9	669	2	AC2661	hypothetical prote
940	140	5.9	710	2	S28014	ouid protein - Brw
941	140	5.9	888	2	I58378	tyrosine kinase -
942	140	5.9	1788	2	T31095	vitellogenin precu
943	140	5.9	5627	2	C83339	holotricin 3 precu
944	139.5	5.9	104	2	JC4190	steroid receptor p
945	139.5	5.9	543	2	A32693	defomed epidermal
946	139.5	5.9	576	2	S69214	extracellular seri
947	139.5	5.9	591	2	AC3528	hypothetical prote
948	139.5	5.9	653	2	T34356	steroid receptor p
949	139.5	5.9	746	2	B32693	hypothetical prote
950	139.5	5.9	845	2	D96799	hypothetical prote
951	139.5	5.9	900	2	B70694	probable intB - My
952	139.5	5.9	914	2	T08081	probable myrosinas
953	139.5	5.9	282	2	T16036	cuticle collagen c
954	139	5.9	294	2	T35892	hypothetical prote
955	139	5.9	328	2	T27644	hypothetical prote
956	139	5.9	328	2	G68499	protein K04G7.10 l
957	139	5.9	524	2	T27043	hypothetical prote
958	139	5.9	860	2	S43846	xyylanase B - rumen
959	139	5.9	1209	2	T13153	brhma associated
960	139	5.9	1279	2	A47363	RNA helicase A - h
961	139	5.9	1839	2	S77626	mannuronan C-5-epi
962	138.5	5.9	152	2	G36010	hypothetical expor
963	138.5	5.9	299	2	T05494	glycine-rich prote
964	138.5	5.9	469	2	T36097	probable ATP-bindi
965	138.5	5.9	576	1	S22453	colicin E7 (BC 3.1
966	138.5	5.9	735	2	T45059	hypothetical prote
967	138.5	5.9	859	2	D66502	hypothetical prote
968	138.5	5.9	949	2	D90803	Aida-I adhesin-lik
969	138.5	5.9	1005	2	H85611	probable adhesin Z
970	138.5	5.9	1111	2	T29070	hypothetical prote
971	138.5	5.9	1411	2	T48529	hypothetical prote
972	138.5	5.9	2441	2	D71623	erythrocyte membra
973	138	5.8	283	2	T19141	hypothetical prote
974	138	5.8	532	2	T35119	probable aminotran
975	138	5.8	640	2	T08179	LR05 protein - Chi
976	138	5.8	1087	2	T30844	serine-repeat anti
977	137.5	5.8	165	2	T03583	glycine-rich RNA-b
978	137.5	5.8	448	1	A56018	transcription fact



1125	131.5	5.6	479	2	A38307	metalloproteinase	1198	129	5.5	551	1	NRECE3	colicin E3 (EC 3.1
1126	131.5	5.6	510	2	T37541	probable glycolipid	1199	129	5.5	581	1	NDECE2	colicin E2 (EC 3.1
1127	131.5	5.6	520	2	AB1183	ATP-dependent RNA	1200	129	5.5	626	2	T01485	probable polygalact
1128	131.5	5.6	525	2	A35596	nuclear pore glyco	1201	129	5.5	632	2	T07587	probable polygalact
1129	131.5	5.6	589	2	AD2263	hypothetical prote	1202	129	5.5	670	2	F84540	hypothetical prote
1130	131.5	5.6	713	2	UC2534	RVG protein - fat	1203	129	5.5	707	2	A46302	PTB-associated spl
1131	131.5	5.6	940	2	D89723	protein F39D8.1b f	1204	129	5.5	895	2	AD0541	outer membrane flm
1132	131.5	5.6	945	2	T21998	hypothetical prote	1205	129	5.5	1442	2	T42607	transcription acti
1133	131.5	5.6	962	2	S03818	carboxymethylcellu	1206	129	5.5	1741	2	S74910	hemolysin - Synech
1134	131.5	5.6	1039	2	T35878	hypothetical prote	1207	129	5.4	157	1	S14857	glycine-rich prote
1135	131.5	5.6	1130	2	T33021	repetin - mouse	1208	128.5	5.4	271	2	A47156	hexamer-binding pr
1136	131.5	5.6	1704	2	T43141	vitellinogenin 1 - m	1209	128.5	5.4	401	2	A46423	engrailed homeodom
1137	131.5	5.6	1732	2	T43026	probable DNA-direc	1210	128.5	5.4	427	2	A33372	female-specific do
1138	131	5.5	180	2	UC7876	piron protein homo	1211	128.5	5.4	549	2	B32372	male-specific doub
1139	131	5.5	184	1	CGRT28	collagen alpha 2(I	1212	128.5	5.4	564	1	KRHUB8	keratin 6b, type I
1140	131	5.5	304	2	T16107	hypothetical prote	1213	128.5	5.4	564	2	I61771	keratin 6f, type I
1141	131	5.5	307	2	T37287	collagen 36 - Caen	1214	128.5	5.4	634	2	A54495	knob protein precu
1142	131	5.5	355	2	F71435	probable nuclear a	1215	128.5	5.4	710	2	T31502	hypothetical prote
1143	131	5.5	440	2	S71795	transcription fact	1216	128.5	5.4	1275	2	T49362	hypothetical prote
1144	131	5.5	485	2	B40552	bindin fertilizati	1217	128.5	5.4	1367	2	T13703	lamu protein - fru
1145	131	5.5	642	2	S27806	homeoic protein B	1218	128.5	5.4	1621	2	T30200	protein-tyrosine k
1146	131	5.5	653	1	S44749	COG64.2 protein -	1219	128	5.4	185	2	JC4085	glycine-rich cutic
1147	131	5.5	724	2	A48569	antigen Bml00 - Ei	1220	128	5.4	321	2	A36712	glycine-rich cutic
1148	131	5.5	728	2	S21913	BRcore-TMT1-Q1-Z1	1221	128	5.4	339	2	S20880	fibrillarlin [valid
1149	131	5.5	753	2	A27041	reverse transcript	1222	128	5.4	514	2	S21914	homeoic protein H
1150	131	5.5	1053	2	T07965	lysosine kinase-re	1223	128	5.4	547	2	S21914	BRcore-Z protein -
1151	131	5.5	1148	2	A71446	hypothetical prote	1224	128	5.4	547	2	C90842	partial probable a
1152	131	5.5	1332	2	T15670	hypothetical prote	1225	128	5.4	598	2	A84616	hypothetical prote
1153	131	5.5	2703	1	A24420	notch protein - fr	1226	128	5.4	606	2	A13367	Om(1D) protein - f
1154	130.5	5.5	163	2	UC6571	cold-inducible RNA	1227	128	5.4	640	2	A41726	homeoic protein B
1155	130.5	5.5	251	2	D96010	hypothetical expor	1228	128	5.4	733	2	S10932	probable protein k
1156	130.5	5.5	286	2	S34665	collagen, cuticula	1229	128	5.4	918	2	A88188	protein C189.3 f1
1157	130.5	5.5	369	2	S11980	variable major pro	1230	128	5.4	1870	2	S37671	MHC class III hist
1158	130.5	5.5	381	2	A54415	transcription fact	1231	128	5.4	1970	1	S21054	DNA-directed RNA p
1159	130.5	5.5	473	2	F70031	cell wall-binding	1232	128	5.4	2248	1	D42088	adenylate cyclase
1160	130.5	5.5	643	2	I50539	intermediate filam	1233	127.5	5.4	290	2	B88638	protein F58F6.2 f1
1161	130.5	5.5	748	2	T04011	hypothetical prote	1234	127.5	5.4	321	2	F60110	repetitive protein
1162	130.5	5.5	1036	1	A34755	nitrogen regulator	1235	127.5	5.4	325	2	T16324	hypothetical prote
1163	130.5	5.5	2154	2	F83068	hypothetical prote	1236	127.5	5.4	373	2	S43455	hypothetical prote
1164	130.5	5.5	2440	2	S39162	transcription coac	1237	127.5	5.4	550	1	F6RTA	fibrinogen alpha c
1165	130	5.5	123	2	C39777	hypothetical prote	1238	127.5	5.4	693	3	UC7925	nucleolin - common
1166	130	5.5	182	1	KRBO2A	keratin, 68k type	1239	127.5	5.4	817	2	T22442	hypothetical prote
1167	130	5.5	250	2	B35026	flaggrin B - mous	1240	127.5	5.4	827	2	JC4900	transferrin entry
1168	130	5.5	253	2	SS3618	major prion protei	1241	127.5	5.4	1641	2	T10955	early nodulin bind
1169	130	5.5	323	2	SS3619	major prion protei	1242	127.5	5.4	1872	2	S36152	MHC class II hist
1170	130	5.5	331	2	F70820	hypothetical glyci	1243	127.5	5.4	1940	2	F75393	hypothetical prote
1171	130	5.5	334	2	SS3490	RNA-binding protei	1244	127	5.4	228	2	T49891	glycine-rich prote
1172	130	5.5	448	2	S05355	hypothetical prote	1245	127	5.4	241	2	S71048	major prion protei
1173	130	5.5	563	2	A36054	mucin homolog - bo	1246	127	5.4	253	1	UWHU	major prion protei
1174	130	5.5	625	2	T41603	hypothetical prote	1247	127	5.4	253	2	SS3617	major prion protei
1175	130	5.5	635	2	T41603	alpha-amylase - fi	1248	127	5.4	253	2	SS3635	major prion protei
1176	130	5.5	676	2	S61977	transcription fact	1249	127	5.4	253	2	SS3614	major prion protei
1177	130	5.5	1618	2	S21424	nestin - human	1250	127	5.4	253	2	I37032	major prion protei
1178	130	5.5	1872	2	T30888	vitellinogenin - Ath	1251	127	5.4	253	2	I61847	major prion protei
1179	130	5.5	3705	2	AD0123	probable autotrans	1252	127	5.4	253	2	SS3616	major prion protei
1180	129.5	5.5	142	2	C33910	bal homeoic prote	1253	127	5.4	298	2	A40616	34k antigen - Myco
1181	129.5	5.5	287	2	T15779	hypothetical prote	1254	127	5.4	370	2	I57555	c-Maf protein - mo
1182	129.5	5.5	296	2	A31219	collagen I - Caeno	1255	127	5.4	378	1	OZQOAV	citruamporozoite p
1183	129.5	5.5	564	1	KRHU8A	keratin 6a, type I	1256	127	5.4	409	2	A70647	probable PPE prote
1184	129.5	5.5	666	2	T05432	hypothetical prote	1257	127	5.4	496	2	AS4770	N-acetylglucosam
1185	129.5	5.5	732	2	T08430	1-phosphatidylinos	1258	127	5.4	579	2	B83144	hypothetical prote
1186	129.5	5.5	900	2	B87957	protein Y1066D.7	1259	127	5.4	644	1	I40712	endo-1,4-beta-xyla
1187	129.5	5.5	948	2	T26417	hypothetical prote	1260	127	5.4	718	2	D84675	hypothetical prote
1188	129.5	5.5	1706	1	OYBRC	cyclolysin - Borde	1261	127	5.4	719	2	S61046	ARPI protein - yea
1189	129.5	5.5	4776	2	E95206	cell wall surface	1262	127	5.4	720	2	T51007	hypothetical prote
1190	129	5.5	155	2	S20846	glycine-rich prote	1263	127	5.4	748	2	S19652	cellohextrinase C
1191	129	5.5	156	2	S41771	glycine-rich RNA-b	1264	127	5.4	1145	2	G87288	hypothetical prote
1192	129	5.5	201	2	G01204	twist protein homo	1265	127	5.4	1705	2	SS1672	adenylate cyclase
1193	129	5.5	256	2	JU00268	major prion protei	1266	127	5.4	1787	2	AG1360	probable tape-meas
1194	129	5.5	256	2	S37149	prion protein - go	1267	126.5	5.4	301	2	T21314	hypothetical prote
1195	129	5.5	256	2	AS4281	major prion protei	1268	126.5	5.4	342	2	S18649	homeoic protein H
1196	129	5.5	323	2	S16318	homeoic protein H	1269	126.5	5.4	420	2	T14911	bZIP DNA-binding p
1197	129	5.5	456	1	KRHU5	keratin 15, type I	1270	126.5	5.4	590	2	A29904	keratin 5, type II

1271	126.5	5.4	742	2	JC7595	1344	124.5	5.3	1374	2	AE3259	extracellular seri
1272	126.5	5.4	764	2	H71607	1345	124.5	5.3	1613	2	T06678	hypothetical prote
1273	126.5	5.4	910	2	A34721	1346	124.5	5.3	2960	2	A45259	deemoyokin - human
1274	126.5	5.4	911	2	B34721	1347	124.5	5.3	3591	1	S21010	filamentous hemag
1275	126.5	5.4	929	2	C96623	1348	124	5.2	254	2	A34759	prion protein - Ch
1276	126.5	5.4	989	2	D89852	1349	124	5.2	285	2	T31503	hypothetical prote
1277	126.5	5.4	993	2	AE1905	1350	124	5.2	437	2	B90996	probable tail fibre
1278	126.5	5.4	2059	2	D82671	1351	124	5.2	452	1	EA9595	cyclokeratin 15 - m
1279	126.5	5.4	2142	2	B35098	1352	124	5.2	452	2	T30082	hypothetical prote
1280	126	5.3	144	2	S35716	1353	124	5.2	459	2	T45911	hypothetical prote
1281	126	5.3	199	2	S32224	1354	124	5.2	486	1	A57601	transcription fact
1282	126	5.3	284	2	A35419	1355	124	5.2	562	2	T49788	related to merzoi
1283	126	5.3	302	2	T15936	1356	124	5.2	580	2	S11890	serine proteinase
1284	126	5.3	305	2	S33690	1357	124	5.2	784	2	AC1091	5'-nucleotidase, p
1285	126	5.3	320	2	T09555	1358	124	5.2	787	2	T00798	hypothetical prote
1286	126	5.3	324	2	A31920	1359	124	5.2	856	2	T13159	ElB-55kDa-associat
1287	126	5.3	340	2	A83401	1360	124	5.2	1325	2	A64905	yedK protein - Bsc
1288	126	5.3	417	2	JC7092	1361	124	5.2	1360	2	T34302	cell polarity prot
1289	126	5.3	518	2	T23745	1362	124	5.2	1428	2	T13926	probable protein p
1290	126	5.3	622	2	AF0169	1363	124	5.2	4550	2	T18440	hypothetical prote
1291	126	5.3	720	2	T48302	1364	124	5.2	7463	2	T36248	Cdk peptide synthe
1292	126	5.3	910	2	S68983	1365	123.5	5.2	152	2	T07858	glycine-rich prote
1293	126	5.3	1022	2	T17406	1366	123.5	5.2	198	2	T06813	dehydrin 3 - garde
1294	126	5.3	1070	2	A10484	1367	123.5	5.2	260	2	S22373	proline-rich prote
1295	125.5	5.3	165	2	T03392	1368	123.5	5.2	280	2	T24454	hypothetical prote
1296	125.5	5.3	199	2	A15603	1369	123.5	5.2	310	2	T43147	hypothetical prote
1297	125.5	5.3	226	2	A53892	1370	123.5	5.2	369	1	TYFVAP	transforming prote
1298	125.5	5.3	222	2	T23966	1371	123.5	5.2	371	2	T36871	probable pseudori
1299	125.5	5.3	453	2	S18804	1372	123.5	5.2	378	2	D88042	protein F56D12.5 (
1300	125.5	5.3	627	2	T05789	1373	123.5	5.2	646	2	H96665	protein F22C12.10
1301	125.5	5.3	634	2	A28412	1374	123.5	5.2	651	2	S18874	nucleolin - Africa
1302	125.5	5.3	933	2	S41539	1375	123.5	5.2	730	2	T43317	ppl-1 protein - Ca
1303	125.5	5.3	936	2	F75622	1376	123.5	5.2	761	2	AI0074	probable autotrans
1304	125.5	5.3	960	1	A39651	1377	123.5	5.2	770	2	TS1024	related to C2H2 zi
1305	125.5	5.3	1148	2	S72635	1378	123.5	5.2	771	2	T29177	hypothetical prote
1306	125.5	5.3	1475	2	F86399	1379	123.5	5.2	1035	2	A84693	autotransporter pr
1307	125.5	5.3	1611	2	T06677	1380	123.5	5.2	1064	2	AD3203	outer membrane pro
1308	125	5.3	179	2	A85217	1381	123.5	5.2	1230	2	BE4664	ecdysone-induced p
1309	125	5.3	224	1	UHR1H	1382	123.5	5.2	1237	2	A34598	ecdysone-induced p
1310	125	5.3	254	2	B34759	1383	123.5	5.2	1237	2	B34598	mannuronan C-5-epi
1311	125	5.3	296	2	T24827	1384	123.5	5.2	1403	2	S77624	domancy-associate
1312	125	5.3	323	2	I51417	1385	123	5.2	129	2	T06256	glycine-rich prote
1313	125	5.3	338	2	T23006	1386	123	5.2	144	2	SA4984	glycine-rich prote
1314	125	5.3	343	2	A29319	1387	123	5.2	149	2	S04069	major prion PrP27-
1315	125	5.3	354	2	T06487	1388	123	5.2	257	2	A23545	probable secreted
1316	125	5.3	425	2	T11619	1389	123	5.2	318	2	T35213	anther-specific pr
1317	125	5.3	438	2	D90734	1390	123	5.2	321	2	S13550	protein C10G8.8 (I
1318	125	5.3	458	2	S62453	1391	123	5.2	385	2	H89046	probable tail fibre
1319	125	5.3	440	2	S37303	1392	123	5.2	407	2	G90907	keratin 12 - mouse
1320	125	5.3	466	2	T35164	1393	123	5.2	483	2	A55033	Balbini ring 1 pr
1321	125	5.3	509	2	T09572	1394	123	5.2	511	2	S24345	nucleoporin p62 -
1322	125	5.3	534	2	T33903	1395	123	5.2	522	2	S41819	MSHA biogenesis pr
1323	125	5.3	570	2	S56132	1396	123	5.2	559	2	G82326	probable polygalac
1324	125	5.3	635	2	F75477	1397	123	5.2	624	2	T02289	endo-1,4-beta-xyla
1325	125	5.3	642	1	S34416	1398	123	5.2	656	1	S59631	ISCC2, transposase
1326	125	5.3	712	2	B47021	1399	123	5.2	841	2	G87331	hypothetical prote
1327	125	5.3	943	2	JC4081	1400	123	5.2	902	2	T26775	hypothetical prote
1328	125	5.3	955	2	G64866	1401	123	5.2	1070	2	S75712	cellulase (EC 3.2.
1329	125	5.3	1315	2	T050300	1402	123	5.2	1334	2	T50568	calcium-binding pr
1330	124.5	5.3	177	2	S37749	1403	123	5.2	1560	2	T30282	hypothetical prote
1331	124.5	5.3	341	2	T22551	1404	122.5	5.2	160	2	T26289	hypothetical prote
1332	124.5	5.3	355	2	A33821	1405	122.5	5.2	296	2	B39581	GRSAG protein 9u
1333	124.5	5.3	360	2	G85014	1406	122.5	5.2	391	2	A49645	transcription fact
1334	124.5	5.3	458	2	T31631	1407	122.5	5.2	437	2	A55662	keratin 13, type I
1335	124.5	5.3	481	2	A26483	1408	122.5	5.2	532	2	B35621	spore germination
1336	124.5	5.3	516	2	AC1540	1409	122.5	5.2	626	2	F85295	hypothetical prote
1337	124.5	5.3	682	2	JC7670	1410	122.5	5.2	685	2	JC6331	rho-type guanine e
1338	124.5	5.3	687	2	F83671	1411	122.5	5.2	748	2	TS1738	RNA helicase RH3 (
1339	124.5	5.3	710	2	A31641	1412	122.5	5.2	867	2	T27136	hypothetical prote
1340	124.5	5.3	812	1	MMECOP	1413	122.5	5.2	871	2	T27135	hypothetical prote
1341	124.5	5.3	995	2	T32466	1414	122.5	5.2	930	2	D86546	polymorphic outer
1342	124.5	5.3	997	2	B71617	1415	122.5	5.2	930	2	D72078	polymorphic outer
1343	124.5	5.3	1262	2	T30524	1416	122.5	5.2	930	2	A81591	polymorphic membra

1417	122.5	5.2	1436	2	SS7238	forked protein 5.4
1418	122.5	5.2	1449	2	SS7237	forked protein 5.6
1419	122.5	5.2	1480	2	T05566	hypothetical prote
1420	122.5	5.2	1883	2	T13944	chromodomain helic
1421	122	5.2	157	2	S04536	embryonic abundant
1422	122	5.2	194	2	S33691	GAR1 protein - fls
1423	122	5.2	222	2	S19931	glycine-rich prote
1424	122	5.2	252	2	S16148	major prion protei
1425	122	5.2	253	2	SS3624	major prion protei
1426	122	5.2	253	2	SS3623	major prion protei
1427	122	5.2	253	2	SS3620	major prion protei
1428	122	5.2	253	2	SS3625	major prion protei
1429	122	5.2	253	2	S184423	major prion protei
1430	122	5.2	253	2	S71055	major prion protei
1431	122	5.2	265	2	A59141	silaffin sllp pre
1432	122	5.2	281	2	S26052	hypothetical prote
1433	122	5.2	281	2	T32921	hypothetical prote
1434	122	5.2	305	2	UC4525	nucleic acid-bind
1435	122	5.2	313	2	T33010	hypothetical prote
1436	122	5.2	392	2	B85436	homeotic protein e
1437	122	5.2	415	2	B85436	hypothetical prote
1438	122	5.2	428	2	S35215	sodium channel pro
1439	122	5.2	439	2	A85741	hypothetical prote
1440	122	5.2	473	2	UC4313	keratin 16, type I
1441	122	5.2	583	2	S56781	esterase D - pseud
1442	122	5.2	649	1	B37953	transcription regu
1443	122	5.2	660	2	A32378	probable ATP-depen
1444	122	5.2	667	2	A41311	transcription fact
1445	122	5.2	674	2	T05264	probable serine/th
1446	122	5.2	677	2	AC0303	conserved hypotet
1447	122	5.2	715	2	UC4908	alkaline serine pr
1448	122	5.2	785	2	AB1455	5'-nucleotidase, p
1449	122	5.2	989	2	A54505	serine-repeat anti
1450	122	5.2	1139	2	T33275	hypothetical prote
1451	122	5.2	1205	2	A55015	binetamide-sensiti
1452	122	5.2	1239	2	T13809	probable disintegr
1453	122	5.2	1908	2	T42707	hypothetical prote
1454	122	5.2	2150	2	S71629	sensory transducti
1455	122	5.2	2761	2	T29285	hypothetical prote
1456	121.5	5.1	220	2	S30977	gene 32 protein -
1457	121.5	5.1	320	2	F64909	hypothetical prote
1458	121.5	5.1	330	2	A40855	homeotic protein H
1459	121.5	5.1	339	2	T11751	transcription repr
1460	121.5	5.1	348	2	T29288	hypothetical prote
1461	121.5	5.1	390	2	T03241	G-box binding fact
1462	121.5	5.1	508	2	SS9870	fork head domain p
1463	121.5	5.1	633	2	H84854	probable ATP-depen
1464	121.5	5.1	759	2	C41843	pefD protein - Xan
1465	121.5	5.1	1159	2	S62562	probable nuclear p
1466	121.5	5.1	1325	1	S73723	probable lipoprote
1467	121.5	5.1	1603	2	S17983	gene posterior sex
1468	121	5.1	252	2	SS3634	major prion protei
1469	121	5.1	272	2	G71618	mezozyte surface
1470	121	5.1	301	2	A53570	collectin-43 - bov
1471	121	5.1	306	2	S08607	chorion protein s3
1472	121	5.1	324	2	T18763	hypothetical prote
1473	121	5.1	361	2	H90877	probable tail fibe
1474	121	5.1	380	2	S75348	hypothetical prote
1475	121	5.1	411	2	S15816	Brn-3.2 - mouse
1476	121	5.1	419	2	T36272	hypothetical prote
1477	121	5.1	493	2	A12314	hypothetical prote
1478	121	5.1	503	2	S31223	transcription fact
1479	121	5.1	503	2	G75262	hypothetical prote
1480	121	5.1	666	2	S15268	class A helix-loop
1481	121	5.1	795	2	T35688	probable-penicilli
1482	121	5.1	807	2	A34581	oxysterol-binding
1483	121	5.1	849	2	T20432	hypothetical prote
1484	121	5.1	967	2	H86334	T20H2.10 protein -
1485	121	5.1	1030	2	T16114	hypothetical prote
1486	121	5.1	1280	2	AB1981	hypothetical prote
1487	121	5.1	1697	2	T00079	hypothetical prote
1488	120.5	5.1	205	2	S19634	nucleolar protein
1489	120.5	5.1	252	2	JC6175	prion protein - ra

1490	120.5	5.1	280	2	H71320	hypothetical prote
1491	120.5	5.1	284	2	T28887	collagen dpy-10 -
1492	120.5	5.1	303	2	T28899	hypothetical prote
1493	120.5	5.1	360	2	G71444	hypothetical prote
1494	120.5	5.1	442	2	G84778	probable bZIP tran
1495	120.5	5.1	526	2	A56573	nuclear pore compl
1496	120.5	5.1	602	2	F84432	probable C2H2-type
1497	120.5	5.1	877	2	F90070	clumping factor B
1498	120.5	5.1	2399	2	H71879	toxin-like outer m
1499	120.5	5.1	4180	2	G83559	hypothetical prote
1500	120	5.1	126	2	S53786	collagen alpha cna

## ALIGNMENTS

## RESULT 1

B70807 hypothetical glycine-rich protein RV3512 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C:Accession: B70807

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: B70807

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1079 <COL>

A:Cross-references: UNIPARC:UPI00000D3AEA; GB:AL022022; GB:AL123456; NID:93261554; PIDN

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV3512

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match	19.1%	Score 450.5	DB 2	Length 1079
Best Local Similarity	30.5%	Pred. No. 9.8e-17		
Matches 139	Conservative 40	Mismatches 181	Indels 95	Gaps 15
17	GSGEAGPIQSGEBSSTNIGETLGH-----GLGDALSEGVKALIGKGAAGSKYSE	69		
336	GNNGAAGATAGSNAGCTGSAAGNGTGRGSGAGAGDGIQVGVGKGNAGDGEVGG	395		
70	ALGGSTREAVGTGVYQVPG-----FGAADALGNRVGEAAH-ALGNTHG	111		
396	AGGAG-----GSGPNTSPGNGNGGCGGCGGSGAGAAAGAGAGANTGAGCGGAGG	450		
112	ETGRQAEVDVIRHGDVAVRSGWGVPGHSGAMETSG-----GHGIFGSGGGLGG--QG	161		
451	TGGAAPASATVNGSGGCGAGTGDDGSGAGGTGAGTGAAGDGGGCGGAGCGAGG	510		
162	QGNPGGLGTPVWVHGVPGN-----SAGSFGMNPQGAIPVGGCGNGCPNFGTNTD-G	210		
511	QGGAGGAGGTGANG--GNITGTAGTACGAAAGAGGAGGCGGTGG-----GTGGGCG	564		
211	AVAQGVGVSRVANSQNEGCTNPPPSGGSGSSNSG-----GSGSGSGSGSGSG	258		
565	AGGDDGAGCTGDTGTGGGTVPAGSGGGGAGNAGGAGGAGGAGDGGSGGDDGAGTGANG	624		
259	SNGDNNNGSSSGSGSSSGSGSGSGSG--GSSGSGSGNAGSGRSDSGSSSGSSTGSS	317		
625	GNCGNRNBSNGTGGAGCGNGGAGGAGGAGGAGSGGCTGNGGAGGADADAANGNGCTG	684		
318	SGNTHGSG-----GANGHKPGCEKPGNEFARSGSGGIGTFRGGVSSNMREISREGNEL	372		
685	NGANGNGNGIAGMGNG-----GGAGTSSGNGGNGSGGANG-----GNAGM	724		
373	GGSGDNVRCGSSSGSGGDAVGVGNTVNSTSPG	407		

Db 725 GGNSTGTGGDGGAGGNGGAAAGTGTGGDLTGTG 759

## RESULT 2

A70934 Hypothetical glycine-rich protein Rv0578c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C:Accession: A70934

R: Cole, S.T.; Broesch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Fellous, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A: Reference number: A70500; MUID: 98295987; PMID: 9634230

A: Accession: A70934

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-1306 <COL>

A: Cross-references: UNIPROT: O53775; UNIPARC: UP100000DAFC8; GB: AL021942; GB: AL123456; NID

C: Genetics:

A: Experimental source: strain H37RV

C: Superfamily: collagen alpha 1(IV) chain

## Query Match

Best Local Similarity 18.6%; Score 439.5; DB 2; Length 1306;

Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

17 GSSEAGPLSGSEESTGTN-IGBALGHLGDLSEGVKAIGK-----EAGGAAGSKV 67

567 GHAAAL-----GVNGVGAAGHG-GD---PVGAGAGGCGSSSTPANKAPNTP 615

68 SEA-LGGTREAIVGTGVQVPGFPAADALGNRYGE-AAHALGNTGHE---IGRQAEV 120

616 TSGNGNGNGRGADATGFGGTGASGGRGDGLVGNAGAGAGNGSKGLPGLRLGNP- 674

121 IRRGALAVGSMGVGSHGAMETSGHGIFGSGGICGGC-----QGNPG 166

675 --GLDGTGTGNGAGAGSGGAMNGGTGAGGTGVTGSGSSDGVNCSAGADGHPG 731

167 GLGTPTVHVGPGNSAGSFGKNPQO---APWGGGNGPFPNFTN-----TOG 210

732 GTGAGVGTGKGGDGGDGAAPNGVAGSQCPGAGGCGGTGCGVGNCRGIDGADATAG 791

211 AVAQPVGYSVRASNONEGCTNP---PSGS---GGSSNSGCGSGSQSGSSGSGND 262

792 ARGQDGAAGAGGKGRGCTGPGGAGPAGTTTSGAGNGCGSGGTGDPDGGNGANS 851

263 --NNNGSSSGSSSGSSSGSSSGSSG-----GSS-----GSSGNSG----- 298

852 VFTNNIGTGGNGAGNAGPAGAGSGAGSTFGATGSSSIHVNGGNGNGNDHALSG 911

299 -GSRGDSGSSSWGSSSTGS--SGNHHGSG-----GANGHKPCCEKPNENARSGESGI 349

912 NGAGNGGNGGNGSLRGSGAGGHHGNGGNGNAGSGMGDDGTGAGGAGGAGGAGG 971

350 OGFRGCGVSNMREISKENR-----LIGSGDNYRGGSSGSGGDAVGV---NTVNS 402

972 GGGGGTGGDGNPAITGSGRGDGGVGGGGSVAAGGADGGRGAGGTGTGTRGTTGA 1031

403 ETSPEKFN 410

1032 TGATGTFD 1039

Db

RESULT 3

T49109

glycine-rich protein - Arabidopsis thaliana

N: Alternate names: protein AT4g22020

C: Species: Arabidopsis thaliana (mouse-ear cress)

C: Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C: Accession: T49109

R: Bevan, M.; Medler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.;

submitted to the Protein Sequence Database, May 2000

A: Reference number: Z25016

A: Accession: T49109

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-396 <BEV>

A: Cross-references: UNIPROT: O65450; UNIPARC: UP100000AABP9; EMBL: AL022140; GSPDB: GN00062

A: Experimental source: cultivar Columbia; BAC clone FIN20

C: Genetics:

A: Gene: ATSP:AT4g22020

A: Map position: 4

C: Superfamily: Phaseolus glycine-rich cell wall protein 1.8

## Query Match

Best Local Similarity 17.9%; Score 423; DB 2; Length 396;

Matches 133; Conservative 22; Mismatches 169; Indels 76; Gaps 14;

17 GSSEAGPLSGSEESTGTNIGBALGHLGDLSEGVKAIGKAGGAAGSKVSEALGQGT 76

63 GGGGGGGGGGEGDGYGHBGTGAGAGMSGTGVGGGGRGGEGSSANGSGHSSG 122

77 EAVGTGV-RQVPGFPAADALGNRYGEAAHALGNTGHEIGRQAEVIRHGAADAVRSGWGV 135

123 SGAGAGVGTGTGVTGGGGGGGGGGEGGSSGSGSH-----GSGSGA 164

136 PSHGAMETSGHGIFGSGGICGGCQCGCPGLTPTVHVGPGNSAGSFGKNPQAPMGQ 195

165 GAGAGVGGSSGAG--GGGGGGGGEGGAGANGSG--HG-----SGAGAGVGGAGAGV 214

196 GGNPGPFPNFTNIGAVAPGYSVRASNONEGCTNPSPSGGSSNSGSGSGSGSS 255

215 GGGG--GGGEGGAGANGSGSHS-----GSAAGGVSGAAGGGGGGGGG 258

256 GSGSN---GDNNGNSGSSSGSSSGSSSGSSSGSSSGSSSGSGSRDPSGSSWSGS 312

259 GSGGSKVGGYGHSSGFGGVTGFPNGSGGGGGGGGGGGGGGNGSG---YGSSTGYGS 314

313 STGSSGNGHSGGCGNGHKPCCEKPNENARSGES-GTQFRGCGVSNMREISKENRL 371

315 GMKRGSGGGGGGGGGGGGGGSGSGS--GSGRGYGMGAGGATG----- 356

372 LGSGDNYRGGSSWSG--GGDAVGG---VNTVNSPSP 406

357 NGGGGVTGFWGIGTIGTGGSGGAGTGTTLTGDKNSP 396

Db

RESULT 4

E70806

hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV)

C: Species: Mycobacterium tuberculosis

C: Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C: Accession: E70806

R: Cole, S.T.; Broesch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Fellous, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A: Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A: Reference number: A70500; MUID: 98295987; PMID: 9634230

A: Accession: E70806

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-1381 <COL>

A: Cross-references: UNIPARC: UP100000DAE7; GB: AL022022; GB: AL123456; NID: g3261554; PIDN

C: Genetics:

A: Experimental source: strain H37RV

C: Superfamily: collagen alpha 1(IV) chain

## Query Match

Best Local Similarity 17.6%; Score 415.5; DB 2; Length 1381;

Matches 133; Conservative 22; Mismatches 169; Indels 76; Gaps 14;

17 GSSEAGPLSGSEESTGTNIGBALGHLGDLSEGVKAIGKAGGAAGSKVSEALGQGT 76

63 GGGGGGGGGGEGDGYGHBGTGAGAGMSGTGVGGGGRGGEGSSANGSGHSSG 122

77 EAVGTGV-RQVPGFPAADALGNRYGEAAHALGNTGHEIGRQAEVIRHGAADAVRSGWGV 135

123 SGAGAGVGTGTGVTGGGGGGGGGGEGGSSGSGSH-----GSGSGA 164







A;Cross-references: UNIPARC:UPI00000DB07, GB:AL021841, GB:AL123456, NID:g3261517, PIDN:  
A;Experimental source: strain H37Rv  
C;Genetics:  
A;Gene: RV3345c  
C;Superfamily: collagen alpha 1(IV) chain

Query Match 16.9%; Score 400.5; DB 2; Length 1538;  
Best Local Similarity 32.4%; Pred. No. 5.7e-14;  
Matches 144; Conservative 41; Mismatches 175; Indels 85; Gaps 23;

QY 17 GSGRAGPLQSGEESTGTNIGALGHG--LGDALSF---GYCKALCKXKAGAGAKSVBEA 70  
DB 979 GSGAAGG--NGNNGSGSLNGGDA--GNGGNGGALNMQAFGTGKKGNGNGNGAG--MINGG 1035  
QY 71 LGQGTREAVGTGVRQVPG--FGAADALGNRVGEAAHALNTGHEITGRQAEVIRHGDADV 129  
DB 1036 LG--GFGAGAGGADVATTTGAGAGNGAGAFSTGLGPGAGGPGAGDPASVGVG 1094  
QY 130 GSWQGVPHSGAMETSGHGIFSGQGLGQGGQ--GNPGGLGT PWHVGY PGNASAGSFGMNP 188  
DB 1095 GA-----GGDGA-----GGVGFPGQGGIGEGRTGNGSG-----GDCGGISLGG 1138  
QY 189 QGAWGQGGNGGPNFGTNTGQAAVAQPRYGSVRASNONEGCTNPPSGSGGSSNSG--G 246  
DB 1139 NG---GLGNGGVSETFG--GAGANGGYGPGPEBNGGLGNGAGANGGVSTTGDDG 1193  
QY 247 GSGSGSSSGSGSN---GDNNGSSSG---GSSSGSSSGSSSGSGSGS-----289  
DB 1194 GAGKKGNGDGGVNGVGLGDDSGGAGANGGIGTIDAGAGAGAGAGAGGAGGSSKSTTTGNA 1253  
QY 290 -SGGSGSN-----SGSRDGSSEBSWSSSTGSSSGNHGSGGCGNGKPKCEKPNMEA 341  
DB 1254 GSGGAGNGGCTGMLNAG 1306  
QY 342 R--GSGSGTGGFFGQGVSNMREIS--KEGNRLIGSGGDN-----YKQGSWSGSG- 389  
DB 1307 TTGAGAGKGGNGSGAAGSGGVVVTAGHGNGGNGGNGGNGAGAGAGAGAGAGAGAG 1366  
QY 390 -----GDAVGVNTVNSERSPCM 408  
DB 1367 HGGGATGDDGNGGNGGNGSGNSTGV 1391

## RESULT 10

A70896  
hypothetical glycine-rich protein RV1091 - Mycobacterium tuberculosis (strain H37Rv)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 15-Sep-2003  
C;Accession: A70896  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: A70896  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-853 <COL>  
A;Cross-references: UNIPARC:UPI00000DF9A; GB:AL021897; GB:AL123456; NID:g3256022; PIDN:  
A;Experimental source: strain H37Rv  
C;Genetics:  
A;Gene: RV1091

Query Match 16.9%; Score 399.5; DB 2; Length 853;  
Best Local Similarity 31.2%; Pred. No. 3.8e-14;  
Matches 149; Conservative 30; Mismatches 187; Indels 111; Gaps 22;  
QY 17 GSGRAGPLQSGEESTGTNIGALGHGDLSEGVKAIGKAGAGASKVSSEALGGQTR 76  
DB 333 GGGGTGGLLFGNGAGAGH--GAAAGNL--AAGNVSSSGGAGAGGTG-----AGDGA 384

QY 77 EAVGTGVR-----QVFGAADALGNRVGE--AAHALNTGHEIGR-----Q 116  
DB 385 GAGAGNARLWGVGAG 444  
QY 117 AEDV-----RHAD-----AVRSGWQVPHSGAMETSGHGIFSGQGLGQ-----160  
DB 445 AAGLLVGTGCGGDDGAGAAVVKGDGGAAGTGT--AGAGRGGAGGSGSGGGGGGAA 503  
QY 161 -----GQNGPGLGT PWHVGY PGNASAGSFGMNP--PGAPWQGGNGGP-----ENF 204  
DB 504 GPAGMLPDDGAG 563  
QY 205 GTNTGQAVA--QPRYGSVRASNONEGCTN-----PPSGSGGSSNSG-----245  
DB 564 GAGGAGATAG 623  
QY 246 GSGSGSSSGSGS-----GSGDNNGSSSG--GSSSSSGSSSGSGSGSGSG-----291  
DB 624 GAGGDRGAGGTGFPISDGDGAGDGDGNGAGAGGTGTLFGAGAGNGGPGSGGGAADTGG 683  
QY 292 -GSGSGSGRDSSEBSWSSSTGSSSGNHGSGGCGN-----GHKPKCEKPNMEA- 341  
DB 684 NGAGNGGCTGNGG--NGSGGAGSGGDDGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 740  
QY 342 --RGSBSGTGGFFGQGVSNMREISKEGNRLIGSGGDNRYRQGSWSGSGGDAVVG 396  
DB 741 GGLGGSGTGLRLNGSGGDDGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795

## RESULT 11

A70807  
hypothetical glycine-rich protein RV3511 - Mycobacterium tuberculosis (strain H37Rv)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C;Accession: A70807  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: A70807  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-714 <COL>  
A;Cross-references: UNIPARC:UPI00000D3AE9; GB:AL022022; GB:AL123456; NID:g3261554; PIDN:  
A;Experimental source: strain H37Rv  
C;Genetics:  
A;Gene: RV3511  
C;Superfamily: elastin

Query Match 16.7%; Score 395; DB 2; Length 714;  
Best Local Similarity 29.9%; Pred. No. 5.7e-14;  
Matches 138; Conservative 28; Mismatches 169; Indels 126; Gaps 19;

QY 17 GSGRAGPLQSGEESTGTNIGEA---LGHGLDALSEGVKA--IGKAGAGASKVSSEAL 71  
DB 164 GSGGAG-----GTGAPGNGGNAAGMLYGRG-----GVGAGAGIGGGTGAGGH--AWLF 210  
QY 72 GQGTREAVGTGVRQVPGGADALGNRVGEAAHALNTGHEITGRQAEVIRHGDADVRS 131  
DB 211 GHGTTGIGGG---PG-----GNGGMLLNGGH-----GAGGIGGG 244  
QY 132 MQGVPHSGAMETSGHGIFSGGCG-----LGSGQGNPGLG-----T 170  
DB 245 SCGAGAGNGMLLNGGIGGAGGTGGAGAGTGGANAAMLLGGGTGGAGGIGGANGHGANG 304  
QY 171 PWHVGYPGNSAGSFGMNPQAPWQGVNGGPNFGTNTGQAAVAQPRYGSVRASNONEGCT 230  
DB 305 GMLLNGNGN--GGLGDDGPGGTGGHGGNGGNGPMLLTGTAAGGAGAGAGSTTACGSGGT 363  
QY 231 NPPSGSGGSGSNNG-----GSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGS 276





GenCore version 6.2  
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OM protein - protein search, using sw model

Run on: March 28, 2007, 21:02:50 ; Search time 349 Seconds

(without alignments)  
1351.676 Million cell updates/sec

Title: US-10-063-561-52

Perfect score: 2363  
Sequence: 1 MKRQGPLACLLALCLGSGE.....KLGFINMDAINKQRSSRIP 440

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2363	100.0	440	2 Q6UXC7 HUMAN	Q6UXC7 homo sapien
2	2098	88.8	398	2 Q32M66 HUMAN	Q32M66 homo sapien
3	2030	85.9	386	2 Q32M67 HUMAN	Q32M67 homo sapien
4	1996	84.5	476	2 Q6E0U4 HUMAN	Q6E0U4 homo sapien
5	1043	44.1	517	2 Q6E0U6 MOUSE	Q6E0U6 mus musculu
6	1038.5	43.6	508	2 Q6P253 MOUSE	Q6P253 mus musculu
7	1030	43.6	493	2 Q6S2J9 MOUSE	Q6S2J9 mus musculu
8	486	20.6	1553	2 Q6FPR0 CANGA	Q6FPR0 candida gla
9	471	19.9	1274	2 Q6CHN8 YARLI	Q6CHN8 yarrowia li
10	460.5	19.5	1938	2 Q7TWC0 MYCBO	Q7TWC0 mycobacteri
11	450.5	19.1	1079	2 Q6MW7 MYCTU	Q6MW7 mycobacteri
12	439.5	18.6	1306	2 Q7D9L6 MYCTU	Q7D9L6 mycobacteri
13	439.5	18.6	1306	2 Q6MX28 MYCTU	Q6MX28 mycobacteri
14	439.5	18.6	1306	2 Q7U107 MYCBO	Q7U107 mycobacteri
15	433	18.3	725	2 Q7SEB7 NEUCR	Q7SEB7 neurospora
16	430	18.2	1391	2 Q6C6W0 YARLI	Q6C6W0 yarrowia li
17	428.5	18.1	1143	2 Q54GV8 DICI1	Q54GV8 dictyosteli
18	428	18.1	528	2 Q63WJ8 BURPS	Q63WJ8 burkholderi
19	426.5	18.0	1815	2 Q6CF66 YARLI	Q6CF66 yarrowia li
20	426	18.0	512	2 Q6ZHK1 BURMA	Q6ZHK1 burkholderi
21	423	17.9	366	2 Q6S4S0 ARATH	Q6S4S0 arabidopsis
22	422.5	17.9	579	2 Q3EAC9 ARATH	Q3EAC9 arabidopsis
23	420.5	17.8	1384	2 Q8V1Z1 MYCTU	Q8V1Z1 mycobacteri
24	415.5	17.6	1381	2 Q6MMW9 MYCTU	Q6MMW9 mycobacteri
25	414	17.5	517	2 Q1BU84 BURK	Q1BU84 burkholderi
26	412.5	17.5	484	2 Q6MW11 MYCTU	Q6MW11 mycobacteri
27	412.5	17.5	1360	2 Q7TWC4 MYCBO	Q7TWC4 mycobacteri
28	412	17.4	636	2 Q3UV88 BURP1	Q3UV88 burkholderi
29	406	17.2	1901	1 FG54 MYCTU	FG54 mycobacteri
30	404.5	17.1	532	2 Q7D7F8 MYCTU	Q7D7F8 mycobacteri
31	403	17.1	1224	2 Q6CN84 KTULU	Q6CN84 kluyveromye

32	403	17.1	1489	2 Q6MMW6 MYCTU	Q6MMW6 mycobacteri
33	401	17.0	623	2 Q1SG97 GARAC	Q1SG97 deinopis sp
34	400.5	16.9	992	2 Q7TWB8 MYCBO	Q7TWB8 mycobacteri
35	400.5	16.9	1538	2 Q6MMY0 MYCTU	Q6MMY0 mycobacteri
36	399.5	16.9	853	2 Q7PFS5 MYCTU	Q7PFS5 mycobacteri
37	399	16.9	786	2 Q18740 CANPA	Q18740 canis famli
38	398	16.8	850	2 Q7U0P1 MYCBO	Q7U0P1 mycobacteri
39	397.5	16.8	743	2 Q6RHW0 MOUSE	Q6RHW0 mus musculu
40	397.5	16.8	763	2 Q7U0R0 MYCBO	Q7U0R0 mycobacteri
41	397.5	16.8	1217	2 Q8V1Y9 MYCTU	Q8V1Y9 mycobacteri
42	397.5	16.8	1460	2 Q7TWC3 MYCBO	Q7TWC3 mycobacteri
43	397.5	16.8	1507	2 Q8VJ23 MYCTU	Q8VJ23 mycobacteri
44	397	16.8	897	2 Q6Q294 AGRAP	Q6Q294 agelenopsis
45	396.5	16.8	1715	2 Q8V1Z0 MYCTU	Q8V1Z0 mycobacteri
46	395.5	16.7	1296	2 Q1U097 9MYCO	Q1U097 mycobacteri
47	395	16.7	714	2 Q6MMW8 MYCTU	Q6MMW8 mycobacteri
48	395	16.7	749	2 Q7TWC6 MYCBO	Q7TWC6 mycobacteri
49	395	16.7	1660	2 Q79FD4 MYCTU	Q79FD4 mycobacteri
50	395	16.7	1665	2 Q7D721 MYCTU	Q7D721 mycobacteri
51	393	16.6	626	2 Q7TWM2 MYCBO	Q7TWM2 mycobacteri
52	392.5	16.6	923	2 Q79FU3 MYCTU	Q79FU3 mycobacteri
53	392.5	16.6	923	2 Q7U0X8 MYCBO	Q7U0X8 mycobacteri
54	392	16.6	731	2 Q6MWX5 MYCTU	Q6MWX5 mycobacteri
55	392	16.6	775	2 Q79FP2 MYCTU	Q79FP2 mycobacteri
56	392	16.6	1329	2 Q8VJ15 MYCBO	Q8VJ15 mycobacteri
57	392	16.6	1408	2 Q8VK17 MYCTU	Q8VK17 mycobacteri
58	392	16.6	5263	1 F1RH BOMMO	F1RH bombyx mori
59	391.5	16.6	389	2 Q2AXE1 9ERACT	Q2AXE1 bacillus we
60	391	16.5	2249	2 Q9NHM4 NEPCU	Q9NHM4 nephila cia
61	390.5	16.5	635	2 Q8VK71 MYCTU	Q8VK71 mycobacteri
62	389.5	16.5	1408	2 Q7U022 MYCBO	Q7U022 mycobacteri
63	388	16.4	63	2 Q7TYG8 MYCBO	Q7TYG8 mycobacteri
64	387.5	16.4	619	2 Q91P09 EBVG	Q91P09 cyromolagus
65	387.5	16.4	796	2 Q62M2 MYCVN	Q62M2 mycobacteri
66	386.5	16.4	1302	2 Q1TH56 9MYCO	Q1TH56 mycobacteri
67	386.5	16.4	1302	2 Q1B5T5 9MYCO	Q1B5T5 mycobacteri
68	386	16.3	778	1 PG46 MYCBO	PG46 mycobacteri
69	385	16.3	778	1 PG46 MYCTU	PG46 mycobacteri
70	385.5	16.3	518	2 Q67WRO ORISA	Q67WRO oryza sativ
71	383.5	16.2	767	2 Q79FT0 MYCTU	Q79FT0 mycobacteri
72	383	16.2	641	1 EBNM1 EBV	E1BNM1 Epstein-Bar
73	383	16.2	641	2 Q777E1 EBVG	Q777E1 Epstein-Bar
74	382.5	16.2	738	2 Q4P459 USFMA	Q4P459 usf1ago ma
75	381.5	16.1	838	2 Q8VK15 MYCTU	Q8VK15 mycobacteri
76	381.5	16.1	741	2 Q79FP1 MYCTU	Q79FP1 mycobacteri
77	381.5	16.1	774	2 Q7U0P7 MYCBO	Q7U0P7 mycobacteri
78	381	16.1	390	2 Q9M3V2 MHBAT	Q9M3V2 triticum ae
79	380.5	16.1	563	2 Q39D10 BURS3	Q39D10 burkholderi
80	380.5	16.1	749	2 Q7D9D4 MYCTU	Q7D9D4 mycobacteri
81	380.5	16.1	837	2 Q79FY9 MYCTU	Q79FY9 mycobacteri
82	380.5	16.1	2401	2 Q7RFS2 PIAYO	Q7RFS2 plasmodium
83	380	16.1	850	2 Q1SG94 GARAC	Q1SG94 deinopis sp
84	379.5	16.1	628	2 Q8VJ19 MYCTU	Q8VJ19 mycobacteri
85	379.5	16.1	1618	2 Q6F010 CANGA	Q6F010 candida gla
86	379	16.0	465	1 GSR2 PHAYU	P14096 phaseolus v
87	379	16.0	1378	2 Q2U2U4 ASPOR	Q2U2U4 aspergillus
88	378.5	16.0	490	2 Q7VEP6 MYCBO	Q7VEP6 mycobacteri
89	378	16.0	588	2 Q6MMX7 MYCTU	Q6MMX7 mycobacteri
90	378	16.0	617	2 Q46172 NEPCU	Q46172 nephila cia
91	376.5	15.9	749	2 Q79FV7 MYCTU	Q79FV7 mycobacteri
92	375	15.9	914	1 MA22 MYCBO	P06687 mycobacteri
93	375	15.9	914	1 MA22 MYCTU	P06687 mycobacteri
94	374	15.8	831	2 Q7U2D6 MYCBO	P06686 mycobacteri
95	373.5	15.8	831	2 Q7TWC4 MYCBO	Q7TWC4 mycobacteri
96	373.5	15.8	584	2 Q7D580 MYCTU	Q7D580 mycobacteri
97	373.5	15.8	667	2 Q7D8M7 MYCTU	Q7D8M7 mycobacteri
98	373.5	15.8	667	2 Q79FT3 MYCTU	Q79FT3 mycobacteri
99	373.5	15.8	1382	2 Q6BN56 DBBHA	Q6BN56 debaryomyce
100	373	15.8	871	2 Q44358 NEPCU	Q44358 nephila cia
101	372	15.7	694	2 Q7D724 MYCTU	Q7D724 mycobacteri
102	372	15.7	909	2 Q7U1D3 MYCBO	Q7U1D3 mycobacteri
103	371.5	15.7	671	2 Q7U0R1 MYCBO	Q7U0R1 mycobacteri
104	371	15.7	400	2 Q8GTU0 ORISA	Q8GTU0 oryza sativ

105	371	15.7	615	2	Q6MX26_MYCTU	Q6mx26 mycobacteri	178	355	15.0	868	2	Q7U2D8_MYCBO	Q7u2d8 mycobacteri
106	371	15.7	615	2	Q7TXQ0_MYCBO	Q7txq0 mycobacteri	179	355	15.0	1087	2	Q59X60_HUMAN	Q59x60 candida alb
107	371	15.7	644	2	Q8MSM4_NEPCU	Q8msm4 nephila cla	180	354.5	15.0	316	2	Q5XKP8_HUMAN	Q5xkp8 homo sapien
108	371	15.7	747	1	SPD1_NEBCL	P19837 nephila cla	181	354.5	15.0	340	2	Q8LIE8_BACOR	Q8lie8 bacillus ce
109	370.5	15.7	491	2	Q79FF3_MYCTU	Q79ff3 mycobacteri	182	353	14.9	588	2	Q91P08_EBVG	Q91p08 cynomolgus
110	370.5	15.7	641	2	Q3KSS4_EBVG	Q3kss4 epstein-bar	183	353	14.9	624	2	Q7T2L0_MYCBO	Q7t2l0 mycobacteri
111	369.5	15.6	491	2	Q7U027_MYCBO	Q7u027 mycobacteri	184	352.5	14.9	384	1	GRP1_PERTHY	P09789 petunia hyb
112	369.5	15.6	795	2	Q7U020_MYCBO	Q7u020 mycobacteri	185	352	14.9	603	1	PG24_MYCTU	Q10637 mycobacteri
113	369.5	15.6	1428	2	Q44341_HALRU	Q44341 halictis ru	186	351.5	14.9	895	2	Q6FFM8_CANGA	Q6ffm8 candida gla
114	369	15.6	557	2	Q6BYD0_DEBHA	Q6byd0 debaryomyce	187	351	14.9	316	2	Q6FHY3_HUMAN	Q6fhy3 homo sapien
115	369	15.6	622	2	Q8VKX3_MYCTU	Q8vnx3 mycobacteri	188	351	14.9	957	1	PE03_MYCTU	P66877 mycobacteri
116	368	15.6	686	2	Q5B9E7_EMENI	Q5b9e7 emericella	189	350.5	14.8	461	2	Q79FC3_MYCTU	Q79fc3 mycobacteri
117	367.5	15.6	606	2	Q7U2C0_MYCBO	Q7u2c0 mycobacteri	190	350.5	14.8	476	2	Q79DM4_MYCTU	Q79dm4 mycobacteri
118	367.5	15.6	608	2	Q7U125_MYCBO	Q7u125 mycobacteri	191	350.5	14.8	879	2	Q8VKD2_MYCTU	Q8vkd2 mycobacteri
119	366.5	15.5	877	2	Q7U247_MYCBO	Q7u247 mycobacteri	192	350	14.8	316	1	LORI_HUMAN	P23490 homo sapien
120	366.5	15.5	4202	2	Q4IDY5_GIBZE	Q4idy5 gibberella	193	349.5	14.8	560	2	Q2HH46_CHABE	Q2hh46 chaetomium
121	366	15.5	408	2	Q43688_VIGIN	Q43688 vigna ungu	194	349	14.8	618	2	Q79F89_MYCTU	Q79f89 mycobacteri
122	366	15.5	538	2	Q4V506_DROME	Q4v506 dirosophila	195	349	14.8	882	2	Q79FV6_MYCTU	Q79fv6 mycobacteri
123	366	15.5	610	2	Q9V5V8_DROME	Q9v5v8 dirosophila	196	348	14.7	392	2	Q1SV89_MEDTR	Q1sv89 medicago tr
124	366	15.5	691	2	Q9BIU3_DOLTE	Q9biu3 dolomedes t	197	348	14.7	1065	2	Q206M2_9ARAC	Q206m2 latrodectus
125	365.5	15.5	496	2	Q79G09_MYCTU	Q79g09 mycobacteri	198	347.5	14.7	462	2	Q15G95_9ARAC	Q15g95 delinopsis sp
126	365.5	15.5	496	2	Q7U2U5_MYCBO	Q7u2u5 mycobacteri	199	347.5	14.7	464	2	Q77I83_MYCBO	Q77i83 mycobacteri
127	365.5	15.5	533	2	Q8VKR5_MYCTU	Q8vkr5 mycobacteri	200	347.5	14.7	544	2	Q46171_NEPCU	Q46171 nephila cla
128	365	15.4	576	2	P71664_MYCTU	P71664 mycobacteri	201	347	14.7	312	2	Q5T869_HUMAN	Q5t869 homo sapien
129	365	15.4	591	2	Q6MX50_MYCTU	Q6mx50 mycobacteri	202	347	14.7	570	2	Q25VM6_MYCVN	Q25vm6 mycobacteri
130	365	15.4	663	2	Q8VTC0_MYCTU	Q8vtc0 mycobacteri	203	346	14.6	648	2	Q9BIU7_ARGTR	Q9biu7 argyiope tri
131	364.5	15.4	524	2	Q817U1_9ARAC	Q817u1 araneus ven	204	346	14.6	974	1	GH42_CAEEL	Q96619 caenorhabdi
132	364.5	15.4	801	1	PG10_MYCTU	Q53810 mycobacteri	205	345.5	14.6	298	2	Q1S3H1_MEDTR	Q1s3h1 medicago tr
133	364.5	15.4	907	2	Q44359_NEPCU	Q44359 nephila cla	206	345	14.6	672	1	PHXR5_MOUSE	P08379 mus musculu
134	364	15.4	421	2	Q9DEY1_CYPCA	Q9dey1 cyprinus ca	207	345	14.6	966	1	FIBA1_PETMA	Q26174 petromyzon
135	364	15.4	606	2	Q79FV3_MYCTU	Q79fv3 mycobacteri	208	344.5	14.6	797	2	Q7UID4_MYCBO	Q7uid4 mycobacteri
136	364	15.4	609	2	Q8VKC5_MYCTU	Q8vkc5 mycobacteri	209	344	14.6	525	2	Q79FB3_MYCTU	Q79fb3 mycobacteri
137	364	15.4	626	2	Q9NWM1_9ARAC	Q9nwm1 nephila ina	210	344	14.6	651	2	Q9BIU9_ARGTR	Q9biu9 argyiope tri
138	364	15.4	1086	2	Q59XU0_CANAL	P27483 arabiidopsis	211	344	14.6	783	2	Q7D9C6_MYCTU	Q7d9c6 mycobacteri
139	363.5	15.4	349	1	GRP1_ARATH	Q97419 mycobacteri	212	344	14.6	783	2	Q79FW8_MYCTU	Q79fw8 mycobacteri
140	363	15.4	639	2	Q79FJ9_MYCTU	Q79fj9 mycobacteri	213	343.5	14.5	548	2	Q5JUN9_ORYSA	Q5jun9 oryza sativ
141	363	15.4	650	2	Q8VJM1_MYCTU	Q8vjm1 mycobacteri	214	343	14.5	538	2	Q7U2R0_MYCBO	Q7u2r0 mycobacteri
142	363	15.4	1114	2	Q6CCAL_YARLI	Q6ccal yarrowia li	215	342.5	14.5	636	5	Q16987_ARADI	Q16987 aradus dia
143	362.5	15.3	561	2	Q8VKR1_MYCTU	Q8vkr1 mycobacteri	216	342	14.5	515	1	BG34_MYCTU	Q9G0B5_GALME
144	362.5	15.3	2850	1	HORN_HUMAN	Q86y33 homo sapien	217	341.5	14.5	1468	2	Q681A9_ARATH	Q681a9 arabiidopsis
145	362.5	15.3	2850	2	Q5DIT0_HUMAN	Q5dit0 homo sapien	218	341	14.4	674	2	Q7U049_MYCBO	Q7u049 mycobacteri
146	362.5	15.3	2850	2	Q5UIF4_HUMAN	Q5ulf4 homo sapien	219	340.5	14.4	452	2	Q25UJ5_MYCVN	Q25uj5 mycobacteri
147	362	15.3	486	1	LORI_MOUSE	P18165 mus musculu	220	340	14.4	557	2	Q27DN7_MYCVN	Q27dn7 mycobacteri
148	361.5	15.3	339	2	Q4MOF5_BACCE	Q4mof5 bacillus ce	221	339.5	14.4	367	2	Q27DN7_MYCVN	Q27dn7 mycobacteri
149	361.5	15.3	422	2	Q6Z142_ORYSA	Q6z142 oryza sativ	222	339.5	14.4	487	2	Q79G08_MYCTU	Q79g08 mycobacteri
150	361	15.3	540	2	Q7TZI3_MYCBO	Q7tzi3 mycobacteri	223	339	14.3	614	2	Q9LH97_ARATH	Q9lh97 arathi
151	360.5	15.3	342	2	Q6HNZ6_BACHK	Q6hnz6 bacillus th	224	339	14.3	937	1	HYR1_CANAL	Q5ALC8_CANAL
152	360	15.2	562	2	Q79FQ7_MYCTU	Q79fq7 mycobacteri	225	339	14.3	937	2	Q5ALC8_CANAL	Q5alc8 candida alb
153	360	15.2	562	2	Q7U0B1_MYCBO	Q7u0b1 mycobacteri	226	338	14.3	429	2	Q817F9_9ARAC	Q817f9 araneus ven
154	360	15.2	586	2	Q7DBJ2_MYCTU	Q7dbj2 mycobacteri	227	337.5	14.3	2819	2	Q3XTQ2_9PROT	Q3xtq2 megalococc
155	359.5	15.2	340	2	Q63G11_BACCE	Q63g11 bacillus ce	228	337	14.3	270	2	Q700C3_ARATH	Q700c3 arabiidopsis
156	359.5	15.2	773	2	Q7U160_MYCBO	Q7u160 mycobacteri	229	337	14.3	290	2	Q7Y218_ARATH	Q7y218 arabiidopsis
157	359.5	15.2	1011	2	Q7DBJ7_MYCTU	Q7dbj7 mycobacteri	230	337	14.3	840	2	Q95YF6_PATYE	Q95yf6 patinopecte
158	359.5	15.2	1011	2	Q79FL8_MYCTU	Q79fl8 mycobacteri	231	337	14.3	1002	2	Q9BIU8_ARGTR	Q9biu8 argyiope tri
159	359.5	15.2	1018	2	Q7TZU3_MYCBO	Q7tzu3 mycobacteri	232	336.5	14.2	358	2	Q8VJ24_MYCTU	Q8vj24 mycobacteri
160	359	15.2	463	1	PG20_MYCTU	Q53416 mycobacteri	233	336	14.2	235	2	Q20V63_ORYSA	Q20v63 oryza sativ
161	359	15.2	854	2	Q9BIU4_DOLTE	Q9biu4 dolomedes t	234	336	14.2	1153	2	Q627B0_CAEER	Q627b0 caenorhabdi
162	358.5	15.2	486	2	Q9A8Z3_ORYSA	Q9a8z3 oryza sativ	235	335	14.2	581	2	Q7U1U2_MYCBO	Q7u1u2 mycobacteri
163	358.5	15.2	988	2	Q17434_NEPCU	Q17434 nephila cla	236	334.5	14.2	489	2	Q270G6_MYCVN	Q270g6 mycobacteri
164	358	15.2	359	2	Q6Z498_ORYSA	Q6z498 oryza sativ	237	334.5	14.2	531	2	Q6BZJ0_DEBHA	Q6bzj0 debaryomyce
165	358	15.2	641	2	Q1HVF7_EBVG	Q1hvf7 epstein-bar	238	334	14.1	255	2	Q9SIH2_ARATH	Q9sih2 arabiidopsis
166	358	15.2	764	2	Q868B4_CAEEL	Q868b4 caenorhabdi	239	334	14.1	284	2	Q73E49_BACCU	Q73e49 bacillus ce
167	357.5	15.1	966	2	Q2GSO1_CHABE	Q2gs01 chaetomium	240	334	14.1	498	1	PE33_MYCTU	Q50615 mycobacteri
168	357	15.1	760	2	Q6PY84_KUKHI	Q6py84 kuklicania	241	334	14.1	861	1	Q15G88_9ARAC	Q15g88 uloborus di
169	357	15.1	766	2	Q6CV63_KIUTA	Q6cv63 kluyveromyc	242	333.5	14.1	501	2	Q66R21_MYCBO	Q66r21 mycobacteri
170	357	15.1	1713	2	Q2MOY7_DROPS	Q2moy7 dirosophila	243	333	14.1	466	2	Q7TZG4_MYCTU	Q7tzg4 mycobacteri
171	357	15.1	1884	2	Q9NHM2_9ARAC	Q9nhm2 nephila ina	244	332.5	14.1	342	2	Q9VKR8_DROME	Q9vkr8 dirosophila
172	356	15.1	281	2	Q22843_CAEEL	Q22843 caenorhabdi	245	332.5	14.1	356	2	Q6NYS8_DROME	Q6nys8 dirosophila
173	356	15.1	603	2	Q7U079_MYCBO	Q7u079 mycobacteri	246	332.5	14.1	491	1	PE36_MYCBO	Q6a689 mycobacteri
174	355.5	15.0	924	2	Q6ORH5_CAEER	Q6orh5 caenorhabdi	247	332.5	14.1	501	2	Q7TZH0_MYCBO	Q7tzh0 mycobacteri
175	355	15.0	291	2	Q39337_BRANA	Q39337 brassica na	248	332.5	14.1	563	2	Q6J6N0_9ARAC	Q6j6n0 araneus ven
176	355	15.0	831	2	Q7U159_MYCBO	Q7u159 mycobacteri	249	332.5	14.1	1197	2	Q2KPB7_CAEER	Q2kpb7 caenorhabdi
177	355	15.0	831	2	Q7U159_MYCBO	Q7u159 mycobacteri	250	332.5	14.1	1197	2	Q2KPB7_CAEER	Q2kpb7 caenorhabdi

251	331.5	14.0	493	2	Q1LAU6_PALME	Q1LAU6_ralstonia m	324	308.5	13.1	251	2	Q0UEV7_YARLI	Q0UEV7_yarrowia li
252	331.5	14.0	622	2	Q8VKJ6_MYCTU	Q8VKJ6_mycobacteri	325	308.5	13.1	2639	2	Q67R86_ANTPE	Q67R86_anttheraea p
253	330.5	14.0	919	2	Q5AL03_CANAL	Q5AL03_candida alb	326	308	13.0	271	2	Q08529_TOBAC	Q08529_nicotiana t
254	330	14.0	447	2	Q0BIV1_ARGAU	Q0BIV1_argiole aur	327	308	13.0	1042	2	Q5CHW4_CRYHO	Q5CHW4_cryptospori
255	330	14.0	513	2	Q61067_PLACH	Q61067_plasmodium	328	308	13.0	2496	1	HORN_MOUSE	HORN_mouse
256	329.5	13.9	504	2	Q7TXZ9_MYCBO	Q7TXZ9_mycobacteri	329	307	13.0	526	2	Q6WEQ9_ARLYL	Q6WEQ9_arabidopsi
257	329.5	13.9	2174	2	Q6CD35_YARLI	Q6CD35_yarrowia li	330	306.5	13.0	419	1	CSP_PLACM	CSP_placm
258	329	13.9	549	2	Q19318_CABEL	Q19318_caenorhabdi	331	306.5	13.0	572	2	Q3WTH7_GPRITZ	Q3WTH7_grietz
259	326	13.8	552	2	Q25VK3_MYCVN	Q25VK3_mycobacteri	332	306.5	13.0	639	2	Q54M35_DICTED	Q54M35_dictyosteli
260	325.5	13.8	439	2	Q6MWY6_MYCTU	Q6MWY6_mycobacteri	333	306.5	13.0	904	2	Q76271_MYTED	Q76271_mytilus edu
261	325.5	13.8	452	2	Q91M52_ARATH	Q91M52_arabidopsis	334	306	12.9	284	2	Q21073_CABEL	Q21073_caenorhabdi
262	325.5	13.8	905	2	Q4XV89_PLACH	Q4XV89_plasmodium	335	306	12.9	752	2	Q4XQTE_PLACH	Q4XQTE_plasmodium
263	325.5	13.8	2391	2	Q5D862_HUMAN	Q5D862_homo sapien	336	306	12.9	1034	2	Q6FX23_CANCA	Q6FX23_candida gla
264	324.5	13.7	460	2	Q278J9_MYCFV	Q278J9_mycobacteri	337	305.5	12.9	267	2	Q61417_BACAN	Q61417_bacillus an
265	324.5	13.7	1198	2	Q206M1_PARAC	Q206M1_lactrodectus	338	305.5	12.9	343	2	Q8FUS3_ARATH	Q8FUS3_arabidopsi
266	324.5	13.7	1458	2	Q910B9_ONCMY	Q910B9_oncorhynch	339	305.5	12.9	405	2	Q7PWP8_ANOGA	Q7PWP8_anopheles g
267	324	13.7	258	2	Q2XQA3_MAIZE	Q2XQA3_zea mays (m	340	305.5	12.9	511	2	Q91333_PGAMA	Q91333_cercopithe
268	323.5	13.7	436	2	Q8VIX6_MYCTU	Q8VIX6_mycobacteri	341	305.5	12.9	902	2	Q16161_MYTED	Q16161_mytilus edu
269	323.5	13.7	1729	2	Q9VIR6_DROME	Q9VIR6_drosophila	342	305.5	12.9	905	2	Q8MW55_MYTGA	Q8MW55_mytilus gal
270	323	13.7	268	2	Q9FIQ2_ARATH	Q9FIQ2_arabidopsis	343	305.5	12.9	922	2	Q8MW53_MYTGA	Q8MW53_mytilus gal
271	323	13.7	7342	2	Q3XS91_PPROT	Q3XS91_magnetococc	344	305	12.9	404	2	Q6C7V4_YARLI	Q6C7V4_yarrowia li
272	322.5	13.6	355	2	Q7VEL2_MYCBO	Q7VEL2_mycobacteri	345	305	12.9	494	2	Q15G93_PARAC	Q15G93_dainopsis sp
273	322	13.6	1169	2	Q21535_CABEL	Q21535_caenorhabdi	346	305	12.9	597	2	Q60Y26_CABBR	Q60Y26_caenorhabdi
274	321.5	13.6	431	2	Q692G4_NEPCU	Q692G4_nephila cia	347	304	12.9	1024	2	Q5DU15_PARTE	Q5DU15_parnecium
275	321.5	13.6	646	2	Q61QV1_CABBR	Q61QV1_caenorhabdi	348	303.5	12.8	1884	2	Q7S737_NEUCR	Q7S737_neurospora
276	321	13.6	697	2	Q5YZX6_NOCFA	Q5YZX6_nocardia fa	349	303	12.8	246	2	Q5Z412_ORYSA	Q5Z412_oryza sativ
277	320.5	13.6	756	2	Q8J1W4_CLAPU	Q8J1W4_claviceps p	350	302	12.8	678	2	Q93486_ONCMY	Q93486_oncorhynch
278	320.5	13.6	1071	2	Q7YU48_DROME	Q7YU48_drosophila	351	302	12.8	426	2	Q8Y293_PALSO	Q8Y293_ralstonia s
279	320.5	13.6	1713	2	Q9VIR6_DROME	Q9VIR6_drosophila	352	302	12.8	592	2	Q9PF60_XYLFA	Q9PF60_xyella fas
280	320.5	13.6	2069	2	Q2VLR2_PARAC	Q2VLR2_mycobacteri	353	301.5	12.7	285	2	Q69TW7_ORYSA	Q69TW7_oryza sativ
281	320	13.5	594	2	Q6MX30_MYCTU	Q6MX30_mycobacteri	354	301	12.7	152	2	Q32M65_HUMAN	Q32M65_homo sapien
282	320	13.5	620	1	RESIL_DROME	Q9V7U0_drosophila	355	301	12.7	388	2	Q7SXQ3_BRARE	Q7SXQ3_brachydantio
283	320	13.5	668	2	Q4X874_PLACH	Q4X874_plasmodium	356	301	12.7	485	1	CSP_PLABR	CSP_plabr
284	320	13.5	1778	2	Q1GY83_METPL	Q1GY83_methylobacti	357	301	12.7	1157	2	Q2LIT8_BORAI	Q2LIT8_borali
285	320	13.5	1953	2	Q9BIT7_PARAC	Q9BIT7_nephila ina	358	300.5	12.7	623	1	K1C9_HUMAN	K1C9_homo sapien
286	319.5	13.5	1424	2	Q54QY4_DICDI	Q54QY4_dicyosteli	359	300	12.7	166	2	Q3F4R6_9BURK	Q3F4R6_burkholderi
287	319.5	13.5	1493	2	Q3E9M3_ARATH	Q3E9M3_arabidopsis	360	300	12.7	170	2	Q32W62_HUMAN	Q32W62_homo sapien
288	318	13.5	301	2	Q4X9Y1_PLACH	Q4X9Y1_plasmodium	361	300	12.7	555	2	Q2H458_CHAGB	Q2H458_chaetomium
289	318	13.5	1464	2	Q6P9I2_XENLA	Q6P9I2_xenopus lae	362	300	12.7	661	2	Q2VLR1_ARGTR	Q2VLR1_argiole tri
290	317	13.4	495	2	Q46Q49_PALEJ	Q46Q49_ralstonia e	363	300	12.7	738	2	Q02402_PINPU	Q02402_pinctea fu
291	317	13.4	2655	2	Q664F4_ANTYA	Q664F4_antheraea y	364	299.5	12.7	1346	2	Q8BUU3_ONCKE	Q8BUU3_oncorhynch
292	316.5	13.4	419	2	Q4DILA3_TRYCR	Q4DILA3_trypanosoma	365	300	12.7	490	2	Q6V5D8_OLIPU	Q6V5D8_olimarabido
293	316	13.4	546	2	Q7TY98_MYCBO	Q7TY98_mycobacteri	366	299.5	12.7	618	2	Q8C1S9_RAT	Q8C1S9_rattus norv
294	316	13.4	1036	2	Q6FX21_CANCA	Q6FX21_candida gla	367	299.5	12.7	2199	2	Q4UTZ8_RICPE	Q4UTZ8_rickettsia
295	315	13.3	256	2	Q2XQA2_MAIZE	Q2XQA2_zea mays (m	368	299.5	12.7	3199	2	Q26638_STRPU	Q26638_streptomyce
296	315	13.3	302	2	Q9SL09_ARATH	Q9SL09_arabidopsis	369	299	12.7	280	2	Q7XUDU_ORYSA	Q7XUDU_oryza sativ
297	315	13.3	462	2	Q3NHM3_NEPCU	Q3NHM3_nephila cia	370	299	12.7	373	2	Q9BIT9_PARAC	Q9BIT9_lactrodectus
298	314.5	13.3	543	1	PG44_MYCTU	Q50630_mycobacteri	371	299	12.7	1077	2	Q175A1_AEDAE	Q175A1_aedes aegypt
299	314	13.3	259	2	Q2XQA4_MAIZE	Q2XQA4_zea mays (m	372	299	12.7	1292	2	Q4ITHD_GIBZE	Q4ITHD_gibberella
300	314	13.3	387	2	Q7XU17_LYCES	Q7XU17_lycopersisico	373	298.5	12.6	210	2	Q41187_ARATH	Q41187_arabidopsis
301	314	13.3	387	2	Q692G3_NEPCU	Q692G3_nephila cia	374	298.5	12.6	250	2	Q1S3N0_MEDTR	Q1S3N0_medicago tr
302	314	13.3	521	2	Q6V5C3_CARAS	Q6V5C3_cardamomops	375	298.5	12.6	262	2	Q8MYJ1_DICTED	Q8MYJ1_dicyosteli
303	314	13.3	906	2	Q15G92_PARAC	Q15G92_dainopsis sp	376	298.5	12.6	262	2	Q551Z1_DICTED	Q551Z1_dicyosteli
304	313.5	13.3	582	2	Q2GPM9_CHAGB	Q2GPM9_chaetomium	377	298.5	12.6	284	2	Q94C18_LYCES	Q94C18_lycopersisico
305	313.5	13.3	3659	2	Q98LNE_RHILIO	Q98LNE_rhizobium l	378	298.5	12.6	381	2	Q4XDC6_PLACH	Q4XDC6_plasmodium
306	313	13.2	1016	2	Q15G91_PARAC	Q15G91_dainopsis sp	379	298.5	12.6	485	2	Q88M46_9CAUD	Q88M46_cyanophagu
307	313	13.2	1249	2	Q59X47_CANAL	Q59X47_candida alb	380	298.5	12.6	922	2	Q44367_MYTED	Q44367_mytilus edu
308	313	13.2	1449	2	Q910C0_ONCMY	Q910C0_oncorhynch	381	298.5	12.6	2174	2	Q92UB8_RHIME	Q92UB8_rhizobium m
309	312.5	13.2	252	1	GRPI_PHAUV	Q10495_phaseolus v	382	298	12.6	214	2	Q6PY82_KUKHI	Q6PY82_kukulcania
310	312.5	13.2	452	2	Q5ARI3_EMENT	Q5ARI3_emeritella	383	298	12.6	2359	2	Q81519_PLAF7	Q81519_plasmodium
311	312	13.2	691	2	Q5PLP2_AZOSE	Q5PLP2_azocarcus sp	384	297.5	12.6	270	2	Q7XDR4_ORYSA	Q7XDR4_oryza sativ
312	312	13.2	691	2	Q4LHC2_PBURK	Q4LHC2_burkholderi	385	297.5	12.6	681	2	Q61QD5_CABBR	Q61QD5_caenorhabdi
313	312	13.2	1680	2	Q4IAH2_GIBZE	Q4IAH2_gibberella	386	296.5	12.5	429	2	Q812V8_NEUCR	Q812V8_neurospora
314	311.5	13.2	795	2	Q61CK9_CABBR	Q61CK9_caenorhabdi	387	296.5	12.5	480	2	Q551D0_DICTED	Q551D0_dicyosteli
315	310.5	13.1	607	2	Q23B00_TETTH	Q23B00_tetrahymena	388	296.5	12.5	480	2	Q8RT215_DICTED	Q8RT215_dicyosteli
316	310.5	13.1	775	2	Q6BGP1_DEBHA	Q6BGP1_debaryomyce	389	296.5	12.5	486	2	Q54KD5_DICTED	Q54KD5_dicyosteli
317	310	13.1	321	2	Q69XV3_ORYSA	Q69XV3_oryza sativ	390	296.5	12.5	637	2	Q2VLR3_PARAC	Q2VLR3_lactrodectus
318	310	13.1	551	2	Q25VVS_MYCVN	Q25VVS_mycobacteri	391	296.5	12.5	855	2	Q5TUR4_ANOGA	Q5TUR4_anopheles g
319	310	13.1	4248	2	Q43DN2_9CHLB	Q43DN2_chlorobium	392	296.5	12.5	1047	2	Q7UNU7_RHOBA	Q7UNU7_rhodospirella
320	309.5	13.1	265	2	Q69K59_ORYSA	Q69K59_oryza sativ	393	296	12.5	486	2	Q8PAP6_HORVU	Q8PAP6_hordewum cui
321	309.5	13.1	509	2	Q7TYG7_MYCBO	Q7TYG7_mycobacteri	394	296	12.5	627	1	SPD2_NEPCU	SPD2_nephila cia
322	309	13.1	454	2	Q8VUD7_MYCTU	Q8VUD7_mycobacteri	395	296	12.5	1124	2	Q6C7C1_YARLI	Q6C7C1_yarrowia li
323	309	13.1	515	2	Q4G1V2_PARAC	Q4G1V2_lactrodectus	396	296	12.5	1450	2	Q91TB4_CYNPY	Q91TB4_cynops pyrr

397	295.5	12.5	859	2	Q267B3_MYCVN	Q267b3_mycobacteri	470	283	12.0	1198	2	Q99PM6_MOUSE	Q99pm6_mus musculus
398	295.5	12.5	894	2	Q8MM54_MYTGA	Q8mm54_mytillus gal	471	283	12.0	1198	2	Q924G8_MOUSE	Q924g8_mus musculus
399	295.5	12.5	1285	2	Q4MX6_BACCE	Q4mx6_bacillus ce	472	283	12.0	1260	2	Q7TSJ9_MOUSE	Q7tsj9_mus musculus
400	295	12.5	1352	2	Q8UTU4_ONCKE	Q8utu4_oncohychnu	473	283	12.0	1346	2	Q801M5_XENLA	Q801m5_xenopus lae
401	294.5	12.5	614	2	Q87AH4_XYLFT	Q87ah4_xylella fas	474	283	12.0	1736	2	Q80TJ5_MOUSE	Q80tj5_mus musculus
402	294.5	12.5	1352	2	Q5NT95_PAROL	Q5nt95_parallelchry	475	283	12.0	1976	2	Q99PB3_MOUSE	Q99pb3_mus musculus
403	294	12.4	248	2	Q7Y215_ARATH	Q7y215_arabidopsi	476	283	12.0	2087	2	Q6D1C6_MOUSE	Q6d1c6_mus musculus
404	294	12.4	373	2	Q4WLVA_ASPFU	Q4wlva_aespergillus	477	282.5	12.0	666	2	Q3R8A9_XYLFA	Q3r8a9_xylella fas
405	294	12.4	1293	2	Q216N3_9DELT	Q216n3_uncultured	478	282.5	12.0	666	2	Q3RGH3_XYLFA	Q3rggh3_xylella fas
406	294	12.4	1356	1	Q01A2_ONCMY	Q01a2_oncohychnu	479	282.5	12.0	1447	2	Q91B91_XENLA	Q91b91_xenopus lae
407	293.5	12.4	222	2	Q7XDV2_ORYSA	Q7xdv2_oryza sativ	480	282	11.9	338	2	Q60354_HUMAN	Q60354_homo sapien
408	293.5	12.4	333	2	Q25VM4_MYCVN	Q25vm4_mycobacteri	481	282	11.9	394	2	Q7SHJ4_NEUCR	Q7shj4_neutrospora
409	293.5	12.4	586	2	Q9VHM5_DROME	Q9vhm5_drosophila	482	282	11.9	400	1	RFOA_DICDI	P546h1_dictyosteli
410	293.5	12.4	794	2	P93560_SAGSA	P93560_sagittaria	483	282	11.9	543	2	Q9LYO9_ARATH	Q9lyo9_arabidopsi
411	293	12.4	256	2	Q79FHH2_MYCTU	Q79fhh2_mycobacteri	484	281.5	11.9	185	1	G8P2_ORYSA	P298h3_oryza sativ
412	293	12.4	257	2	Q81Z75_BACAN	Q81z75_bacillus an	485	281.5	11.9	1147	2	Q733CI_BACCI	Q733ci_bacillus ce
413	293	12.4	542	2	Q4G1Y1_PARAC	Q4g1y1_lactodectus	486	281	11.9	821	2	Q7PZ88_ANOGA	Q7pzb8_anopheles g
414	292.5	12.4	421	2	Q7PXP5_ANOGA	Q7pxp5_anopheles g	487	281	11.9	1150	1	MOCAP_PIG	P12021_sus scrofa
415	292.5	12.4	707	2	Q61869_MOUSE	Q61869_mus musculu	488	281	11.9	1439	2	Q97406_HALDI	Q97406_haliotis di
416	292	12.3	912	2	Q9BIR2_PLETR	Q9bir2_plectreurys	489	281	11.9	1463	2	Q4W6W6_GCHON	Q4w6w6_raja kenje
417	291.5	12.3	367	2	Q86KL5_DICDI	Q86kl5_dictyosteli	490	280.5	11.9	325	2	Q4XND7_PLACH	Q4xnd7_plasmodium
418	291.5	12.3	357	2	Q55AD6_DICDI	Q55ad6_dictyosteli	491	280.5	11.9	476	2	Q80890_CHV12	Q80890_cercopithec
419	291.5	12.3	502	2	Q9ZTR5_HORVU	Q9ztr5_hordum vul	492	280.5	11.9	1449	2	Q6NZ15_BRARE	Q6nzt5_brachydantio
420	291	12.3	332	2	Q3TF92_MOUSE	Q3tf92_mus musculu	493	280	11.8	444	2	Q9BIU6_ARGTR	Q9biu6_argiope tri
421	291	12.3	821	2	Q8VPM9_9MICC	Q8vpm9_micrococcus	494	280	11.8	1380	1	DXH3_MOUSE	Q701j3_mus musculu
422	290.5	12.3	274	2	Q7OIN7_ANOGA	Q7oin7_anopheles g	495	280	11.8	1466	1	Q03A1_HUMAN	P02461_homo sapien
423	290.5	12.3	406	2	Q825Z4_STRAM	Q825z4_streptomyce	496	280	11.8	1466	2	Q53S91_HUMAN	O53s91_homo sapien
424	290.5	12.3	707	2	Q3TTF5_MOUSE	Q3ttf5_m_10 days n	497	280	11.8	1466	2	Q541P8_HUMAN	Q541p8_homo sapien
425	290.5	12.3	1109	2	Q3YQW8_PARTE	Q3yqwm8_parmecium	498	280	11.8	2362	2	Q5CQ07_CRYPV	Q5cq07_cryptospori
426	290.5	12.3	1387	1	TROP_HUMAN	Q12816_homo sapien	499	279.5	11.8	1046	2	Q640B2_XENTR	Q640b2_xenopus tro
427	290	12.3	543	2	Q43302_ARATH	Q43302_arabidopsi	500	279.5	11.8	1449	2	Q5TR04_ANOGA	Q5tr04_anopheles g
428	290	12.3	751	2	Q7M3J9_RIPPA	Q7m3j9_riftia pach	501	279	11.8	452	2	Q5TR04_ANOGA	Q5tr04_anopheles g
429	290	12.3	1435	2	Q4LIR7_GBURK	Q4lij7_burkholderi	502	279	11.8	1096	2	Q5A2Y2_CANAL	Q5a2y2_candida alb
430	290	12.3	1435	2	Q1B6G4_GBURK	Q1b6g4_burkholderi	503	278.5	11.8	225	2	Q5SNV5_CRYNE	Q5snv5_cryptococcu
431	289.5	12.3	533	2	Q94FQ4_ARATH	Q94fq4_arabidopsi	504	278.5	11.8	526	1	FUS_HUMAN	Q5KBY1_CRYNE
432	289.5	12.3	559	2	Q1DEA0_MYXXA	Q1deo0_myxococcus	505	278.5	11.8	526	2	Q5KBY1_CRYNE	Q5kby1_cryptococcu
433	289.5	12.3	3069	2	Q2G505_NOVAD	Q2g505_novosphingo	506	278.5	11.8	526	2	Q5KBY1_CRYNE	Q5kby1_cryptococcu
434	289	12.2	1414	2	Q26634_STRPU	Q26634_strongyloce	507	278.5	11.8	526	2	Q5KBY1_CRYNE	Q5kby1_cryptococcu
435	288.5	12.2	477	2	Q11U73_MCIEL	Q11j73_acidobacter	508	278.5	11.8	929	2	Q5NBJ3_DROME	Q5nbj3_drosophila
436	288.5	12.2	499	2	Q6C268_YARLI	Q6c268_yarrowia li	509	278.5	11.8	929	2	Q5NBJ3_DROME	Q5nbj3_drosophila
437	288.5	12.2	538	2	Q13344_HUMAN	Q13344_homo sapien	510	278.5	11.8	939	2	Q5NHQ0_DROME	Q5nhq0_drosophila
438	288.5	12.2	543	2	Q94FF0_ARATH	Q94ff0_arabidopsi	511	278.5	11.8	939	2	Q5NBJ3_DROME	Q5nbj3_drosophila
439	288	12.2	1051	2	Q6MU51_BDEBA	Q6mj51_bdellovibri	512	278.5	11.8	978	2	Q6BLF5_DEBHA	Q6blf5_debaryomyce
440	288	12.2	1962	2	Q873R2_EMENT	Q873r2_emeritella	513	278.5	11.8	2280	2	Q5VBR6_DROME	Q5vbr6_drosophila
441	287.5	12.2	185	2	Q6PY83_KUKHI	Q6py83_kukulcania	514	278.5	11.8	2302	2	Q5N693_DROME	Q5n693_drosophila
442	287.5	12.2	2363	2	Q6ALH2_DESPS	Q6alh2_desulfocale	515	278.5	11.8	2407	2	Q1QIX3_NITHX	Q1qix3_nitrobacter
443	287	12.1	483	2	Q3EDB7_ARATH	Q3edb7_arabidopsi	516	278	11.8	220	2	Q39367_BRAOL	Q39367_brassica ol
444	287	12.1	2795	2	Q70BL5_PARLI	Q70bl5_parencroto	517	278	11.8	270	2	Q61764_MOUSE	Q61764_mus musculu
445	287	12.1	13288	2	Q18758_PIG	Q18758_sus scrofa	518	278	11.8	290	2	Q2CA03_9RHO8	Q2ca03_oceanicola
446	286.5	12.1	857	2	Q6RHX3_9HYME	Q6rhx3_dinocampus	519	278	11.8	1447	2	Q6PAU1_BRARE	Q6pau1_brachydantio
447	286	12.1	399	2	Q7ZXJ3_XENLA	Q7zxj3_xenopus lae	520	278	11.8	2219	2	Q6P405_USTMA	Q6p405_ustillego ma
448	286	12.1	497	2	Q22112_TETTH	Q22112_tetrahymena	521	277.5	11.7	230	2	Q7XDU2_ORYSA	Q7xd2_oryza sativ
449	286	12.1	533	2	Q94FP9_ARATH	Q94fp9_arabidopsi	522	277.5	11.7	621	2	Q8VJK6_MYCTU	Q8vjk6_mycobacteri
450	286	12.1	563	2	Q9BIR5_9ARAC	Q9bir5_nephila ina	523	277.5	11.7	1378	2	Q97405_HALDI	Q97405_haliotis di
451	286	12.1	594	2	Q212L9_TETTH	Q212l9_tetrahymena	524	277.5	11.7	1449	2	Q802B5_XENLA	Q802b5_xenopus lae
452	286	12.1	2112	2	Q9VEL9_DROME	Q9vel9_drosophila	525	277.5	11.7	1449	2	Q6PXR9_BRARE	Q6pxr9_brachydantio
453	285.5	12.1	1370	2	Q6C3B8_YARLI	Q6c3b8_yarrowia li	526	277	11.7	226	2	Q24568_MAIZE	Q24568_zea mays (m
454	285	12.1	227	2	Q6ZBR3_ORYSA	Q6zbr3_oryza sativ	527	277	11.7	335	2	Q61H99_DROME	Q61h99_drosophila
455	285	12.1	250	2	Q92PB4_RHIME	Q92pb4_rhizobium m	528	277	11.7	370	2	Q2GPI7_CHAGB	Q2gpi7_chaetomium
456	284.5	12.0	481	2	Q1GV78_9SPHN	Q1gv78_sphingomyxi	529	277	11.7	1355	1	Q01A2_RANCA	Q01a2_rana catesb
457	284.5	12.0	844	2	Q51UC1_CIOIN	Q51uc1_ciona intes	530	277	11.7	1447	2	Q6UIJ5_BRARE	Q6uij5_brachydantio
458	284	12.0	293	2	Q9DEX9_CYPCA	Q9dex9_cyprinus ca	531	276.5	11.7	682	2	Q22537_CAERL	Q22537_caenorhabdi
459	284	12.0	236	2	Q6Z495_ORYSA	Q6z495_oryza sativ	532	276.5	11.7	748	2	Q636W5_BACCC	Q636w5_bacillus ce
460	284	12.0	543	2	Q94FQ0_ARATH	Q94fq0_arabidopsi	533	276.5	11.7	1372	1	Q01A2_RAT	Q01a2_rattus norv
461	283.5	12.0	379	2	Q692G2_NEPCL	Q692g2_nephila cla	534	276.5	11.7	2175	2	Q47JH7_DECAR	Q47jh7_dechloromon
462	283	12.0	248	2	Q21XW8_HOHP	Q21xw8_rhodofexia	535	276.5	11.7	2332	2	Q6ALH4_DESPS	Q6alh4_desulfocale
463	283	12.0	464	2	Q7XDI5_ORYSA	Q7xd5_oryza sativ	536	276	11.7	1366	2	Q7Z5S6_HUMAN	Q7z5s6_homo sapien
464	283	12.0	464	2	Q9FWK8_ORYSA	Q9fwk8_oryza sativ	537	276	11.7	1366	2	Q51577_HUMAN	Q51577_homo sapien
465	283	12.0	655	2	Q2IN11_ANADE	Q2in11_aanaeromyxob	538	276	11.7	1447	2	Q5NT96_PAROL	Q5nt96_parallelchry
466	283	12.0	689	2	Q8BSKO_MOUSE	Q8bsko_mus musculu	539	276	11.7	1553	2	Q387F2_9TRYP	Q387f2_trypanosoma
467	283	12.0	1051	2	Q26055_PARLI	Q26055_parencroto	540	275.5	11.7	423	2	Q7PXF0_ANOGA	Q7pxf0_anopheles g
468	283	12.0	1160	2	Q9MUN1_MOUSE	Q9mun1_mus musculu	541	275.5	11.7	1976	2	Q412S1_GIBBEZ	Q412s1_gibberella
469	283	12.0	1160	2	Q8R564_MOUSE	Q8r564_mus musculu	542	275	11.6	193	2	Q7YMO8_CABEL	Q7ym8_caenorhabdi



543	275	11.6	950	2	Q9VK59_DROME	Q9VK59_drosophila	616	267	11.3	320	2	Q4MFS1_BACCE	Q4MFS1_bacillus ce
544	275	11.6	1156	1	GLH4_CAEEL	Q76743 caenorhabdi	617	266.5	11.3	259	2	Q615C9_CAEBR	Q615C9 caenorhabdi
545	274.5	11.6	929	1	Q9NGW5_DROME	Q9ngw5 drosophila	618	266.5	11.3	561	1	Q615C9_CAEBR	Q615C9 caenorhabdi
546	274.5	11.6	1376	2	Q7SSB8_NEUCR	Q7ssb8 neurospora	619	266.5	11.3	987	2	Q89C58_BRALJA	Q89C58 bradyrhizob
547	274.5	11.6	1399	2	Q4SB89_TETNG	Q4sb89 tetraodon n	620	266	11.3	243	2	Q98DS7_RHIL0	Q98ds7 rhizobium l
548	274	11.6	429	2	Q6OR78_CAEBR	Q6or78 caenorhabdi	621	266	11.3	343	2	Q8SK59_DROME	Q8sk59 drosophila
549	274	11.6	443	2	Q2DL96_DELT	Q2dl96 geobacter u	622	266	11.3	586	2	Q9BDM2_LEPIN	Q9bdm2 leptospira
550	274	11.6	460	2	Q6COR1_YARLI	Q6cor1 yarrowia li	623	266	11.3	683	2	Q9PDW2_XYLFA	Q9pdw2 xyloella fas
551	274	11.6	593	1	KIC10_HUMAN	P1645 homo sapien	624	266	11.3	1088	2	Q69UP6_ORRSA	Q69up6 oryza sativ
552	274	11.6	730	2	Q9ZUJ3_ARATH	Q9zuJ3 arabidopsis	625	265.5	11.2	175	2	Q91SN6_ARATH	Q91sn6 arabidopsi
553	274	11.6	1025	2	Q4N1K0_THERP	Q4n1k0 theileria p	626	265.5	11.2	265	2	Q69PC6_ORRSA	Q69pc6 oryza sativ
554	274	11.6	1676	2	Q3JMU6_TERTH	Q3jmu6 tetrahymena	627	265.5	11.2	461	2	Q6V5F7_9BRAS	Q6v5f7 pinella ma
555	274	11.6	3016	2	P73590_SYNY3	P73590 synchocyst	628	265.5	11.2	568	2	Q9N1J8_YBLVA	Q9n1j8 pinctada m
556	273.5	11.6	544	2	Q2GRY1_XANP2	Q2gry1 xanthobacte	629	265.5	11.2	614	2	Q7TYR8_MYCBO	Q7tyr8 mycobacteri
557	273	11.6	485	2	Q22XP9_TERTH	Q22xp9 tetrahymena	630	265.5	11.2	615	2	Q7D7A1_MYCTU	Q7d7a1 mycobacteri
558	273	11.6	790	2	Q2OR13_ORYSA	Q2or13 oryza sativ	631	265	11.2	331	2	Q692G6_NEUCR	Q692g6 neurospora
559	273	11.6	1168	2	Q6HP99_BACHK	Q6hp99 bacillus th	632	265	11.2	380	2	Q17QLE_BOVIN	Q17qle bovin
560	273	11.6	1491	2	Q7ZTW4_XENLA	Q7ztw4 xenopus lae	633	265	11.2	717	2	Q75FL0_LEPIC	Q75fl0 leptospira
561	273	11.6	1491	2	Q91718_XENLA	Q91718 xenopus lae	634	265	11.2	1119	2	Q75DC8_ASHGO	Q75dc8 ashbya gos
562	272.5	11.5	405	2	Q2TM01_PLAVI	Q2tm01 plasmodium	635	265	11.2	2256	2	Q5CV62_CRYPV	Q5cv62 cryptospori
563	272.5	11.5	604	2	Q9L252_STRCO	Q9l252 streptomyce	636	264.5	11.2	297	2	Q7XDU7_ORYSA	Q7xdw7 oryza sativ
564	272.5	11.5	1241	2	Q3TUE2_MOUSE	Q3tue2 mus musculu	637	264.5	11.2	536	1	FAEB_PIRRO	FAEB_PIRRO
565	272.5	11.5	1372	1	COL1A2_MOUSE	Q01149 mus musculu	638	264.5	11.2	1820	2	Q91907_PAGMA	Q91907 pagrus majo
566	272.5	11.5	1372	2	Q3TX57_MOUSE	Q3tx57 m osteoclas	639	264	11.2	227	2	Q84W21_ARATH	Q84w21 arabidopsi
567	272.5	11.5	1372	2	Q3TUE4_MOUSE	Q3tue4 mus musculu	640	264	11.2	267	2	Q245T1_TERTH	Q245t1 tetrahymena
568	272.5	11.5	1445	2	Q93251_PANCA	Q93251 rana cateab	641	264	11.2	741	2	Q6RCF4_9CAUD	Q6rcf4 vibrio phage
569	272.5	11.5	2104	2	Q8IKG1_PLAF7	Q8ikg1 plasmodium	642	264	11.2	818	2	Q812V5_BACCR	Q812v5 bacillus ce
570	272.5	11.5	2310	2	Q9G9A9_DROME	Q9g9a9 drosophila	643	264	11.2	1163	2	Q8N6U4_HUMAN	Q8n6u4 homo sapien
571	272	11.5	375	1	SAINT_PLAFV	P05959 plasmodium	644	263.5	11.2	548	2	Q1TX12_9MYCO	Q1tx12 mycobacteri
572	272	11.5	1925	2	Q4DD65_TREYCR	Q4dd65 trypanosoma	645	263.5	11.2	548	2	Q1TXN3_9MYCO	Q1txn3 mycobacteri
573	271.5	11.5	370	2	Q79FP0_MYCTU	Q79fp0 mycobacteri	646	263.5	11.2	548	2	Q1B433_9MYCO	Q1b433 mycobacteri
574	271.5	11.5	370	2	Q7U007_MYCBO	Q7u007 mycobacteri	647	263.5	11.2	561	2	Q7W721_BORPA	Q7w721 borrelia
575	271.5	11.5	375	2	Q7D8E3_MYCTU	Q7d8e3 mycobacteri	648	263.5	11.2	763	1	Q5Y770_9TRYR	Q5y770 strongyloe
576	271.5	11.5	594	2	Q3R7F1_XYLFA	Q3r7f1 xyloella fas	649	263.5	11.2	1017	2	Q5Y770_9TRYR	Q5y770 strongyloe
577	271.5	11.5	1366	1	COL1A2_HUMAN	P08123 homo sapien	650	263.5	11.2	1412	2	Q8WUP5_HYDAT	Q8wup5 hydat atten
578	271	11.5	681	2	Q8YTC9_ANASP	Q8ytc9 anabaena sp	651	263.5	11.2	1418	2	Q9W7R9_CYNPY	Q9w7r9 cynops pyrr
579	271	11.5	1364	1	COL1A2_BOVIN	P02465 bos taurus	652	263.5	11.2	2147	2	Q96M68_RHIL0	Q96m68 rhizobium l
580	270.5	11.4	360	2	Q7TYPI_MYCBO	Q7typi mycobacteri	653	263	11.1	435	2	Q7Z152_CAEEL	Q7z152 caenorhabdi
581	270.5	11.4	1027	1	CAEF_RIPPA	P30754 riftia pach	654	263	11.1	486	2	Q292N1_DROPS	Q292n1 drosophila
582	270.5	11.4	1079	2	Q3VYG8_PACTO	Q3vyg8 frankia sp.	655	263	11.1	907	2	Q26312_STRPU	Q26312 strongyloe
583	270	11.4	726	2	Q1IUZ9_ACTIBL	Q1iuZ9 acidobacter	656	263	11.1	1097	2	Q6C029_YARLI	Q6c029 yarrowia li
584	270	11.4	854	2	Q09238_9METZ	Q09238 pseudocorti	657	262.5	11.1	1752	2	Q07265_STRPU	Q07265 strongyloe
585	270	11.4	1035	2	Q76C74_YEAST	Q76c74 saccharomyc	658	262.5	11.1	410	2	Q7ZUB3_BRARE	Q7zue3 brachydantio
586	270	11.4	1366	2	Q6N964_RHOPA	Q6n964 rhodopsendo	659	262.5	11.1	645	2	Q79FM4_MYCTU	Q79fm4 mycobacteri
587	270	11.4	1463	1	CO3A1_FAT	P13941 rattus norv	660	262.5	11.1	645	2	Q7U1IC_MYCBO	Q7u1ic mycobacteri
588	270	11.4	1713	2	Q8TGB1_YEAST	Q8tgb1 saccharomyc	661	262.5	11.1	646	2	Q7D9B9_MYCTU	Q7d9b9 mycobacteri
589	270	11.4	1844	2	Q7S6Q1_NEUCR	Q7s6q1 neurospora	662	262.5	11.1	685	2	Q61G02_RAT	Q61g02 rat
590	269.5	11.4	360	2	Q9BIU0_GARAC	Q9biu0 latrodectus	663	262.5	11.1	860	2	Q5CCT7_CRYPV	Q5cct7 cryptospori
591	269.5	11.4	443	2	Q9GUB4_GALME	Q9gub4 galliera me	664	262.5	11.1	1049	1	CO3A1_BOVIN	CO3A1_BOVIN
592	269.5	11.4	690	2	Q3RGA4_9BURK	Q3rga4 burkholderi	665	262.5	11.1	1157	2	Q1YTS6_9GAMM	Q1yts6 marine gamm
593	269.5	11.4	960	2	Q5S3U0_ANOGA	Q5s3u0 anopheles g	666	262.5	11.1	1464	2	Q3UHT2_MOUSE	Q3uht2 mus musculu
594	269	11.4	361	2	Q79FE6_MYCTU	Q79fe6 mycobacteri	667	262	11.1	245	2	Q6HYG2_DEBHA	Q6hyg2 debaryomyce
595	269	11.4	382	2	Q7D777_MYCTU	Q7d777 mycobacteri	668	262	11.1	1549	2	Q48105_PSE14	Q48105 pseudomonas
596	269	11.4	410	2	Q16988_ARADI	Q16988 araneus dia	669	262	11.1	1434	2	Q60444_CRIGR	Q60444 circulella
597	269	11.4	422	2	Q80K33_BRARE	Q80k33 brachydantio	670	262	11.1	2757	2	Q248X6_TERTH	Q248x6 tetrahymena
598	269	11.4	1025	2	Q7MTW0_BORER	Q7mtw0 bordetella	671	261.5	11.1	410	2	Q5UX77_HALMA	Q5ux77 halotartula
599	268.5	11.4	259	2	Q02049_CAEEL	Q02049 caenorhabdi	672	261.5	11.1	605	2	Q7PSS5_ANOGA	Q7pss5 anopheles g
600	268.5	11.4	323	2	Q6BC34_PATYE	Q6bc34 patinopecte	673	261.5	11.1	815	2	Q632M4_BACZ	Q632m4 bacillus ce
601	268.5	11.4	557	2	Q8BQ46_MOUSE	Q8bq46 mus musculu	674	261.5	11.1	1396	2	Q2C9U2_9RHOB	Q2c9u2 oceanicola
602	268.5	11.4	584	2	Q6CAS0_YARLI	Q6cas0 yarrowia li	675	261.5	11.1	2038	1	FSH_DROME	FSH_DROME
603	268.5	11.4	900	2	Q1MSC6_LAMIP	Q1msc6 lawsonia in	676	261	11.0	232	2	Q3ESF2_BACTI	Q3esf2 bacillus th
604	268.5	11.4	2615	2	Q2G6U5_NOVAD	Q2g6u5 novosphingo	677	261	11.0	249	2	Q4FGL0_USTMA	Q4fgl0 uestilago ma
605	268	11.3	193	2	Q59E78_DROME	Q59e78 drosophila	678	261	11.0	967	2	Q5CQR3_CRYPV	Q5cqr3 cryptospori
606	268	11.3	241	2	Q6I1W5_DROME	Q6i1w5 drosophila	679	260.5	11.0	1226	2	Q7UL12_RHOBA	Q7ul12 rhodopirell
607	268	11.3	647	2	Q6HS19_BACAN	Q6hs19 bacillus an	680	260.5	11.0	1033	2	Q4UBV8_THEAN	Q4ubv8 theileria a
608	268	11.3	870	2	Q6FPN0_CANGA	Q6fpn0 candida gla	681	260.5	11.0	1321	2	Q72Z02_BACCL	Q72z02 bacillus ce
609	268	11.3	1055	2	Q6HCR4_BACHK	Q6hcr4 bacillus th	682	260	11.0	359	2	Q81G99_DROME	Q81g99 drosophila
610	268	11.3	1275	2	Q5CTD3_CRYPV	Q5ctd3 cryptospori	683	260	11.0	595	2	Q2WQ09_CLOBE	Q2wq09 clostridium
611	268	11.3	1746	2	Q2G5V5_CHAGB	Q2g5v5 chaetomium	684	260	11.0	730	2	Q26052_PARLI	Q26052 paracentritum
612	267.5	11.3	429	2	Q76966_PODCA	Q76966 podocoryne	685	260	11.0	1366	1	COL1A2_CANFA	COL1A2_CANFA
613	267.5	11.3	871	2	Q5CZV2_BRARE	Q5czv2 brachydantio	686	260	11.0	1486	2	Q7ZT16_XENLA	Q7zt16 xenopus lae
614	267.5	11.3	1207	2	Q9PVF5_BRARE	Q9pvf5 brachydantio	687	260	11.0	1486	2	Q91717_XENLA	Q91717 xenopus lae
615	267.5	11.3	1536	2	Q4T4H8_TETNG	Q4t4h8 tetraodon n	688	259.5	11.0	261	2	Q9ZWM2_CUCSA	Q9zwm2 cucumis bet



689	259.5	11.0	399	2	Q9B1T8_PARAC	Q9b1t8 latrodectus	762	255	10.8	769	2	Q4PAD8_USTWA	Q4pad8 utiilago ma
690	259.5	11.0	476	2	Q4CL13_TRYCR	Q4cl13 trypanosoma	763	255	10.8	853	2	Q40YF4_KINRA	Q40yf4 kinococcus
691	259.5	11.0	487	2	Q412R4_GIBBEA	Q412r4 gibberella	764	255	10.8	1052	2	Q7Y2B4_PLACH	Q7y2b4 plasmodium
692	259.5	11.0	1170	2	Q3MG99_PACTO	Q3mg99 frankia sp.	765	255	10.8	1526	2	Q5KTT4_DROME	Q5ktt4 drosophila
693	259.5	11.0	1186	1	SER11_BOMBO	P07856 bombyx mori	766	254.5	10.8	131	2	Q4LH45_9BURK	Q4lh45 burkholderi
694	259.5	11.0	1222	2	Q8K173_MOUSE	Q8k173 mus musculus	767	254.5	10.8	273	2	Q3M2W9_ANAVT	Q3m2w9 anabena va
695	259.5	11.0	1464	1	CO3A1_MOUSE	P08121 mus musculus	768	254.5	10.8	413	2	Q8IME3_DROME	Q8ime3 drosophila
696	259.5	11.0	1464	2	Q7T732_MOUSE	Q7t732 mus musculus	769	254.5	10.8	496	2	Q7KRL6_DROME	Q7krl6 drosophila
697	259.5	11.0	1464	2	Q8BKX2_MOUSE	Q8bkx2 mus musculus	770	254.5	10.8	502	2	Q7KRL7_DROME	Q7krl7 drosophila
698	259.5	11.0	1464	2	Q8BLM4_MOUSE	Q8blm4 mus musculus	771	254.5	10.8	673	2	Q4BBU6_BURVI	Q4bbu6 burkholderi
699	259.5	11.0	1464	2	Q3TV15_MOUSE	Q3tv15 m osteoclas	772	254.5	10.8	700	2	Q8CTI9_MOUSE	Q8cti9 mus musculus
700	259.5	11.0	1467	2	Q5DTG2_MOUSE	Q5dtg2 mus musculus	773	254.5	10.8	966	2	Q5CKR2_CRYHO	Q5ckr2 cryptospori
701	259	11.0	263	2	Q6ZL79_ORYSA	Q6zl79 oryza sativ	774	254.5	10.8	1981	2	Q56B16_RICBE	Q56b16 rickettsia
702	259	11.0	441	2	Q26062_PLAMA	Q26062 plasmodium	775	254.5	10.8	1981	2	Q1RK84_RICBR	Q1rk84 rickettsia
703	259	11.0	517	2	Q8CRQ9_MOUSE	Q8crq9 mus musculus	776	254	10.7	932	2	Q52P73_PARAC	Q52p73 latrodectus
704	259	11.0	684	2	P90679_ARENA	P90679 arenicola m	777	254	10.7	1419	1	CO2A1_FAT	P05538 rictus norv
705	259	11.0	886	2	Q9VXR7_DROME	Q9vkr7 drosophila	778	254	10.7	1487	2	Q14047_HUMAN	Q14047 homo sapien
706	259	11.0	1000	2	Q4XNS3_PLACH	Q4xns3 plasmodium	779	254	10.7	1487	2	Q1JUQ2_HUMAN	Q1jqh2 homo sapien
707	259	11.0	1132	2	Q3W4W4_PACTO	Q3w4w4 frankia sp.	780	254	10.7	1745	1	CO5A3_HUMAN	P25940 homo sapien
708	259	11.0	3145	2	Q9BMG7_RHITO	Q9bm7 rhizobium 1	781	254	10.7	1747	2	Q26640_STRPU	Q26640 strongyloce
709	258.5	10.9	1309	2	Q4XOM2_PLACH	Q4xom2 plasmodium	782	253.5	10.7	396	2	CO3136_PLAST	CO3136 plasmodium
710	258.5	10.9	1309	2	Q812M4_BACCR	Q812m4 bacillitox	783	253.5	10.7	401	1	CSP_PLACG	CSP_PLACG
711	258	10.9	138	2	Q964C4_ENCCU	Q964c4 encephalito	784	253.5	10.7	509	2	Q875B1_PODAN	Q875b1 podospora a
712	258	10.9	208	2	Q9ZRV2_CICAR	Q9zrv2 cicier ariet	785	253.5	10.7	539	2	Q8MCQ9_CAEEL	Q8mcq9 caenorhabdi
713	258	10.9	387	2	Q59WL5_CANAL	Q59wl5 candida alb	786	253.5	10.7	660	2	Q86D04_CAEEL	Q86d04 caenorhabdi
714	258	10.9	394	1	THYD_CLAPS	Q9uv14 claviiceps f	787	253.5	10.7	1492	2	Q6P4Z2_XENTR	Q6p4z2 xenopus tro
715	258	10.9	417	2	Q2VH44_9PARAC	Q2vh44 latrodectus	788	253	10.7	784	2	Q216N4_9DELT	Q216n4 uncultured
716	258	10.9	541	2	Q4Y842_PLACH	Q4y842 plasmodium	789	253	10.7	818	2	Q9N1P0_BOVIN	Q9n1p0 bos taurus
717	258	10.9	604	2	Q6BQ06_DEBHA	Q6bq06 debaryomyce	790	253	10.7	1217	2	Q17240_BOMMO	Q17240 bombyx mori
718	258	10.9	617	2	Q5B4Q0_EMENT	Q5b4q0 emericella	791	253	10.7	1418	1	CO2A1_HUMAN	P02458 homo sapien
719	258	10.9	1272	2	Q5CLT1_CRYHO	Q5clt1 cryptospori	792	252.5	10.7	496	2	Q7KAB0_DROME	Q7ka80 drosophila
720	258	10.9	1984	2	Q4M001_ASPRU	Q4m001 aspergillus	793	252.5	10.7	934	2	Q17H04_AEDAE	Q17h04 aedes aegypt
721	257.5	10.9	440	2	Q5B200_EMENT	Q5b200 emericella	794	252	10.7	389	2	Q2AC60_9BURK	Q2ac60 acidovorax
722	257.5	10.9	474	2	Q4LKK2_9BURK	Q4lkk2 burkholderi	795	252	10.7	582	2	Q7W9S8_MYCBO	Q7w9s8 mycobacteri
723	257.5	10.9	474	2	Q1BWR3_9BURK	Q1bwr3 burkholderi	796	252	10.7	582	2	Q7D5C5_MYCBO	Q7d5c5 mycobacteri
724	257.5	10.9	503	2	Q734G5_BACCI	Q734g5 bacillus ce	797	252	10.7	656	2	Q46BD8_METFR	Q46bd8 methanosaer
725	257.5	10.9	518	1	FUS_MOUSE	P56959 mus musculu	798	252	10.7	1497	2	Q61431_MOUSE	Q61431 mus musculu
726	257.5	10.9	518	2	Q3UK30_MOUSE	Q3uk30 mus musculu	799	252	10.7	1583	2	Q6C398_YARLI	Q6c398 yarrowia li
727	257.5	10.9	518	2	Q3US74_MOUSE	Q3us74 mus musculu	800	251.5	10.6	343	2	Q01914_PHYIN	Q01914 pyropthor
728	257.5	10.9	518	2	Q564D0_MOUSE	Q564d0 mus musculu	801	251.5	10.6	490	2	Q9S0W9_ARATH	Q9s0w9 arabidopsis
729	257.5	10.9	518	2	Q5POK2_RAT	Q5pqk2 rattus norv	802	251.5	10.6	601	2	Q2T8A1_BURVI	Q2t8a1 burkholderi
730	257.5	10.9	584	2	Q8N175_HUMAN	Q8n175 homo sapien	803	251.5	10.6	627	8	Q20CA8_DROVI	Q20ca8 drosophila
731	257.5	10.9	735	2	Q7Z009_9NEOP	Q7z009 anagasta ku	804	251.5	10.6	810	2	Q9ESZ9_MOUSE	Q9esz9 mus musculu
732	257.5	10.9	934	2	Q2AY81_9BACT	Q2ay81 bacillus we	805	251.5	10.6	860	1	RUN_MOUSE	P54320 mus musculu
733	257	10.9	385	1	RB87F_DROME	P48810 drosophila	806	251.5	10.6	860	2	Q8C9I8_MOUSE	Q8c9i8 mus musculu
734	257	10.9	433	2	Q61152_PLAMA	Q61152 plasmodium	807	251.5	10.6	1723	2	Q9GQ81_HYDAT	Q9gq81 hydra atten
735	257	10.9	499	2	Q1CXL7_MYXXA	Q1cxl7 myxococcus	808	251	10.6	125	2	Q964C1_ENCCU	Q964c1 encephalito
736	257	10.9	561	2	Q2O1N6_PSECI	Q2o1n6 pseudomonas	809	251	10.6	232	2	Q7S4R3_NEUCR	Q7s4r3 neurospora
737	257	10.9	632	2	Q7TX52_MYCBO	Q7tx52 mycobacteri	810	251	10.6	315	2	Q81GPH_DROME	Q81gph drosophila
738	257	10.9	686	2	Q8VJ65_MYCTU	Q8vj65 mycobacteri	811	251	10.6	385	2	Q59W77_CANAL	Q59w77 candida alb
739	257	10.9	998	2	Q8CFM4_MOUSE	Q8cfm4 mus musculu	812	251	10.6	386	2	Q2AC92_9BURK	Q2ac92 acidovorax
740	257	10.9	1180	2	Q216F9_RHOPE	Q216f9 rhodopseudo	813	251	10.6	425	1	Q61151_PLAMA	Q61151 plasmodium
741	257	10.9	1352	2	Q90YU0_BRARE	Q90yu0 brachydanio	814	251	10.6	429	1	CSP_PLAMA	P13815 plasmodium
742	257	10.9	1403	2	Q4RKGS_TETNG	Q4rkgs tetradon n	815	251	10.6	429	2	Q61144_PLAMA	Q61144 plasmodium
743	257	10.9	1491	2	Q21D81_BRARE	Q21d81 brachydanio	816	251	10.6	429	2	Q61148_PLAMA	Q61148 plasmodium
744	256.5	10.9	306	2	Q15G89_9PARAC	Q15g89 uloborus di	817	251	10.6	429	2	Q62597_PLAMA	Q62597 plasmodium
745	256.5	10.9	508	2	Q7KH10_DROME	Q7kh10 drosophila	818	251	10.6	1420	2	Q6FWM4_CANGA	Q6fwm4 candida gla
746	256.5	10.9	809	2	Q93485_ONCMY	Q93485 oncorhynch	819	251	10.6	1453	1	CO1A1_RAT	P02458 rattus norv
747	256.5	10.9	1329	2	Q11W91_BRARE	Q11w91 brachydanio	820	250.5	10.6	360	2	Q16985_ARADI	Q16985 artans dia
748	256.5	10.9	1352	2	Q610X2_BRARE	Q610x2 brachydanio	821	250.5	10.6	373	2	Q60TWS_CAEER	Q60tws caenorhabdi
749	256	10.8	421	2	Q93119_ANTPE	Q93119 anthraes p	822	250.5	10.6	540	2	Q7N1J1_GLOVI	Q7n1j1 gloeobacter
750	256	10.8	429	2	Q61150_PLAMA	Q61150 plasmodium	823	250.5	10.6	585	2	Q8NN98_CORGL	Q8nn98 corynebacte
751	256	10.8	436	2	Q96778_ANTPE	Q96778 anthraes p	824	250.5	10.6	587	2	Q54L58_DICDI	Q54l58 dictyosteli
752	256	10.8	743	2	Q6R6B2_9CAUD	Q6r6b2 vibrio phag	825	250	10.6	315	2	Q7KRL5_DROME	Q7krl5 drosophila
753	256	10.8	1487	2	Q77753_CANPA	Q77753 caenis fami	826	250	10.6	326	2	Q854M0_9CAUD	Q854m0 mycobacteri
754	256	10.8	1556	2	Q4FYR4_LEIMA	Q4fyf4 leishmania	827	250	10.6	603	2	Q8VJ65_MYCTU	Q8vj65 mycobacteri
755	255.5	10.8	501	2	Q86X94_HUMAN	Q86x94 homo sapien	828	250	10.6	813	2	Q636M4_BACCR	Q636m4 bacillus ce
756	255.5	10.8	592	1	RBPF6_HUMAN	Q92804 homo sapien	829	250	10.6	1497	2	Q7TMS0_MOUSE	Q7tms0 mus musculu
757	255.5	10.8	1269	2	Q6V5D4_OLIPU	Q6v5d4 olimarrabido	830	250	10.6	1570	2	Q6TNP8_XENLA	Q6tnp8 xenopus lae
758	255.5	10.8	2532	2	Q6229H6_CAEER	Q6229h6 caenorhabdi	831	250	10.6	1658	2	Q59G3D_HUMAN	Q59g3d homo sapien
759	255	10.8	357	2	Q6V5F6_9BRAS	Q6v5f6 capsella ru	832	249.5	10.6	395	2	Q7M3X0_PLAVI	Q7m3x0 plasmodium
760	255	10.8	492	2	Q4DKB7_TRYCR	Q4dkb7 trypanosoma	833	249.5	10.6	589	2	Q7TXX3_MYCBO	Q7txx3 mycobacteri
761	255	10.8	632	2	Q9N2N7_HEMPU	Q9n2n7 hemientroct	834	249.5	10.6	669	2	Q182R7_CLODI	Q182r7 clostridium

835	249.5	10.6	1033	1	IP2_STRCO	08c3j8 streptomyc	908	245	10.4	1684	2	080815 ARATH	080815 arabidopsis
836	249.5	10.6	1300	2	Q4WVJ1_BACCE	Q4wv1 bacillus ce	909	245	10.4	1759	1	CO4A1_CAEEL	P17139 caenorhabdi
837	249.5	10.6	1300	2	Q3UT74_MOUSE	Q3ut74 mus musculu	910	245	10.4	1804	1	COB41_MOUSE	061245 mus musculu
838	249.5	10.6	1477	2	Q3TVR2_MOUSE	Q3tvr2 mus musculu	911	245	10.4	1910	2	O1E7F2_COCIM	O1ef2 coccitoides
839	249.5	10.6	1497	2	Q3UHK7_MOUSE	Q3uhk7 mus musculu	912	244.5	10.3	761	2	O1IPU0_ACTIBL	O1ipu0 actiodacter
840	249.5	10.6	1497	2	Q3VLU6_MOUSE	Q3vlu6 mus musculu	913	244.5	10.3	825	2	O212W2_9ARRAC	O212w2 latrodectus
841	249.5	10.6	1497	2	Q3U962_MOUSE	Q3u962 mus musculu	914	244.5	10.3	939	1	COLL3_MIMIV	O5upx3 miltivirus.
842	249	10.5	516	2	Q6XBJ0_MAIZE	Q6xjb0 zea mays (m	915	244.5	10.3	1453	1	COLA1_CHICK	P02457 brachydanto
843	249	10.5	793	2	Q6MX04_MYCTU	Q6mx04 mycobacteri	916	244.5	10.3	1461	2	O76045_HUMAN	P02452 homo sapien
844	249	10.5	770	2	Q95TR3_DROME	Q95tr3 dirosophila	917	244.5	10.3	1464	1	COLA1_HUMAN	P02452 homo sapien
845	249	10.5	1215	2	Q9W2K4_DROME	Q9w2k4 dirosophila	918	244.5	10.3	1464	1	COLA1_HUMAN	P02452 homo sapien
846	249	10.5	2465	2	Q6CB66_YARLI	Q6cb66 yarrowia li	919	244.5	10.3	1467	2	Q8A473_HUMAN	Q8a473 homo sapien
847	248.5	10.5	305	1	YA090_ASPFU	Q4wlb9 aspergillus	920	244.5	10.3	1737	2	O9104_RAT	Q9104 ratu
848	248.5	10.5	597	2	Q8ISB3_ANTMY	Q8isb3 antheraea m	921	244	10.3	504	2	Q4MXK2_BACCE	Q4mxk2 bacillus ce
849	248.5	10.5	502	2	Q7PIQ0_ANOGA	Q7piq0 anopheles g	922	244	10.3	537	2	O1TX11_9MYCO	O1tx11 mycobacteri
850	248.5	10.5	710	2	Q8WMD1_STRCO	Q8wmd1 streptomyc	923	244	10.3	1398	2	Q2QZB8_ORYSA	Q2qz8 oryza sativ
851	248.5	10.5	1011	2	Q7YXS7_BORPE	Q7yxs7 bordetella	924	244	10.3	1849	2	Q1LWXS_BRARE	Q1lwxs brachydanto
852	248.5	10.5	1016	2	Q9XTX5_CAEEL	Q9xtx5 caenorhabdi	925	243.5	10.3	413	2	Q8UQ01_BRANA	Q8uq01 bradyrhizob
853	248.5	10.5	1442	2	Q62033_MOUSE	Q62033 mus musculu	926	243.5	10.3	615	2	Q8MS22_DROME	Q8ms22 dirosophila
854	248.5	10.5	1442	2	Q62031_MOUSE	Q62031 mus musculu	927	243.5	10.3	1046	1	IP2_STRAM	Q8rk53 streptomyc
855	248.5	10.5	1459	1	CO2A1_MOUSE	P28481 mus musculu	928	243.5	10.3	1641	2	Q5SKX0_CRYNE	O5skx0 cryptococcu
856	248.5	10.5	1459	1	Q62032_MOUSE	Q62032 mus musculu	929	243.5	10.3	1641	2	Q5SZK6_CRYNE	O5szk6 cryptococcu
857	248	10.5	117	2	Q964C2_ENCCU	Q964c2 encephalito	930	243.5	10.3	1759	2	Q61I05_CAEER	Q61i05 caenorhabdi
858	248	10.5	200	2	Q61TM4_CAEER	Q61tm4 caenorhabdi	931	243	10.3	237	2	Q7TW10_MYCBO	Q7tw10 mycobacteri
859	248	10.5	343	2	Q81761_ARATH	Q81761 arabidopsis	932	243	10.3	424	2	Q42626_BRANA	Q42626 brassica na
860	248	10.5	364	2	Q4E3X5_TRYCR	Q4e3x5 trypanosoma	933	243	10.3	555	2	Q8SX80_DROME	Q8sx80 dirosophila
861	248	10.5	385	1	RO32_XENLA	P51992 xenopus lae	934	243	10.3	712	2	Q6H198_BACHK	Q6h198 bacillus th
862	248	10.5	425	2	Q61147_PLAMA	Q61147 plasmodium	935	243	10.3	1069	2	Q6LAN8_HUMAN	Q6lan8 homo sapien
863	248	10.5	712	2	Q4S272_TETNG	Q4s272 tetraodon n	936	243	10.3	1192	2	Q964R2_THETI	Q964r2 theileria t
864	247.5	10.5	279	2	Q57148_9BETA	Q57148 human herpe	937	243	10.3	1060	2	Q7YXC8_CAEEL	Q7yxc8 caenorhabdi
865	247.5	10.5	347	2	Q01916_PHYIN	Q01916 phytophthor	938	243	10.3	1357	2	Q9W4M4_DROME	Q9w4m4 dirosophila
866	247.5	10.5	354	2	Q3YSW9_PLAVI	Q3ysw9 plasmodium	939	243	10.3	2884	2	O17JN1_AEDAE	O17jn1 aedes aegypt
867	247.5	10.5	399	1	CAZ_DROME	Q27294 dirosophila	940	243	10.3	3822	2	Q1BG63_9BURK	Q1bg63 burkholderi
868	247.5	10.5	481	2	Q97641_HORSE	Q97641 equus caball	941	242.5	10.3	205	2	Q22432_PINTA	Q22432 pinus taeda
869	247.5	10.5	1208	2	Q4RX03_TETNG	Q4rx03 tetraodon n	942	242.5	10.3	243	2	Q67WQ9_ORYSA	Q67wq9 oryza sativ
870	247.5	10.5	1418	2	Q28396_HORSE	Q28396 equus caball	943	242.5	10.3	423	2	Q9FM47_ARATH	Q9fm47 arabidopsis
871	247.5	10.5	1419	2	Q80VY3_MOUSE	Q80vy3 mus musculu	944	242.5	10.3	803	2	Q7XJ46_CHIRE	Q7xj46 chlamydomon
872	247.5	10.5	1419	2	Q80X38_MOUSE	Q80x38 mus musculu	945	242.5	10.3	940	1	PE1RA_HUMAN	O66c60 homo sapien
873	247.5	10.5	1487	2	Q64IK3_MOUSE	Q64ik3 mus musculu	946	242.5	10.3	940	2	Q21610_HUMAN	O21610 homo sapien
874	247.5	10.5	1739	2	Q9JL12_MOUSE	Q9jll2 mus musculu	947	242.5	10.3	1475	2	Q4S5W8_TETNG	Q4s5w8 tetraodon n
875	247.5	10.5	2090	2	Q1GWM9_9SPHN	Q1gwm9 sphingopyxi	948	242.5	10.3	1496	1	CO5A2_HUMAN	P05997 homo sapien
876	247.5	10.5	3275	2	Q8VNM3_MYCBCT	Q8vnm3 mycobacteri	949	242.5	10.3	1466	2	Q53WR4_HUMAN	Q53wr4 homo sapien
877	247.5	10.5	3300	2	Q6WX44_MYCTU	Q6wx44 mycobacteri	950	242.5	10.3	1562	2	Q6G0S7_MOUSE	O6g0s7 mus musculu
878	247.5	10.5	3507	2	Q7U270_MYCBO	Q7u270 mycobacteri	951	242.5	10.3	1669	2	Q3UHR4_MOUSE	Q3uhr4 m. edna, rik
879	247	10.5	879	2	Q4RR11_GIBZE	Q4irr11 gibberella	952	242.5	10.3	1775	1	CO4A1_DROME	P08120 dirosophila
880	247	10.5	425	2	Q61146_PLAMA	Q61146 plasmodium	953	242	10.2	193	2	Q7XDR9_ORYSA	Q7xd9 oryza sativ
881	247	10.5	583	2	Q218X9_PETMA	Q218x9 petromyxon	954	242	10.2	220	2	Q3XEU2_PSEEP	Q3xeu2 pseudomonas
882	246.5	10.4	360	2	Q2U7Q7_ASPOR	Q2u7q7 aspergillus	955	242	10.2	347	2	Q9GZC7_TRYCR	Q9gzc7 trypanosoma
883	246.5	10.4	382	2	Q2G4P7_NOVAD	Q2g4p7 novosphingo	956	242	10.2	385	2	Q934Z4_CAEEL	Q934z4 caenorhabdi
884	246.5	10.4	1453	1	CO1A1_MOUSE	P11087 mus musculu	957	242	10.2	421	2	Q61145_PLAMA	O61145 plasmodium
885	246.5	10.4	1460	1	CO1A1_CANPA	Q9xst7 canis famli	958	242	10.2	457	2	Q2ASD3_SBACT	Q2asd3 bacillus we
886	246.5	10.4	1958	1	Q69340_9ALPH	Q69340 suid herpes	959	242	10.2	1286	2	Q3TSR6_MOUSE	Q3tsr6 mus musculu
887	246	10.4	182	2	Q9VTB7_DROME	Q9vct1 m o day neo	960	242	10.2	1804	2	Q80WR4_MOUSE	O80wr4 mus musculu
888	246	10.4	250	2	Q9VTB7_DROME	Q9vct7 dirosophila	961	241.5	10.2	185	2	Q7XMD7_ORYSA	Q7xmd7 oryza sativ
889	246	10.4	447	2	Q1A087_9CAUD	Q1a087 mycobacteri	962	241.5	10.2	349	2	Q4CZ27_TRYCR	Q4cz27 trypanosoma
890	246	10.4	817	2	COLLA_MIMIV	Q5up87 mimivirus.	963	241.5	10.2	608	2	Q9SUX1_ARATH	Q9sux1 arabidopsis
891	246	10.4	886	2	Q8CEP7_MOUSE	Q8cep7 mus musculu	964	241.5	10.2	685	2	Q6CE66_YARLI	Q6ce66 yarrowia li
892	246	10.4	959	2	Q3TFP8_MOUSE	Q3tfp8 mus musculu	965	241.5	10.2	1258	2	Q8A8W1_BRARE	Q8a8w1 brachydanto
893	246	10.4	1262	1	CO3A1_CHICK	P12105 gallus gall	966	241.5	10.2	1347	2	Q96OB3_HUMAN	Q96ob3 homo sapien
894	246	10.4	1721	2	OLYNG6_BRARE	OLYng6 brachydanto	967	241	10.2	342	2	Q9BIT1_GASMA	Q9bit1 gastrocanc
895	245.5	10.4	185	2	Q7XDT5_ORYSA	Q7xdt5 oryza sativ	968	241	10.2	380	2	Q07138_MYCPR	Q07138 microciona
896	245.5	10.4	354	2	Q79FR3_MYCTU	Q79ft3 mycobacteri	969	241	10.2	678	2	Q7TZK3_MYCBO	Q7tzk3 mycobacteri
897	245.5	10.4	457	2	Q61C49_CAEER	Q61c49 caenorhabdi	970	241	10.2	1783	2	Q29108_DROSP	Q29108 dirosophila
898	245.5	10.4	795	2	Q54M14_DICDI	Q54m14 dicystoselei	971	241	10.2	1928	2	Q8T9H1_DROME	Q8t9h1 drospophila
899	245.5	10.4	1459	2	Q3F163_9BURK	Q3f163 burkholderi	972	240.5	10.2	232	2	Q5AKR0_HUMAN	Q5akr0 candida alb
900	245.5	10.4	1669	2	Q3UJEF_MOUSE	Q3ujef mus musculu	973	240.5	10.2	273	2	Q5UNY9_9ARRAC	Q5uny9 arract
901	245	10.4	275	2	Q5AXC7_EMENTI	Q5axc7 emeritella	974	240.5	10.2	528	2	Q3WGL0_PACTO	Q3wgl0 frankia sp.
902	245	10.4	373	2	Q23062_CAEEL	Q23062 caenorhabdi	975	240.5	10.2	889	2	Q4D590_TRYCR	Q4d590 trypanosoma
903	245	10.4	518	2	Q43PNS_SOLUS	Q43pns solibacter	976	240.5	10.2	1499	2	Q591P2_PIG	O591p2 sus scrofa
904	245	10.4	535	2	Q3R0S5_XYLEFA	Q3r0s5 xylella fas	977	240	10.2	170	2	Q43539_LILLO	O43539 lilium long
905	245	10.4	892	2	Q3V4Q4_9VIRU	Q3v4q4 acylanus t	978	240	10.2	421	2	Q61149_PLAMA	O61149 plasmodium
906	245	10.4	894	1	ILF3_HIDMAN	O12906 h. interieuk	979	240	10.2	503	2	O15G96_PARRAC	O15g96 brachyid sp
907	245	10.4	1349	2	Q8AW17_BRARE	O8aw17 brachydanto	980	240	10.2	512	1	FUS_BOVIN	Q28009 bos taurus

981	240	10.2	678	1	PPE21_MYCTU	Q10778	mycobacteri	1054	236.5	10.0	747	1	CO2A1_BOVIN	P02459	bos taurus
982	240	10.2	630	2	Q50WH0_ENTHI	Q01000	entamoeba h	1055	236.5	10.0	844	2	Q7Q3C5_ANOGA	Q7Q3C5	anophelis g
983	240	10.2	974	2	Q406F5_LEIMA	Q406F5	leishmania	1056	236.5	10.0	961	2	Q7RM88_NEUCR	Q7RM88	neurospora
984	240	10.2	987	2	Q37161_RHOBA	Q37161	rhodospseudo	1057	236.5	10.0	963	2	Q2U109_ASPOB	Q2U109	aspergillus
985	240	10.2	1015	2	Q7XZU9_HORVU	Q7XZU9	hordeum vul	1058	236.5	10.0	977	2	Q8X005_NEUCR	Q8X005	neurospora
986	240	10.2	1348	2	Q4ZW16_PSEU2	Q4ZW16	pseudomonas	1059	236.5	10.0	1474	2	Q61406_CAEBR	Q61406	caenorhadi
987	239.5	10.1	268	2	Q52ID4_ORYSA	Q52ID4	oryza sativ	1060	236.5	10.0	1733	1	VNUA_PRYVA	Q5PPC8	caenorhadi
988	239.5	10.1	426	2	Q55IB8_CRYNE	Q55IB8	crypococcu	1061	236.5	10.0	1733	1	Q5PPC8_PALPH	Q5PPC8	caenorhadi
989	239.5	10.1	426	2	Q5K7V5_CRYNE	Q5K7V5	crypococcu	1062	236.5	10.0	1736	1	COBA2_MOUSE	Q5K7V5	caenorhadi
990	239.5	10.1	444	2	Q55IB9_CRYNE	Q55IB9	crypococcu	1063	236.5	10.0	464	2	Q5LOV0_STIRO	Q5LOV0	stiro
991	239.5	10.1	444	2	Q5K7V6_CRYNE	Q5K7V6	crypococcu	1064	236.5	10.0	504	2	Q6FL55_CANGA	Q6FL55	candida gla
992	239.5	10.1	469	2	Q8IKL9_BACAN	Q8IKL9	bacillus an	1065	236.5	10.0	518	2	Q8MQC8_CAEEL	Q8MQC8	caenorhadi
993	239.5	10.1	538	2	Q8NOR6_TURMA	Q8NOR6	turbo marmo	1066	236.5	10.0	524	2	Q02123_CAEEL	Q02123	caenorhadi
994	239.5	10.1	617	2	Q3J151_BURPI	Q3J151	burkholderi	1067	236.5	10.0	888	2	Q90796_CHICK	Q90796	chick
995	239.5	10.1	663	2	Q81ZY6_STEPAW	Q81ZY6	streptomyce	1068	236.5	10.0	991	2	Q1BWM4_BURTA	Q1BWM4	burkholderi
996	239.5	10.1	706	2	Q41972_MHV68	Q41972	murid herpe	1069	236.5	10.0	1139	2	Q5PR22_HUMAN	Q5PR22	homo sapien
997	239.5	10.1	727	2	Q41973_MHV68	Q41973	murid herpe	1070	236.5	10.0	1827	2	Q8U0M5_ORYLA	Q8U0M5	oryzias lat
998	239.5	10.1	732	2	Q2WBX4_PLADU	Q2WBX4	platynereis	1071	235.5	10.0	341	2	Q1E584_COCIM	Q1E584	coccidioid
999	239.5	10.1	774	2	Q41971_MHV68	Q41971	murid herpe	1072	235.5	10.0	643	1	KZC1_HUMAN	Q9VRM2	homo sapien
1000	239.5	10.1	812	2	Q06452_EPHMU	Q06452	ephyratia m	1073	235.5	10.0	682	2	Q2TR93_BURTA	Q2TR93	burkholderi
1001	239.5	10.1	1502	2	Q59GR4_HUMAN	Q59GR4	homo sapien	1074	235.5	10.0	827	2	Q59EX5_HUMAN	Q59EX5	homo sapien
1002	239.5	10.1	1669	1	CO4A1_MOUSE	P02463	mus musculu	1075	235.5	10.0	867	2	Q7Z5L5_HUMAN	Q7Z5L5	homo sapien
1003	239.5	10.1	519	2	Q417C0_GIBZE	P02463	gibberella	1076	235.5	10.0	1714	2	Q7Z5L5_HUMAN	Q7Z5L5	homo sapien
1004	239.5	10.1	584	2	Q6ZBE4_BURMA	Q6ZBE4	burkholderi	1077	235.5	10.0	1714	2	Q5VY50_HUMAN	Q5VY50	homo sapien
1005	239.5	10.1	826	2	Q8KON6_MOUSE	Q8KON6	mus musculu	1078	235.5	10.0	1714	2	Q17RM2_HUMAN	Q17RM2	homo sapien
1006	239.5	10.1	1041	2	Q6SS51_OIKDI	Q6SS51	oikopleura	1079	235.5	10.0	1770	2	Q7O1Y4_ANOGA	Q7O1Y4	anophelis g
1007	239.5	10.1	1463	1	COA1_BOVIN	P02453	bos taurus	1080	235.5	10.0	1877	2	Q4RMT3_TETNG	Q4RMT3	tetrahodon n
1008	239.5	10.1	1642	2	Q4BLE7_BURVI	Q4BLE7	burkholderi	1081	235.5	9.9	244	2	Q380R5_ANOGA	Q380R5	anophelis g
1009	238.5	10.1	212	2	Q964C5_ENCCU	Q964C5	encephalito	1082	235.5	9.9	448	2	Q18265_CAEEL	Q18265	caenorhadi
1010	238.5	10.1	121	1	BGG1_SCHJA	P19470	schistosoma	1083	235.5	9.9	568	2	Q6E1Z0_CANGA	Q6E1Z0	canis famli
1011	238.5	10.1	267	2	Q9B0B8_BPMB1	Q9B0B8	plasmocacteri	1084	235.5	9.9	839	2	Q9RXS7_DEIRA	Q9RXS7	deinococcus
1012	238.5	10.1	387	2	Q7M3W9_PLAVI	Q7M3W9	plasmocacteri	1085	235.5	9.9	891	2	Q80V58_MOUSE	Q80V58	mus musculu
1013	238.5	10.1	387	2	Q7M3W8_PLAVI	Q7M3W8	plasmocacteri	1086	235.5	9.9	1047	2	Q4D324_TRYCR	Q4D324	trypanosoma
1014	238.5	10.1	450	1	SWP1_ENCCU	Q9XZV1	encephalito	1087	235.5	9.9	1269	2	Q7T227_CHICK	Q7T227	gallus galli
1015	238.5	10.1	502	2	Q3RGN8_XYLPA	Q3RGN8	xyliella fas	1088	234.5	9.9	207	1	BGG2_SCHJA	Q42638	brassica ol
1016	238.5	10.1	615	2	Q9VYL7_DROME	Q9VYL7	dirosophila	1089	234.5	9.9	419	2	Q7M3J7_9ANOE	Q7M3J7	paratyneil
1017	238.5	10.1	689	2	Q7SEH4_ASHGO	Q7SEH4	aashya goss	1090	234.5	9.9	438	2	Q7M3J7_9ANOE	Q7M3J7	paratyneil
1018	238.5	10.1	1430	2	Q90W37_CHICK	Q90W37	gallus galli	1091	234.5	9.9	455	2	Q28495_MACMG	Q28495	maccaca mlla
1019	238.5	10.1	518	2	Q3TIE4_MOUSE	Q3TIE4	mus musculu	1092	234.5	9.9	1736	1	COBA2_BOVIN	Q3TIE4	bos taurus
1020	238.5	10.1	558	2	Q21N17_SACD2	Q21N17	saccharoph	1093	234.5	9.9	2109	1	PGCA_CHICK	PGCA	chick
1021	238.5	10.1	963	2	Q9UVL2_NEUCR	Q9UVL2	neurospora	1094	234.5	9.9	2585	2	Q23587_CAEEL	Q23587	caenorhadi
1022	238.5	10.1	1011	2	Q6CF27_YARLI	Q6CF27	yarrowia li	1095	234.5	9.9	2944	1	CO7A1_HUMAN	CO7A1	homo sapien
1023	238.5	10.1	1736	1	COBA2_HUMAN	P13942	homo sapien	1096	234.5	9.9	237	2	Q6D166_PLAVI	Q6D166	plasmocacteri
1024	238.5	10.1	1804	1	COBA1_HUMAN	P12107	homo sapien	1097	234.5	9.9	237	2	Q6DXX9_PLAVI	Q6DXX9	plasmocacteri
1025	238.5	10.1	1991	2	Q7RFD0_PLAVO	Q7RFD0	plasmocacteri	1098	234.5	9.9	301	2	Q01927_THYIN	Q01927	thyridophthor
1026	238.5	10.1	2037	2	Q9PV22_XENLA	Q9PV22	xenopus lae	1099	234.5	9.9	309	2	Q8V6M8_VYIRU	Q8V6M8	halorubrum
1027	237.5	10.1	185	2	Q7XDT6_ORYSA	Q7XDT6	oryza sativ	1100	234.5	9.9	339	2	Q941H8_SOLTU	Q941H8	solanum tub
1028	237.5	10.1	247	2	Q6DY38_PLAVI	Q6DY38	plasmocacteri	1101	234.5	9.9	395	2	Q4DNB3_TRYCR	Q4DNB3	trypanosoma
1029	237.5	10.1	349	2	Q9BIV0_ARGAV	Q9BIV0	argiole aur	1102	234.5	9.9	436	2	Q1BLC3_9BURK	Q1BLC3	burkholderi
1030	237.5	10.1	495	2	Q2VSC9_9GAMA	Q2VSC9	ovine herpe	1103	234.5	9.9	685	2	Q4MXS4_BACCE	Q4MXS4	baacillus ce
1031	237.5	10.1	495	2	Q918P0_9GAMA	Q918P0	ovine herpe	1104	234.5	9.9	1626	2	Q8NFW1_HUMAN	Q8NFW1	homo sapien
1032	237.5	10.1	712	2	Q4JF01_PLADU	Q4JF01	platynereis	1105	234.5	9.9	1655	2	Q47F54_DROVI	Q47F54	dirosophila
1033	237.5	10.1	940	1	PIPIA_MACMG	Q5T6M1	maccaca mlla	1106	234.5	9.9	2236	1	AR11B_HUMAN	AR11B	homo sapien
1034	237.5	10.1	940	1	PIPIA_MACMG	Q5T6M1	maccaca mlla	1107	234.5	9.9	171	2	Q04335_ARATH	Q04335	arabidopsi
1035	237.5	10.1	940	2	Q1XHY0_PANTR	Q1XHY0	pan troglod	1108	233.5	9.9	180	2	P91207_CAEEL	P91207	caenorhadi
1036	237.5	10.1	1362	1	CO1A2_CHICK	P02467	gallus galli	1109	233.5	9.9	239	2	Q7PKP4_ANOGA	Q7PKP4	anophelis g
1037	237.5	10.1	1650	2	Q5UP94_HUMAN	Q5UP94	homo sapien	1110	233.5	9.9	336	2	Q5ULN4_ORYSA	Q5ULN4	oryza sativ
1038	237.5	10.1	1693	2	Q5STP6_HUMAN	Q5STP6	homo sapien	1111	233.5	9.9	811	2	Q9AD50_STRCO	Q9AD50	streptomyce
1039	237.5	10.1	1693	2	Q5SUI8_HUMAN	Q5SUI8	homo sapien	1112	233.5	9.9	966	2	Q01385_NEUCR	Q01385	neurospora
1040	237.5	10.1	2944	2	Q63870_MOUSE	Q63870	mus musculu	1113	233.5	9.9	1438	2	Q4S012_TETNG	Q4S012	tetrahodon n
1041	237.5	10.1	309	2	Q9FNR1_ARATH	Q9FNR1	arabidopsi	1114	233.5	9.9	1617	2	Q6MGH2_RAT	Q6MGH2	rattus norv
1042	237.5	10.1	365	2	Q6IP29_XENLA	Q6IP29	xenopus lae	1115	233.5	9.9	2936	2	Q7YRK8_CANGA	Q7YRK8	canis famli
1043	237.5	10.1	369	2	Q61H15_CAEER	Q61H15	caenorhadi	1116	233.5	9.9	237	2	Q6DXX7_PLAVI	Q6DXX7	plasmocacteri
1044	237.5	10.1	430	2	Q9V948_DROME	Q9V948	dirosophila	1117	233.5	9.9	296	2	Q8RU50_ARATH	Q8RU50	arabidopsi
1045	237.5	10.1	535	2	Q7WLD1_BORER	Q7WLD1	bordetella	1118	233.5	9.9	373	1	RO31_XENLA	RO31	xenla
1046	237.5	10.1	642	2	Q6G364_BARBE	Q6G364	bartonella	1119	233.5	9.9	427	2	Q4IM18_GIBZE	Q4IM18	gibberella
1047	237.5	10.1	854	2	Q81VT9_HUMAN	Q81VT9	homo sapien	1120	233.5	9.9	526	2	Q16TFS_AEDAE	Q16TFS	aedes aegy
1048	237.5	10.1	953	2	Q22PQ8_TETTH	Q22PQ8	tetrahymena	1121	233.5	9.9	536	2	Q6DKX4_XENLA	Q6DKX4	xenopus lae
1049	237.5	10.1	1024	2	Q6FLAS_CANGA	Q6FLAS	candida gla	1122	233.5	9.9	539	2	Q28EJ3_XENLA	Q28EJ3	xenopus tro
1050	237.5	10.1	1024	2	Q6SSB6_CHLRE	Q6SSB6	chlamydoma	1123	233.5	9.9	578	2	Q4AC44_9SPHN	Q4AC44	spillingomna
1051	236.5	10.0	207	2	Q381S7_SCHJA	Q381S7	schistosoma	1124	233.5	9.9	658	2	Q6FRG1_CANGA	Q6FRG1	candida gla
1052	236.5	10.0	247	2	Q6DY44_PLAVI	Q6DY44	plasmocacteri	1125	233.5	9.9	783	2	Q9XAI1_STRCO	Q9XAI1	streptomyce
1053	236.5	10.0	717	2	Q6MT66_BDEBA	Q6MT66	bellioibri	1126	233.5	9.9	870	1	ELN_RAT	ELN	rattus norv

1127	233	9.9	1827	2	Q589R0_ORYLA	Q589I0 oryzias lat	1200	229.5	9.7	740	2	Q73J82_TREDE	Q73J82 treponema d
1128	232.5	9.8	253	2	Q7XDR2_ORYSA	Q7Xdr2 oryza sativ	1201	229.5	9.7	824	2	Q81B45_BACCR	Q81B45 bacillus ce
1129	230.5	9.8	290	2	Q21294_CAEEL	Q21294 caenorhabdi	1202	229.5	9.7	853	2	Q8VQ00_MYXCO	Q8VQ00 myxococcus
1130	232.5	9.8	342	1	CU36_MANSE	Oemuc manduca sex	1203	229.5	9.7	857	2	Q85783_MYXXA	O85783 myxococcus
1131	232.5	9.8	388	2	Q9VRF7_DROME	O9vrf7 drosophila	1204	229.5	9.7	877	2	Q1CXR4_MYXXA	Q1CXR4 myxococcus
1132	232.5	9.8	515	2	Q4PB86_USTMA	Q4pb86 ustilago ma	1205	229.5	9.7	1557	2	Q4SMJ3_TETNG	Q4smj3 tetragona n
1133	232.5	9.8	652	2	Q86NR7_DROME	Q86nr7 drosophila	1206	229.5	9.7	3018	2	Q29114_DROPS	Q29114 drosophila
1134	232.5	9.8	2109	2	P79787_CHICK	P79787 gallus gall	1207	229	9.7	147	2	Q33701_ORYSA	Q33701 oryza sativ
1135	232	9.8	329	2	Q9DEX0_CYPCA	Q9dex0 cyprinus ca	1208	229	9.7	162	2	Q9M0B4_ARATH	Q9m0b4 arabidopsis
1136	232	9.8	387	2	Q4D462_TRYCR	Q4d462 trypanosoma	1209	229	9.7	192	2	Q7XDR3_ORYSA	Q7Xdr3 oryza sativ
1137	232	9.8	460	1	CYSP7_DICDI	O94504 dictyosteli	1210	229	9.7	391	2	Q65216_WHEAT	Q65216 tritium ae
1138	232	9.8	460	1	Q54X57_DICDI	Q54x57 dictyosteli	1211	229	9.7	370	2	Q8RS16_BACT	Q8rs16 uncultured
1139	232	9.8	463	2	Q97640_FELCA	Q97640 felis silve	1212	229	9.7	929	2	Q5C122_CRYHO	Q5c122 cryptospori
1140	232	9.8	471	2	Q178C5_ABDAA	Q178c5 aedes aegypt	1213	228.5	9.7	197	2	Q9ATP3_PENCL	Q9atp3 penaeum
1141	232	9.8	797	2	Q9GV13_HYDMA	Q9gv13 hydra magni	1214	228.5	9.7	228	2	Q6DXY0_PLAVI	Q6dxy0 plasmodium
1142	232	9.8	802	2	Q7PYX1_ANOGA	Q7pyx1 anopheles g	1215	228.5	9.7	375	2	Q5TM69_ANOGA	Q5tm69 anopheles g
1143	232	9.8	913	2	Q6C979_YARLI	Q6c979 yarrowia li	1216	228.5	9.7	392	2	Q5A818_CANAL	Q5a818 candida alb
1144	232	9.8	1545	2	Q4RYT7_TETNG	Q4ryt7 tetradodon n	1217	228.5	9.7	429	1	DDR48_YEAST	P18899 saccharomyc
1145	232	9.8	1806	2	Q5VT31_HUMAN	Q5vt31 homo sapien	1218	228.5	9.7	560	2	Q50275_MYCPU	Q50275 mycoplasma
1146	231.5	9.8	239	2	Q9BMN2_PLAVI	Q9bm2 plasmodium	1219	228.5	9.7	645	2	Q14664_HUMAN	Q14664 homo sapien
1147	231.5	9.8	444	2	Q9LY08_ARATH	O9ly08 arabidopsis	1220	228.5	9.7	786	2	Q4BIC9_BURVI	Q4bic9 burkholderi
1148	231.5	9.8	487	2	Q9ZB39_UREUR	Q9zb39 ureaplasma	1221	228.5	9.7	800	2	Q6NU13_XENLA	Q6nu13 xenopus lae
1149	231.5	9.8	533	2	Q1TGC9_MYCO	Q1tgc9 mycobacteri	1222	228.5	9.7	1748	2	Q591P1_PIG	Q591p1 sus scrofa
1150	231.5	9.8	533	2	Q1BF76_MYCO	Q1bf76 mycobacteri	1223	228.5	9.7	1860	2	Q4A6E6_JCHON	Q4a6e6 raja kenoje
1151	231.5	9.8	544	2	Q6BU19_DEBHA	Q6bu19 debaryomyce	1224	228.5	9.7	2523	2	Q8TJ58_METAC	Q8tj58 methanosarc
1152	231.5	9.8	881	2	Q11V22_ACIBL	Q11v22 acidobacter	1225	228.5	9.7	5146	2	Q9VXK3_DROME	O9vrx3 drosophila
1153	231.5	9.8	925	1	PP1RA_PIG	Q767X9 sus scrofa	1226	228.5	9.7	189	2	Q7XDS0_ORYSA	Q7xds0 oryza sativ
1154	231.5	9.8	1009	2	Q5TOG3_CANFA	O5tjg3 canis famli	1227	228	9.6	166	1	Q22638_WAIZE	Q22638 zea mays (m
1155	231.5	9.8	1210	2	Q610K8_CAEER	Q610k8 caenorhabdi	1228	228	9.6	196	2	Q58M71_9CAUD	Q58m71 cyanophaga
1156	231.5	9.8	1475	2	Q9XEP3_SORBI	Q9xep3 scorgium bic	1229	228	9.6	597	2	Q73797_MYCPA	Q73797 mycopbacteri
1157	231.5	9.8	1596	2	Q5TJG0_CANFA	O5tjg0 canis famli	1230	228	9.6	690	2	Q82YD4_STRAW	Q82yd4 streptomyce
1158	231.5	9.8	185	2	Q948R3_ORYSA	Q948r3 oryza sativ	1231	228	9.6	738	2	Q09A13_CHICK	P12106 gallus galli
1159	231	9.8	221	2	Q65514_ARATH	Q65514 arabidopsis	1232	228	9.6	920	1	Q4S014_TETNG	Q4s014 tetradodon n
1160	231	9.8	237	2	Q6DYO1_PLAVI	Q6dyo1 plasmodium	1233	228	9.6	1468	2	Q8VA11_WSSV	Q8va11 white spot
1161	231	9.8	237	2	Q6DYO2_PLAVI	Q6dyo2 plasmodium	1234	228	9.6	1684	2	Q8VA11_WSSV	Q8va11 white spot
1162	231	9.8	237	2	Q6DX29_PLAVI	Q6dx29 plasmodium	1235	228	9.6	1684	2	Q91LX9_WSSV	Q91lx9 white spot
1163	231	9.8	237	2	Q7XLA1_ORYSA	Q7xla1 oryza sativ	1236	228	9.6	1684	2	Q8JNB6_WSSV	Q8jnb6 white spot
1164	231	9.8	373	2	Q9P639_NEUCR	Q9p639 neurospora	1237	227.5	9.6	116	2	Q9N104_PLAFA	Q9n104 plasmodium
1165	231	9.8	433	2	Q7VTS4_MYCHO	Q7vts4 mycobacteri	1238	227.5	9.6	372	2	Q7Z008_SNEOP	Q7z008 anagasta ku
1166	231	9.8	433	2	Q7D7A7_MYCTU	Q7d7a7 mycobacteri	1239	227.5	9.6	726	2	Q81ZX1_STRAW	Q81zx1 streptomyce
1167	231	9.8	442	2	Q94K00_ARATH	Q94k00 arabidopsis	1240	227.5	9.6	1130	2	Q6VC1H_KLULA	Q6vc1h kluyveromyce
1168	231	9.8	473	2	Q39H15_BURSA	Q39h15 burkholderi	1241	227.5	9.6	1297	2	Q6VBI9_CANGA	Q6vbi9 candida gla
1169	231	9.8	501	2	Q6GLD1_XENTR	Q6gl1d xenopus tro	1242	227.5	9.6	1389	2	Q414C4_GIBZE	Q414c4 gibberella
1170	231	9.8	536	2	Q7ZXQ2_XENLA	Q7zxq2 xenopus lae	1243	227.5	9.6	1556	2	Q1G0S6_MANSE	Q1g0s6 manduca sex
1171	231	9.8	583	2	Q54CI3_DICDI	Q54ci3 dictyosteli	1244	227.5	9.6	1733	2	Q30D77_MOUSE	Q30d77 mus musculu
1172	231	9.8	583	2	Q218Y0_PETMA	Q218y0 petromycon	1245	227.5	9.6	1758	2	Q61315_CAEER	Q61315 caenorhabdi
1173	231	9.8	898	1	ILF3_MOUSE	Q59hb5 mus musculu	1246	227.5	9.6	1997	2	Q7RXD0_NEUCR	Q7rxd0 neurospora
1174	231	9.8	1017	2	Q59HB5_HUMAN	Q59hb5 mus musculu	1247	227.5	9.6	236	2	Q94F05_ARATH	Q94f05 arabidopsis
1175	231	9.8	1062	2	Q2J778_FRASC	Q2j778 frankia sp.	1248	227	9.6	324	2	Q3SRK6_NITWN	Q3srk6 nitrobacter
1176	231	9.8	1758	1	CO4A2_CAEEL	P17140 caenorhabdi	1249	227	9.6	371	2	Q4S114_CAEEL	Q4s114 caenorhabdi
1177	230.5	9.8	257	2	Q2D940_ACTIC	Q2d940 acidiphiliiu	1250	227	9.6	536	2	Q816B9_DROME	Q816b9 drosophila
1178	230.5	9.8	274	2	Q19YM9_9CAUD	Q19ym9 mycobacteri	1251	227	9.6	544	2	Q816C5_DROME	Q816c5 drosophila
1179	230.5	9.8	274	2	Q19Z23_9CAUD	Q19z23 mycobacteri	1252	227	9.6	645	2	Q63P58_BURPS	Q63p58 burkholderi
1180	230.5	9.8	284	2	Q6EEZ3_9ARAC	Q6eez3 eupyrostheno	1253	227	9.6	703	2	COB82_HUMAN	P25067 homo sapien
1181	230.5	9.8	483	2	Q9UV68_NEOPA	Q9uv68 neocallimas	1254	227	9.6	1060	2	Q4SK66_TETNG	Q4sk66 tetradodon n
1182	230.5	9.8	643	2	Q87E00_XYLFT	Q87e00 xylophila fas	1255	227	9.6	1148	1	ICEN_PSEBX	Q30611 pseudomonas
1183	230.5	9.8	887	2	Q9W4V1_DROME	Q9w4v1 drosophila	1256	227	9.6	1595	1	COLI2_MIMIV	Q87g59 vibrio para
1184	230.5	9.8	1300	2	Q36421_9GAMA	Q36421 alcelaphine	1257	227	9.6	2671	2	Q44M12_CHILI	Q44m12 chlorobium
1185	230.5	9.8	2096	2	Q7TWN7_MYCHO	Q7twn7 mycobacteri	1258	227	9.6	228	2	Q6DYS9_PLAVI	Q6dys9 plasmodium
1186	230.5	9.8	3157	2	Q6MMX9_MYCTU	Q6mmx9 mycobacteri	1259	227	9.6	252	2	Q7VEE9_PROMA	Q7vee9 pneumoloco
1187	230.5	9.8	4061	2	FLTA_HUMAN	P20993 homo sapien	1260	227	9.6	308	2	Q4WA77_ASPFU	Q4wa77 dictyosteli
1188	230	9.7	115	1	SERI_GALME	Q96614 gallieria me	1261	227	9.6	331	2	Q4DK15_TRICR	Q4dk15 trypanosoma
1189	230	9.7	459	2	Q4IMG0_GIBZE	Q4imu0 gibberella	1262	226.5	9.6	359	2	Q61E00_CAEER	Q61e00 caenorhabdi
1190	230	9.7	664	2	Q129G8_PHOPR	Q129g8 photobacter	1263	226.5	9.6	469	2	CS66_WHEAT	P6526 triticum ae
1191	230	9.7	1981	2	NU181_SCHPO	Q9utk4 schistosach	1264	226.5	9.6	637	2	Q9D2R8_MOUSE	Q9d2r8 mus musculu
1192	230	9.7	1981	2	Q4BDP1_BURVI	Q4bdp1 burkholderi	1265	226.5	9.6	1022	1	Q17740_CAEEL	Q17740 caenorhabdi
1193	229.5	9.7	160	2	Q94669_PLARA	Q94669 plasmodium	1266	226.5	9.6	1709	2	Q86L43_DICDI	Q86l43 dictyosteli
1194	229.5	9.7	189	2	Q337P9_ORYSA	Q337p9 oryza sativ	1267	226.5	9.6				
1195	229.5	9.7	228	2	Q6DY00_PLAVI	Q6dy00 plasmodium	1268	226.5	9.6				
1196	229.5	9.7	294	2	Q16986_ARATH	Q16986 araneus dia	1269	226.5	9.6				
1197	229.5	9.7	539	2	Q7TWN9_MYCHO	Q7twn9 mycobacteri	1270	226.5	9.6				
1198	229.5	9.7	569	2	KIC10_MOUSE	P02515 mus musculu	1271	226.5	9.6				
1199	229.5	9.7	708	2	Q7ZWN6_XENLA	Q7zwn6 xenopus lae	1272	226.5	9.6				

1273	226.5	9.6	1709	2	Q558W3	DICDI	0558W3	dictyosteli	1346	223.5	9.5	572	2	Q6UP53	RALEJ	Q6UP53	ralestonia e
1274	226	9.6	189	2	Q7XDS8	ORYSA	Q7XDS8	oryza sativ	1347	223.5	9.5	572	2	Q4LCR8	9ZZZZ	Q4LCR8	incp-1beta
1275	226	9.6	199	2	Q94476	DICDI	Q94476	dictyosteli	1348	223.5	9.5	631	2	Q9N1P1	BOVIN	Q9N1P1	bos taurus
1276	226	9.6	251	2	Q853B6	9CAUD	Q853B6	mycobacteri	1349	223.5	9.5	659	2	Q8MT98	DROME	Q8MT98	drosophila
1277	226	9.6	251	2	Q19XD3	9CAUD	Q19XD3	mycobacteri	1350	223.5	9.5	683	2	Q1ZZM6	PHOFR	Q1ZZM6	photobacter
1278	226	9.6	260	2	Q5J5S0	9CAUD	Q5J5S0	mycobacteri	1351	223.5	9.5	812	1	COLUS5	MIMIV	Q4P9D9	usuliago ma
1279	226	9.6	261	2	Q4UX7	9BURK	Q4UX7	polaronomas	1352	223.5	9.5	869	2	Q9UVL3	NEUTR	Q9UVL3	neutrosora
1280	226	9.6	343	2	Q5XGF4	XENTR	Q5XGF4	xenopus tro	1353	223.5	9.5	974	2	Q9UVL3	NEUTR	Q9UVL3	neutrosora
1281	226	9.6	389	2	Q4CN93	TRYCR	Q4CN93	trypanosoma	1354	223.5	9.5	978	2	P91777	PACIE	P91777	pacifiastacu
1282	226	9.6	544	2	Q81EC7	DROME	Q81EC7	drosophila	1355	223.5	9.5	1075	2	Q86X41	HUMAN	Q86X41	homo sapien
1283	226	9.6	544	2	Q81072	DROME	Q81072	drosophila	1356	223.5	9.5	1427	2	Q8G1Z2	9MOJU	Q8G1Z2	9mopiasma
1284	226	9.6	1014	2	Q5FWM2	XENLA	Q5FWM2	xenopus lae	1357	223.5	9.5	1855	2	Q80ZFO	RAT	Q80ZFO	ratius norv
1285	226	9.6	1579	2	Q4T574	TEITNG	Q4T574	tetradodon n	1358	223.5	9.5	2170	2	Q5CN66	CRYMO	Q5CN66	cryptospori
1286	226	9.6	1600	2	Q9UEH6	HUMAN	Q9UEH6	homo sapien	1359	223	9.4	172	2	Q5VSA0	ORYSA	Q5VSA0	oryza sativ
1287	226	9.6	1669	1	QO4A1	HUMAN	P02462	homo sapien	1360	223	9.4	184	2	Q9ZMM7	MAIRE	Q9ZMM7	zea mays (m
1288	226	9.6	1669	1	Q5VWF6	HUMAN	Q5VWF6	homo sapien	1361	223	9.4	253	2	Q60ZY0	METFA	Q60ZY0	methylococc
1289	226	9.6	1691	1	QO4A6	HUMAN	Q14031	homo sapien	1362	223	9.4	306	2	Q1MM93	PINIU	Q1MM93	pinctada fu
1290	226	9.6	2189	1	Q9B105	EIMTE	Q9B105	eimeria ten	1363	223	9.4	349	2	Q3SSK6	NITWN	Q3SSK6	nitrobacter
1291	225.5	9.5	265	2	Q6DDA7	XENTR	Q6DDA7	xenopus tro	1364	223	9.4	441	2	Q6GAM7	BARIE	Q6GAM7	bartonella
1292	225.5	9.5	491	2	Q178C4	AEDAE	Q178C4	aedes aegypt	1365	223	9.4	544	2	Q81EC3	DROME	Q81EC3	drosophila
1293	225.5	9.5	751	2	Q9R1N9	MOUSE	Q9R1N9	mus musculu	1366	223	9.4	572	2	Q5GRB4	ALCXX	Q5GRB4	alcigenes
1294	225.5	9.5	770	2	Q6B1Y3	DEBHA	Q6B1Y3	debariomyce	1367	223	9.4	678	2	Q4UR20	THEAN	Q4UR20	theileria a
1295	225.5	9.5	809	2	Q76869	DROME	Q76869	saccharomyc	1368	223	9.4	1001	2	Q05164	YEAST	Q05164	saccharomyc
1296	225.5	9.5	1113	1	NU116	YEAST	Q02630	saccharomyc	1369	223	9.4	1200	1	ICEN	PEBSX	ICEN	pebsx
1297	225.5	9.5	1338	2	Q7TWP0	MYCHO	Q7TWP0	pseudoplusi	1370	222.5	9.4	153	2	Q4XVLI	PLACH	Q4XVLI	plasmodium
1298	225.5	9.5	1474	2	Q86G87	PSERC	Q86G87	haloquadrac	1371	222.5	9.4	153	2	Q3SAU8	PIARA	Q3SAU8	piasmodium
1299	225.5	9.5	9159	2	Q1BDN4	9BURP	Q1BDN4	paracoccus	1372	222.5	9.4	361	2	Q4PHE7	USTIA	Q4PHE7	ustilago ma
1300	225	9.5	208	2	Q3PGX4	PARDP	Q3PGX4	drosophila	1373	222.5	9.4	627	2	Q81RV3	DROME	Q81RV3	drosophila
1301	225	9.5	544	2	Q81EC8	DROME	Q81EC8	drosophila	1374	222.5	9.4	655	2	Q70575	MOUSE	Q70575	mus musculu
1302	225	9.5	572	2	Q63IU2	BURPS	Q63IU2	burkholderi	1375	222.5	9.4	739	2	Q70575	MOUSE	Q70575	mus musculu
1303	225	9.5	587	2	Q3JIL4	BURP1	Q3JIL4	burkholderi	1376	222.5	9.4	878	2	Q4LYA1	9BURK	Q4LYA1	9burkholderi
1304	225	9.5	624	2	Q8N1V1	NEUTR	Q8N1V1	neutrosora	1377	222.5	9.4	1063	2	Q9CH86	LACIA	Q9CH86	lactococcus
1305	225	9.5	855	2	Q3WEK6	9ACTO	Q3WEK6	frankia sp.	1378	222.5	9.4	1319	1	MN1	HUMAN	MN1	human
1306	225	9.5	1085	2	Q361Z3	MARRY	Q361Z3	psaendomonas	1379	222.5	9.4	1361	2	Q5T133	HUMAN	Q5T133	homo sapien
1307	225	9.5	1196	1	ICEV	PEBSX	Q34793	psaendomonas	1380	222.5	9.4	1761	2	Q18407	DROME	Q18407	drosophila
1308	224.5	9.5	174	2	Q9LTF5	ARATH	Q9LTF5	arabidopsis	1381	222.5	9.4	2523	2	Q6MMY2	MYCJU	Q6MMY2	mycobacteri
1309	224.5	9.5	192	2	Q7O1B1	ANOCA	Q7O1B1	anopheles g	1382	222	9.4	305	2	Q5APAS	DICDI	Q5APAS	dictyosteli
1310	224.5	9.5	381	2	Q61BS0	CABER	Q61BS0	caenorhabdi	1383	222	9.4	363	2	Q9RCH5	ARATH	Q9RCH5	arabidopsis
1311	224.5	9.5	488	2	Q2UAI0	ASPOR	Q2UAI0	aspergillus	1384	222	9.4	365	1	ROAI	XENLA	ROAI	xenella
1312	224.5	9.5	442	2	Q7PKR2	ANOCA	Q7PKR2	anopheles g	1385	222	9.4	544	2	Q6MMW0	MYCJU	Q6MMW0	mycobacteri
1313	224.5	9.5	561	2	Q8BVU3	MOUSE	Q8BVU3	mus musculu	1386	222	9.4	552	2	Q7TW76	MYCJU	Q7TW76	mycobacteri
1314	224.5	9.5	677	2	Q21HT7	ANADE	Q21HT7	anaeromyxob	1387	222	9.4	582	2	Q8VYU0	MYCJU	Q8VYU0	mycobacteri
1315	224.5	9.5	775	2	Q9FF42	STRCO	Q9FF42	streptomyce	1388	222	9.4	623	2	Q8VYU0	MYCJU	Q8VYU0	mycobacteri
1316	224.5	9.5	801	2	Q8T5G4	ANOCA	Q8T5G4	anopheles g	1389	222	9.4	676	2	Q6DSE0	XENLA	Q6DSE0	xenopus lae
1317	224.5	9.5	897	1	ILF3	RAT	Q9J113	ratius norv	1390	222	9.4	735	2	Q3XK57	9GAMV	Q3XK57	shewanella
1318	224.5	9.5	1019	2	Q37BM1	RHOPA	Q37BM1	rhodopsines g	1391	222	9.4	946	2	Q857Y4	9CAUD	Q857Y4	mycobacteri
1319	224.5	9.5	1724	2	Q7PVR8	ANOCA	Q7PVR8	anopheles g	1392	222	9.4	1041	2	Q5TP94	ANOCA	Q5TP94	anopheles g
1320	224.5	9.5	1770	2	Q29109	DROPS	Q29109	drosophila	1393	222	9.4	1519	2	Q7Z3C4	HUMAN	Q7Z3C4	homo sapien
1321	224	9.5	167	2	Q63115	RAT	Q63115	ratius norv	1394	222	9.4	1680	2	Q5JYH8	HUMAN	Q5JYH8	homo sapien
1322	224	9.5	374	2	Q4DZ50	TRYCR	Q4DZ50	trypanosoma	1395	221.5	9.4	100	2	Q964C3	ENCCT	Q964C3	encephalito
1323	224	9.5	407	2	Q6S7B1	ARATH	Q6S7B1	arabidopsis	1396	221.5	9.4	173	2	Q41191	ARATH	Q41191	arabidopsis
1324	224	9.5	584	2	Q22791	ARATH	Q22791	arabidopsis	1397	221.5	9.4	193	2	Q9VMM4	DROME	Q9VMM4	drosophila
1325	224	9.5	447	2	Q9YRU3	ATHV3	Q9YRU3	ateline her	1398	221.5	9.4	326	2	Q53UR9	ORYSA	Q53UR9	oryza sativ
1326	224	9.5	478	2	Q1IUP2	ACTIBL	Q1IUP2	acidobacter	1399	221.5	9.4	349	2	Q6C605	YARLI	Q6C605	yarrowia li
1327	224	9.5	544	2	Q81EC4	DROME	Q81EC4	drosophila	1400	221.5	9.4	503	2	Q9HEH4	NEUTR	Q9HEH4	neutrosora
1328	224	9.5	655	2	Q61MF3	RAT	Q61MF3	ratius norv	1401	221.5	9.4	1385	2	Q20C79	DROVI	Q20C79	drosophila
1329	224	9.5	655	2	Q58EP8	BRABE	Q58EP8	brachydanio	1402	221	9.4	273	2	Q65X75	ORYSA	Q65X75	oryza sativ
1330	224	9.5	681	2	Q6AZO8	XENLA	Q6AZO8	xenopus lae	1403	221	9.4	310	2	Q90612	CHICK	Q90612	gallus gall
1331	224	9.5	946	2	Q1A142	9CAUD	Q1A142	mycobacteri	1404	221	9.4	333	2	Q1MM95	PINIU	Q1MM95	pinctada fu
1332	224	9.5	1115	2	Q6PFB1	MOUSE	Q6PFB1	mus musculu	1405	221	9.4	544	2	Q81EC0	DROME	Q81EC0	drosophila
1333	224	9.5	1497	1	COHA1	HUMAN	Q9UM93	homo sapien	1406	221	9.4	544	2	Q81EC1	DROME	Q81EC1	drosophila
1334	224	9.5	1691	2	Q9ESQ1	MOUSE	Q9ESQ1	mus musculu	1407	221	9.4	544	2	Q81EC6	DROME	Q81EC6	drosophila
1335	224	9.5	2308	2	Q9WZU7	DROME	Q9WZU7	drosophila	1408	221	9.4	561	2	Q9CXH6	MOUSE	Q9CXH6	mus musculu
1336	223.5	9.5	247	2	Q1SMR2	TRITU	Q1SMR2	tritricum fu	1409	221	9.4	575	2	Q9SB17	HORVU	Q9SB17	hordeum vul
1337	223.5	9.5	311	2	Q4CNA1	TRYCR	Q4CNA1	trypanosoma	1410	221	9.4	594	2	Q67095	SYNTH	Q67095	syntrobacte
1338	223.5	9.5	339	2	Q6CNA1	YARLI	Q6CNA1	yarrowia li	1411	221	9.4	758	2	Q6TEC0	CRAGI	Q6TEC0	crassostrea
1339	223.5	9.5	415	2	Q1B9F8	COCIM	Q1B9F8	coccidioidi	1412	221	9.4	1044	2	Q4DVU1	TRYCR	Q4DVU1	trypanosoma
1340	223.5	9.5	572	2	Q76M30	COMAN	Q76M30	comanomas a	1413	221	9.4	1363	2	Q4LIW7	9BURK	Q4LIW7	burkholderi
1341	223.5	9.5	572	2	P71187	ENTAE	P71187	enterobacte	1414	221	9.4	2053	2	Q54E08	DICDI	Q54E08	dictyosteli
1342	223.5	9.5	572	2	Q3FZB7	9BURK	Q3FZB7	burkholderi	1415	220.5	9.3	141	2	Q9BJP8	PIARA	Q9BJP8	piasmodium
1343	223.5	9.5	572	2	Q36Y6	PSBED	Q36Y6	pseudomonas	1416	220.5	9.3	239	2	Q4D9X5	TRYCR	Q4D9X5	trypanosoma
1344	223.5	9.5	572	2	Q7X3E2	9BACT	Q7X3E2	uncultured	1417	220.5	9.3	316	2	Q19111	CABER	Q19111	caenorhabdi
1345	223.5	9.5	572	2	Q2VLD7	_BURCE	Q2VLD7	burkholderi	1418	220.5	9.3	506	2	Q4XG36	_PLACH	Q4XG36	plasmodium

1419	1419	220.5	9.3	5.6	2	043XV3 SOLUS
1420	1420	220.5	9.3	616	2	05AXP3 EMENTI
1421	1421	220.5	9.3	618	2	07UOK5 MYGEO
1422	1422	220.5	9.3	618	2	079P50 MYCTU
1423	1423	220.5	9.3	636	2	08VKE5 MYCTU
1424	1424	220.5	9.3	639	2	04VAQ2 HUMAN
1425	1425	220.5	9.3	659	1	K22Z HUMAN
1426	1426	220	9.3	192	2	07XDS2 ORYSA
1427	1427	220	9.3	202	2	08MML4 DICI
1428	1428	220	9.3	202	2	055SM5 DICI
1429	1429	220	9.3	332	2	06C127 YARLI
1430	1430	220	9.3	355	2	05RCCK PONPY
1431	1431	220	9.3	413	2	09HJ00 NEUCR
1432	1432	220	9.3	568	2	08CD80 MOUSE
1433	1433	220	9.3	572	2	09AHG8 COMTE
1434	1434	220	9.3	582	2	05GGB4 9CADA
1435	1435	220	9.3	595	2	07XJ24 ORYSA
1436	1436	220	9.3	678	2	04N5H2 THEPA
1437	1437	220	9.3	741	2	035E29 9GAMMA
1438	1438	220	9.3	771	2	03UUI1 MOUSE
1439	1439	220	9.3	954	2	08KAV8 HUMAN
1440	1440	220	9.3	957	2	09HVO3 HUMAN
1441	1441	220	9.3	957	2	09EPF4 HUMAN
1442	1442	220	9.3	1206	2	0869X8 DICI
1443	1443	220	9.3	1213	2	0553Z2 DICI
1444	1444	220	9.3	1333	2	04UZC3 XANC8
1445	1445	220	9.3	1333	2	08PD38 XANCP
1446	1446	220	9.3	1740	2	09HCJ0 HUMAN
1447	1447	220	9.3	1900	2	0435Z2 LYCES
1448	1448	219.5	9.3	207	2	0643Y0 ORYSA
1449	1449	219.5	9.3	214	2	05UNU0 9ARAC
1450	1450	219.5	9.3	244	2	05UNU0 9ARAC
1451	1451	219.5	9.3	262	2	06CBM5 YARLI
1452	1452	219.5	9.3	311	2	08GBM2 9VIRU
1453	1453	219.5	9.3	539	2	081097 DROME
1454	1454	219.5	9.3	634	1	09A333 HUMAN
1455	1455	219.5	9.3	706	2	01APF6 9BACT
1456	1456	219.5	9.3	715	2	021E71 LETNG
1457	1457	219.5	9.3	791	2	021E77 SACD2
1458	1458	219.5	9.3	1191	2	06CKC7 XENIA
1459	1459	219.5	9.3	1642	2	04Q3C2 LEIMA
1460	1460	219.5	9.3	3930	2	05AHF6 DICI
1461	1461	219	9.3	191	2	07XDR3 ORYSA
1462	1462	219	9.3	193	2	070592 RAT
1463	1463	219	9.3	263	2	05EB93 MOUSE
1464	1464	219	9.3	294	2	06WGT3 BDEBA
1465	1465	219	9.3	313	2	05J3M2 MOUSE
1466	1466	219	9.3	342	2	09LH90 ARATH
1467	1467	219	9.3	345	2	07TDH1 9VIRU
1468	1468	219	9.3	364	2	04WD77 TRYCR
1469	1469	219	9.3	368	2	08BPD9 PLAVI
1470	1470	219	9.3	379	1	ROA3 MOUSE
1471	1471	219	9.3	379	1	ROA3 RAT
1472	1472	219	9.3	379	2	05FB19 MOUSE
1473	1473	219	9.3	412	2	05D919 SCHDA
1474	1474	219	9.3	413	2	064939 LOPEL
1475	1475	219	9.3	473	2	084QM1 ARATH
1476	1476	219	9.3	475	2	05E2I3 NOCPA
1477	1477	219	9.3	544	2	049A51 HUMAN
1478	1478	219	9.3	544	2	0816B7 DROSI
1479	1479	219	9.3	544	2	0816B8 DROME
1480	1480	219	9.3	544	2	0816C2 DROME
1481	1481	2				

[illegible]

1492	218.5	9.2	370	2	ROA5TX_DROME
1493	218.5	9.2	378	1	OQ3RW7_HUMAN
1494	218.5	9.2	378	2	OQ3RW7_HUMAN
1495	218.5	9.2	391	1	C6120_WHEAT
1496	218.5	9.2	459	2	Q41SH5_9EURK
1497	218.5	9.2	497	2	O9VVC3_DROME
1498	218.5	9.2	498	2	O46S8B_RALEJ
1499	218.5	9.2	589	2	O66043_GNAMA
1500	218.5	9.2	612	2	Q7X678_CHLRE

ALIGNMENTS

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RESULT 1
O6UXC7_HUMAN
AC O6UXC7_HUMAN PRELIMINARY; PRT; 440 AA.
ID O6UXC7
DE O6UXC7
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 13-JUN-2006, entry version 9.
DE KFOG729.
GN ORENAMES=UNO729;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen Y., Chow B., Choi C., Crowley C., Currell B., Dewel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schenfeld J.,
RA Seehagiri S., Simmons L., Singh U., Smith V., Stinson C., Vogts A.,
RA Vandlen R.L., Watanabe C., Wiand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
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DR EMBL; AY358412; AAC88778.1; -; mRNA.
DR RZPD-ProExp; IOH14207; -.
DR RZPD-ProExp; TI1713; -.
SQ SEQUENCE 440 AA; 42208 MW; BAQCAFDOCAAEI8BD CRC64;

Query Match      100.0%; Score 2363; DB 2; Length 440;
Best Local Similarity    100.0%; Pred. No. 2e-118;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFQGPIALCLILALCLSGGEAGPLOSSESTGTINIGELGHGLGDPAISGVGKAIGKEAG 60
Db 1 MKFQGPIALCLILALCLSGGEAGPLOSSESTGTINIGELGHGLGDPAISGVGKAIGKEAG 60
QY 61 GAAGSKTSEALGGCTREAVGTGVNPFGGAADALGNRVGEAAHALGNTGHEIRORADV 120
Db 61 GAAGSKTSEALGGCTREAVGTGVNPFGGAADALGNRVGEAAHALGNTGHEIRORADV 120
QY 121 IRHGADAVRGSWGCVPGHSAMETSSGGHGFISGGCGLCGGCGGNPFGSLGTPWVGYPGNS 180
Db 121 IRHGADAVRGSWGCVPGHSAMETSSGGHGFISGGCGLCGGCGGNPFGSLGTPWVGYPGNS 180
QY 181 AGSGGNMPPQGA PMWGGNGGEPNCTGTNQGA VAAPGYGVSVAASNOBECTNPPPSGSGGG 240
Db 181 AGSGGNMPPQGA PMWGGNGGEPNCTGTNQGA VAAPGYGVSVAASNOBECTNPPPSGSGGG 240

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```

OY 241 SSNSGSGSGSOGSSGSGSGNDNNNGSSGSGSSSGSSSGSGSSGSGSGSGNSGGS 300
    |||
DB 241 SSNSGSGSGSGSOGSSGSGSGNDNNNGSSGSGSSSGSSSGSGSSGSGSGSGNSGGS 300
OY 301 RGDGSGSSSWGSSSTGSSSGNHGSGGCGNGHKGPCCEKPGNEARSGSGSGIOGFRGQGVSSN 360
    |||
DB 301 RGDGSGSSSWGSSSTGSSSGNHGSGGCGNGHKGPCCEKPGNEARSGSGSGIOGFRGQGVSSN 360
OY 361 MREISKEGNRLGGSGDNRYGSGSSWGSGGDAVGVTNVSSESPGMFNDTFWKNFKS 420
    |||
DB 361 MREISKEGNRLGGSGDNRYGSGSSWGSGGDAVGVTNVSSESPGMFNDTFWKNFKS 420
OY 421 KLGFINMDAINKDORSRIP 440
    |||
DB 421 KLGFINMDAINKDORSRIP 440

RESULT 2
O32W66 HUMAN PRELIMINARY; PRT; 398 AA.
ID O32W66 HUMAN
AC O32W66
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 13-JUN-2006, entry version 6.
DE Dermokine-gamma 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Normal epidermis;
RX PubMed=16374476; DOI=10.1038/sj.jid.5700033;
RA Toulza E., Galliano M.F., Jonca N., Galliano H., Mechin M.C.,
RA Ishida-Yamamoto A., Serre G., Guerrin M.;
RT "The human dermokine gene: description of novel isoforms with
RT different tissue-specific expression and subcellular location.";
RL J. Invest. Dermatol. 126:503-506(2006).
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DR EMBL: AY789697; AAX48747.1; -; mRNA.
DR RZPD-ProcExp; IOH14207; -.
DR RZPD-ProcExp; TI713; -.
SQ SEQUENCE 398 AA; 38238 MW; FAE77055D5142A49 CRC64;

Query Match 88.8%; Score 2098; DB 2; Length 398;
Best Local Similarity 90.2%; Pred. No. 2.6e-104;
Matches 397; Conservative 1; Mismatches 0; Indels 42; Gaps 2;
OY 1 MKFOGFLACLLALCLSGGEAGPLQSGESTGTNIGALGHGLDALSEGVKAIKKEAG 60
    |||
DB 1 MKFOGFLACLLALCLSGGEAGPLQSGESTGTNIGALGHGLDALSEGVKAIKKEAG 60
OY 61 GAAGSKYSEALGGCTREAVGTGVRQVPGFAADALGNRVGBAAHALGNTGHEIGRQAEV 120
    |||
DB 61 GAAGSKYSEALGGCTREAVGTGVRQVPGFAADALGNRVGBAAHALGNTGHEIGRQAEV 120
OY 121 IRRGADAVRSGWGVPGHNGAMETSGGHGIFGSGGGLGQGGQGNPGGLGTPWVHGYPNS 180
    |||
DB 121 IRRGADAVRSGWGVPGHNGAMETSGGHGIFGSGGGLGQGGQGNPGGLGTPWVHGYPNS 180
OY 181 AGSFQNNPQGAIPWGQGGNGGPPNFGTNTQGAVAOPGYGSVYASNONBECTNPPPSGSGG 240
    |||
DB 181 AGSFQNNPQGAIPWGQGGNGGPPNFGTNTQGAVAOPGYGSVYASNONBECTNPPPSGSGG 240
OY 241 SSNSGSGSGSOGSSGSGSGNDNNNGSSGSGSSSGSSSGSGSGSGSGSGNSGGS 300
    |||
DB 241 SSNSGSGSGSOGSSGSGSGNDNNNGSSGSGSSSGSSSGSGSGSGSGSGNSGGS 300
OY 301 RGDGSGSSSWGSSSTGSSSGNHGSGGCGNGHKGPCCEKPGNEARSGSGSGIOGFRGQGVSSN 360
    |||
DB 301 RGDGSGSSSWGSSSTGSSSGNHGSGGCGNGHKGPCCEKPGNEARSGSGSGIOGFRGQGVSSN 360
OY 361 MREISKEGNRLGGSGDNRYGSGSSWGSGGDAVGVTNVSSESPGMFNDTFWKNFKS 420
    |||
DB 361 MREISKEGNRLGGSGDNRYGSGSSWGSGGDAVGVTNVSSESPGMFNDTFWKNFKS 420

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DB 297 RGDGSGSSSWGSSSTGSSSGNHGSGGCGNGHKGPCCEKPGNEARSGSGSGIOGFRGQGVSSN 356
    |||
OY 361 MREISKEGNRLGGSGDNRYGSGSSWGSGGDAVGVTNVSSESPGMFNDTFWKNFKS 420
    |||
DB 357 MR-----NSSTSPGMFNDTFWKNFKS 378
OY 421 KLGFINMDAINKDORSRIP 440
    |||
DB 379 KLGFINMDAINKDORSRIP 398

RESULT 3
O32W67 HUMAN PRELIMINARY; PRT; 386 AA.
ID O32W67 HUMAN
AC O32W67
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DT 13-JUN-2006, entry version 6.
DE Dermokine-gamma 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Normal epidermis;
RX PubMed=16374476; DOI=10.1038/sj.jid.5700033;
RA Toulza E., Galliano M.F., Jonca N., Galliano H., Mechin M.C.,
RA Ishida-Yamamoto A., Serre G., Guerrin M.;
RT "The human dermokine gene: description of novel isoforms with
RT different tissue-specific expression and subcellular location.";
RL J. Invest. Dermatol. 126:503-506(2006).
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DR EMBL: AY789696; AAX48746.1; -; mRNA.
DR RZPD-ProcExp; IOH14207; -.
DR RZPD-ProcExp; TI713; -.
SQ SEQUENCE 386 AA; 36961 MW; 35A84A256833E43D CRC64;

Query Match 85.9%; Score 2030; DB 2; Length 386;
Best Local Similarity 87.5%; Pred. No. 1.1e-100;
Matches 385; Conservative 1; Mismatches 0; Indels 54; Gaps 2;
OY 1 MKFOGFLACLLALCLSGGEAGPLQSGESTGTNIGALGHGLDALSEGVKAIKKEAG 60
    |||
DB 1 MKFOGFLACLLALCLSGGEAGPLQSGESTGTNIGALGHGLDALSEGVKAIKKEAG 60
OY 61 GAAGSKYSEALGGCTREAVGTGVRQVPGFAADALGNRVGBAAHALGNTGHEIGRQAEV 120
    |||
DB 61 GAAGSKYSEALGGCTREAVGTGVRQVPGFAADALGNRVGBAAHALGNTGHEIGRQAEV 120
OY 121 IRRGADAVRSGWGVPGHNGAMETSGGHGIFGSGGGLGQGGQGNPGGLGTPWVHGYPNS 180
    |||
DB 121 IRRGADAVRSGWGVPGHNGAMETSGGHGIFGSGGGLGQGGQGNPGGLGTPWVHGYPNS 180
OY 181 AGSFQNNPQGAIPWGQGGNGGPPNFGTNTQGAVAOPGYGSVYASNONBECTNPPPSGSGG 240
    |||
DB 181 AGSFQNNPQGAIPWGQGGNGGPPNFGTNTQGAVAOPGYGSVYASNONBECTNPPPSGSGG 240
OY 241 SSNSGSGSGSOGSSGSGSGNDNNNGSSGSGSSSGSSSGSGSGSGSGSGNSGGS 300
    |||
DB 241 SSNSGSGSGSOGSSGSGSGNDNNNGSSGSGSSSGSSSGSGSGSGSGSGNSGGS 300
OY 301 RGDGSGSSSWGSSSTGSSSGNHGSGGCGNGHKGPCCEKPGNEARSGSGSGIOGFRGQGVSSN 360
    |||
DB 301 RGDGSGSSSWGSSSTGSSSGNHGSGGCGNGHKGPCCEKPGNEARSGSGSGIOGFRGQGVSSN 360
OY 361 MREISKEGNRLGGSGDNRYGSGSSWGSGGDAVGVTNVSSESPGMFNDTFWKNFKS 420
    |||
DB 361 MREISKEGNRLGGSGDNRYGSGSSWGSGGDAVGVTNVSSESPGMFNDTFWKNFKS 420

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Db 347 -----NSETSPGMFNPDFTWKNKFS 366

QY 421 KLGFINDMADINKDQSSSRIP 440

Db 367 KLGFINDMADINKDQSSSRIP 386

## RESULT 4

Q6E0U4 HUMAN PRELIMINARY; PRT; 476 AA.

AC Q6E0U4

DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.

DT 16-AUG-2004, sequence version 1.

DT 25-JUL-2006, entry version 19.

DE Dermokine-beta (Dermokine).

GN Name=ZD52P10;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

OC Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;

RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katayama S., Morita K.,

RA Miyachi Y., Ono Y., Imai T., Tanigawa Y., Komiya T., Tsukita S.;

RT "Identification of novel keratinocyte-secreted peptides dermokine-

RT alpha/-beta and a new stratified epithelium-secreted protein gene

RT complex on human chromosome 19q13.1.";

RL Genomics 84:384-397(2004).

RL [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Normal epidermis;

RX PubMed=16374476; DOI=10.1038/sj.jid.5700033;

RA Toulza E., Galliano M.F., Jonca N., Galliano H., Mechin M.C.,

RA Ishida-Yamamoto A., Serre G., Guerin M.;

RT "The human dermokine gene: description of novel isoforms with

RT different tissue-specific expression and subcellular location.";

RT J. Invest. Dermatol. 126:503-506(2006).

RL [3]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Skin;

RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,

RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butlerfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).

RL [4]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Skin;

RC NUCLEOTIDE SEQUENCE.

RG NIH MGC Project;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AY622965; AA168269.1; -; mRNA.

DR EMBL; AY789695; AAX48745.1; -; mRNA.

DR EMBL; BC035311; AAH35311.1; -; mRNA.

DR UniGene; Hs.417795; -.

DR Ensembl; ENSG00000161249; Homo sapiens.

DR RZPD-ProtExp; IOH14207; -.

DR RZPD-ProtExp; TI713; -.

SQ SEQUENCE 476 AA; 47010 MW; E2206CCE64AC4992 CRC64;

Query Match 84.5%; Score 1996; DB 2; Length 476;

Best Local Similarity 87.1%; Pred. No. 8.5e-99;

Matches 378; Conservative 2; Mismatches 0; Indels 54; Gaps 2;

QY 1 MKFGPLALCLLALCLGSGEAGPLQSGESTGTNIGALGHLGALSGVKAIGKXG 60

Db 1 MKFGPLALCLLALCLGSGEAGPLQSGESTGTNIGALGHLGALSGVKAIGKXG 60

QY 61 GAAGSKVSEALGQGTREAVGTGVRVPGFGAADALGNRVGEAAHALGNTGHEIGQADV 120

Db 61 GAAGSKVSEALGQGTREAVGTGVRVPGFGAADALGNRVGEAAHALGNTGHEIGQADV 120

QY 121 IRHGADAVRGSWQVPGHSGAWETSGHGIFSGSGGLGQGGQGNPGGLTTPWVHGYPGNS 180

Db 121 IRHGADAVRGSWQVPGHSGAWETSGHGIFSGSGGLGQGGQGNPGGLTTPWVHGYPGNS 180

QY 181 AGSPFANPQAGAPWGGGNGGPPNFGTNTQGAVAOPGYGSVRASNONEGCTNPPPGSGGG 240

Db 181 AGSPFANPQAGAPWGGGNGGPPNFGTNTQGAVAOPGYGSVRASNONEGCTNPPPGSGGG 240

QY 241 SSNSGGSG 300

Db 241 SSNSGGSG 296

QY 301 RGDSSSSSSSG 360

Db 297 RGDSSSSSSSG 346

QY 361 MREISKEGNRLLGSGGDNVYRGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 420

Db 347 -----NSETSPGMFNPDFTWKNKFS 366

QY 421 KLGFINDMADINKDQ 434

Db 367 KLGFINDMADINKDQ 380

RESULT 5

Q6E0U6 MOUSE PRELIMINARY; PRT; 517 AA.

AC Q6E0U6

DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.

DT 16-AUG-2004, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE Dermokine-beta.

GN Name=1110014F24R1k;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;

RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katayama S., Morita K.,

RA Miyachi Y., Ono Y., Imai T., Tanigawa Y., Komiya T., Tsukita S.;

RT "Identification of novel keratinocyte-secreted peptides dermokine-

RT alpha/-beta and a new stratified epithelium-secreted protein gene

RT complex on human chromosome 19q13.1.";

RL Genomics 84:384-397(2004).

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DR EMBL; AY622963; AAT68267.1; -, mRNA.  
 DR Ensembl; ENSMUSG0000060962; Mus musculus.  
 DR MGI; MGI:1920962; 1110014F24Rik.  
 SO SEQUENCE 517 AA; 51660 MW; 61E2974EBB36650B CRC64;

Query Match 44.1%; Score 1043; DB 2; Length 517;  
 Best Local Similarity 48.9%; Pred. No. 7e-48;  
 Matches 231; Conservative 41; Mismatches 102; Indels 98; Gaps 13;

QY 1 MKFQGLPLCLLALCLGSGEAGPLQSGEESTGTGALHGLDALSEVGAIGKAG 60  
 |||||  
 DB 1 MKLQSGSLACLILALCLGGAANPLHSGEGTGA-----SAAHGADALSHGGEAVGQAK 56  
 QY 61 GAAGSKVSEALAGCTREAVGTGVRQVPGFADALGNRVGEAAALNTHGHEIROEDY 120  
 |||||  
 DB 57 EAASSGIGLALGQGHGEGSTLMGSRG---DYFERHLEGAASLGNAGNEIGQAEI 112  
 QY 121 IRHGAADVRSWQGVPGHSGAMETSGHGIFGSGGGLGQGGQGNPGGLGTPWVHGYPGNS 180  
 |||||  
 DB 113 IRGVDVAVH-----NAGSWGTSQGHGAYGSGGAG--VQGNPQGTTPWAG----- 157  
 QY 181 AGSFQMPQCAPWQGGGNGGPPNFGTNTQGAVAOPGYGVASVNASQNEGCTNPPSGS--- 237  
 |||||  
 DB 158 -GNVGTNSLGGSVQGGNGGPGPLNETHAQAQVAPGYGVAGNNGNNGCTNPPSGSHES 216  
 QY 238 ---GGSSNSNG--GSGSQSGSGSGSNG-----DNNNGSSGSGSGSGSGSGSGSS 286  
 |||||  
 DB 217 FSNSSGSSNDGSRSGSGSHSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSS 274  
 QY 287 GSSSG 325  
 |||||  
 DB 275 GNSNSGNSGNSGSGSRDIETSNPDEGYSVSRGTGSRGSGSGSGSGSGSGSGSGSGSG 329  
 QY 326 GGNHGPCEKPGNEARAGSGESGIGFRGQGVSSNMREISKEGNRLIGSGSDNTRGQSS 385  
 |||||  
 DB 330 GGN--KPECNNPGNDVAMAGSGSG-----GSGSGSGSGSGSGSGSGSGSGSGSN 357  
 QY 386 WSGGGDVAVGCVTVNSETSPGMFNPFTPKNPKSKLGFINWDAINDQSS 437  
 |||||  
 DB 358 GGNIGKEAVNGLNTMNSDASTLPFNIDFWENLKSRTFIMWDAINKHAPS 409

RESULT 6  
 Q6P253 MOUSE PRELIMINARY; PRT; 508 AA.  
 AC Q6P253;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 04-APR-2006, entry version 13.  
 DE Dermokine, beta.  
 GN Name=1110014F24Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters K.J., Adamson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RG NIH MGC Project;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

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 CC -----

DR EMBL; BC064724; AAH64724.1; -, mRNA.

DR UniGene; Mm.30138;  
 DR Ensembl; ENSMUSG0000060962; Mus musculus.

DR MGI; MGI:1920962; 1110014F24Rik.

DR GO; GO:0005615; C:extracellular space; IDA.  
 SO SEQUENCE 508 AA; 51057 MW; 1B7913E7275A1926 CRC64;

Query Match 43.9%; Score 1038.5; DB 2; Length 508;  
 Best Local Similarity 50.0%; Pred. No. 1.2e-47;  
 Matches 229; Conservative 44; Mismatches 106; Indels 79; Gaps 13;

QY 1 MKFQGLPLCLLALCLGSGEAGPLQSGEESTGTGALHGLDALSEVGAIGKAG 60  
 |||||  
 DB 1 MKLQSGSLACLILALCLGGAANPLHSGEGTGA-----SAAHGADALSHGGEAVGQAK 56  
 QY 61 GAAGSKVSEALAGCTREAVGTGVRQVPGFADALGNRVGEAAALNTHGHEIROEDY 120  
 |||||  
 DB 57 EAASSGIGLALGQGHGEGSTLMGSRG---DYFERHLEGAASLGNAGNEIGQAEI 112  
 QY 121 IRHGAADVRSWQGVPGHSGAMETSGHGIFGSGGGLGQGGQGNPGGLGTPWVHGYPGNS 180  
 |||||  
 DB 113 IRGVDVAVH-----NAGSWGTSQGHGAYGSGGAG--VQGNPQGTTPWAG----- 157  
 QY 181 AGSFQMPQCAPWQGGGNGGPPNFGTNTQGAVAOPGYGVASVNASQNEGCTNPPSGS--- 237  
 |||||  
 DB 158 -GNVGTNSLGGSVQGGNGGPGPLNETHAQAQVAPGYGVAGNNGNNGCTNPPSGSHES 216  
 QY 238 ---GGSSNSNG--GSGSQSGSGSGSNG-----DNNNGSSGSGSGSGSGSGSGSS 286  
 |||||  
 DB 217 FSNSSGSSNDGSRSGSGSHSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSS 274  
 QY 287 GSSSG 339  
 |||||  
 DB 275 GNSNSGNSGNSGSRDIETSNPDEGYSVSRGTGSRGSGSGSGSGSGSGSGSGSGSG 332  
 QY 340 EARGSGESGIGFRGQGVSSNMREISKEGNRLIGSGSDNTRGQSSWGSGGDVAVGVT 399  
 |||||  
 DB 333 DVRAAGSGSG-----GHSGNSGNIGKEAVNGLNT 362  
 QY 400 VNSETSPGMFNPFTPKNPKSKLGFINWDAINKQSS 437  
 |||||  
 DB 363 MNSDASTLPFNIDFWENLKSRTFIMWDAINKHAPS 400

RESULT 7  
 Q6S2J9 MOUSE PRELIMINARY; PRT; 493 AA.  
 AC Q6S2J9;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE EpiDerma8-specific secreted protein SK89 precursor.  
 GN Name=1110014F24Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.

OX NCHI\_TaxID=10090;  
 [1] NUCLEOTIDE SEQUENCE.  
 RN STRAIN=CD1;  
 RC PubMed:15256262; DOI=10.1016/j.gene.2004.03.010;  
 RA Moffatt P., Salois P., St-Amant N., Gaumond M.-H., Lantrot C.;  
 RT "Identification of a conserved cluster of skin-specific genes encoding  
 secreted proteins";  
 RL Gene 334:123-131(2004).  
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 CC  
 DR EMBL; AY444557; AAR20796.1; -, mRNA.  
 DR MGI; MGI:1920962; 1110014F24Rk.  
 DR GO; GO:0005615; C:extracellular space; IDA.  
 DR InterPro; IPR002952; Eggshell.  
 DR PRINTS; PR01228; EGSSHELL.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 493 AA; 49338 MW; 59A94D74FA1C5978 CRC64;  
 1 22 Potential.  
 Query Match 43.6%; Score 1030; DB 2; Length 493;  
 Best Local Similarity 49.6%; Pred. No. 3.3e-47;  
 Matches 224; Conservative 45; Mismatches 101; Indels 82; Gaps 12;  
 QY 1 MKFOGPLALLALCLSGSEAGPLQSGESTGTGIGALGHGLDGLSEGVKAIKENG 60  
 1 MKLGGSLACLALLCLCGGAANPLHSGEGTGA---SAHAGAGALSHIGEAIVQGA 56  
 DB 1  
 QY 61 GAASKVSSEALGCGTREATVGTGVRQVPGFAADALGNRVGEAAHAGNTGHEIGHQAEV 120  
 57 EAASSGIONALGQGHGEGSGTLMGSRG---DVPFHLRGEAARSLGNAGNEIGHQAEV 112  
 DB 1  
 QY 121 IRHGAADVRSQVGPBGHSAMETSGGHGIFGSGGGLGCGCGNCGIGTPTWVHGYPGNS 180  
 113 IRQVNAH-----NAGSWGTSGGHGPYSGGAG--VQGNPGGTPTWASG----- 157  
 DB 1  
 QY 181 AGSFQMPQAGPAGQCGNGGPNFQTNQGAVAOPGYGSVRAONEGCTMPPEPSSG--- 237  
 158 -GNVGTSLGSSVQCGNGGPLANETNAQGAVAOPGYGTVRKANNNSGCTNPPPSGSHS 216  
 DB 1  
 QY 238 ---GGSSNSGG--GGSGQSGSSGSGSNG-----DNNNGSSGGSSSGSSSGSSGSS 286  
 217 FSNQSGSSNDSSRQSGSHSGSGSGSGSGGQGNSDNNGSS--SSSGSSNSGNSGNS 274  
 DB 1  
 QY 287 GSSGSSGSSGNG--GSRDGSSESSWGSTGSSSGNHGSGGNGHKEPCEKPEAFARSG 345  
 275 GNSNSGNSGNSGSGSRG-----TGRGSGSGSGSGSGGKPEKCNPNPANDVMAAG 323  
 DB 1  
 QY 346 ESGIQFRGQGVSSNMREISKGNRLLGSGSDNYRQSGSSWGSGGDAVGVNTVNSETS 405  
 324 GSGSG-----GHSSNGNQLQKZAVNLNTNNSDAS 353  
 DB 1  
 QY 406 PGMEFPTFMKFKSLGFINMDAINKQRSS 437  
 354 TLPEINIDFWENLXSKTRFINMDAINKHAPS 385  
 DB 1  
 RESULT 8  
 Q6PPO CANGA  
 ID Q6PPO CANGA PRELIMINARY; PRT; 1553 AA.  
 AC Q6PPO;  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 30-MAY-2006, entry version 11.  
 DE Similarities with tr|O08294 Saccharomyces cerevisiae YOL155c.  
 GN Ordered locus names=CAGL0J01771g;  
 OS Candida glabrata (yeast) (Torulopsis glabrata).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5478;  
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 2001 / CBS 138 / IFO 0622 / NRRL Y-65;  
 RX PubMed:15229592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,  
 RA Goffard N., Frangoul L., Aigle M., Anhouard V., Badour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boissarie A., Boyer J., Catolico L., Confantolero F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppe R.,  
 RA Hantave F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrat A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Niclaud J.-M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenouli-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Galliardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts";  
 RL Nature 430:35-44(2004).  
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 CC  
 DR EMBL; CR380956; CAG60731.1; -, Genomic DNA.  
 KW Complete proteome.  
 SQ SEQUENCE 1553 AA; 145623 MW; A17810AE221D7480 CRC64;  
 Query Match 20.6%; Score 486; DB 2; Length 1553;  
 Best Local Similarity 33.6%; Pred. No. 1.1e-17;  
 Matches 143; Conservative 38; Mismatches 204; Indels 40; Gaps 10;  
 QY 17 GSGEAGPLQSGES---TGNTIGMALGHGLDGLSEGVKAIKENGAGKVSBAIQ 73  
 432 GSGSSGSGSGSGSTPBGSGSGSGSGSGSGSGSTPBGSGSGSGSGSGSGAPBGS 491  
 DB 1  
 QY 74 GTREAIVGTGVRQV---GFGAADALGNRVGEAAHAGNTGHEIGHQAEVIRHGAADV 129  
 492 GSGSGSGSGSGSTPBGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSTPBGSGSG 551  
 DB 1  
 QY 130 GSNQVGPBGHSAMETSGGHGIFGSGGIG-----GQCGNPGGLTPTWVHGYPGNSAGSF 184  
 552 GSGSGTGSAGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSTPG--EGSGSGSG 610  
 DB 1  
 QY 185 GNNPQGAPWGCGNGGPNFQTNQGAVAOPGYGSVRAONEGCTNPPPSGSGSG--- 241  
 611 TGSAGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSTPBGSGSGSGSGSGSG 670  
 DB 1  
 QY 242 ---SNSGSGSGSQSGS-----SGSGSGNDNNNGSSSG--GSSSGSSSGSGSGSGSGSG 291  
 671 TGSAGSTPBGSGSGSGSG 730  
 DB 1  
 QY 292 GSSG 346  
 731 SSG 790  
 DB 1  
 QY 347 ---SGIQFRGQGVSSNMREISKGNRLLGSGSDNYRQSGSSWGSGGDAVGVNTVNS 402  
 791 PEGSG 845  
 DB 1  
 QY 403 FTSPG 407  
 846 GSNPG 850  
 DB 1  
 RESULT 9  
 Q6CHN8 YARLI  
 ID Q6CHN8 YARLI PRELIMINARY; PRT; 1274 AA.  
 AC Q6CHN8;  
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
 DT 16-AUG-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 12.  
 DE Similarity (Fragment).  
 GN Ordered locus names=YAL10A06853g;  
 RN [1]

OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=4952;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Clb 122 / E 150.  
 RX PubMed=15229592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Duretts P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Mack C., Neuvéglise C., Talla E.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boissarime A., Boyer J., Catolico L., Confariolieri F., de Darvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicoud J.-M., Nikolaki M., Ozes S., Ozeri-Kalogenopolos O.,  
 RA Pellenz S., Pottier S., Richard G.-F., Straub M.-L., Sileau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., With B.,  
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron J.-L.,  
 RA Wincker P., Souciet J.-L.,  
 RL "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
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 CC EMBL: CR381212; CAG83749.1; -; Genomic\_DNA.  
 DR InterPro: IPR002952; Eggshell.  
 DR PRINTS: PR01228; EGGSHLL.  
 DR Complete proteome.  
 FT NON TER 1  
 SQ SEQUENCE 1274 AA; 116260 MW; 33583C8CE680B3E2 CRC64;  
  
 Query Match: 19.9%; Score 471; DB 2; Length 1274;  
 Best Local Similarity 36.2%; Pred. No. 5.7e-17;  
 Matches 149; Conservative 27; Mismatches 168; Indels 68; Gaps 16;  
  
 QY 17 GSGEAGPIQSGHE-----TGTNIGALGHGLDALSEGVKAIKREAGAGAKYSE 69  
 DB 881 GSGSGGDDTSGNGSGSGGDDTSGNGSSGSGSGSGGDDSSNG-----GGSGSGSG----- 932  
 QY 70 ALGQGTREAVGTGROVPFGAADALGNRVBPAHALCNTGHEIGRAQEDVIRIGADAV- 128  
 DB 933 --GDGTS---GNGSGSGSGSGGDDGSSGNGSGSGSGGDDTSGNGSGSGS-----GGDGTG 981  
 QY 129 ---RSMQGVPRHSGAMETSGCHGIFSGQGLG--CGQGNPGCIGTPVWGHVPRGNSASF 184  
 DB 982 GNGSGSGSGGDDSSNGSGSGGDDTSGSGSGSGSGSGSGSGSGS---DGTSGSGSGS- 1036  
 QY 185 GNNPGCAPWGCGGCGNPGPFNTTNGAVALQPCYGVRAASNQNEGCTNPPPSGSGGCS-- 241  
 DB 1037 -----SGNGG-----SGSGSGSDSGSGSGSGSGSGSGSGSDSGSGSGSGSGSG 1080  
 QY 242 SNGSGGSGSGSGSGSGSGSGNNGNNGSSG--SSSSGSSSGSSSGSGSGSGSSGSGNSG 298  
 DB 1081 SDSGSGSGSGSG--SSSGSGSDSGSGSGSGSGSGSGSDSGSGSGSGSGSGSGSGS 1139  
 QY 299 GSRGDSGSESWGSGSTGSSSGNHGSGGGGNGHKPCCEKPCNENRSG--ESGIGPRGGV 357  
 DB 1140 GSDSGSGSGSGSGSGSGSGSGSGSGSGSGSGSDSGSGSGSGSDSGSGSGSDSGSGSGSGS 1199  
 QY 358 SSNNKEIKEGNRLLGSGDNNRQCGSSSWGSGGADAVGAVTVNSETPGMF 409  
 DB 1200 DSGSGSGSGSGSDSGSGS-----SGSDSGSGSGSGGLG-----TDSGPRDP 1243

DT	01-OCT-2003, sequence version 1.
DT	02-MAY-2006, entry version 12.
DE	PE-PGRS FAMILY PROTEIN.
GN	Name=PE_PGRS5; OrderedLocustNames=Mb3541;
OS	Mycobacterium bovis.
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC	Corynebacteriineae; Mycobacteriaceae; Mycobacterium;
OC	Mycobacterium tuberculosis complex.
OX	NCBI_TaxID=1765;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	STRAIN=AF2122/97;
RX	MEBLIN=22709107; PubMed=12768972; DOI=10.1073/pnas.1130426100;
RA	Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansour H.,
RA	Pryor W., Duthoy S., Grondin S., Lacroix C., Monsemppe C., Simon S.,
RA	Harris B., Atkin J., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA	Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RL	"The complete genome sequence of Mycobacterium bovis.";
RL	Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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CC	-----
DR	EMBL; BX248346; CAD95727.1; -; Genomic_DNA.
DR	GenomeReviews; BX24833 GR; Mb3541.
DR	InterPro; IPR002952; Eggshell1.
DR	InterPro; IPR000202; HMG-CoA_red.
DR	InterPro; IPR000084; PE_region_N.
DR	InterPro; IPR002173; PEK.
DR	Pfam; PF00934; PE; 1.
DR	PRINTS; PR01228; EGGSELL.
DR	ProDom; PD001223; PE_region_N_1.
DR	ProSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1.
DR	ProSITE; PS00583; PPKB_KINASE_1; UNKNOWN_1.
FW	Complete proteome.
QO	SEQUENCE 1938 AA; 152027 MW; 3CC73A507EB0F9C CRC64;

Query Match	Similarity	19.5%	Score 460.5	DB 2	Length 1938
Best Local	Similarity	31.5%	Pred. No. 3.1e-16		
Matches	146	Conservative	36	Mismatches 173	Indels 109
				Gaps	17
Qy	17	GSGEAGPLQSGESTGTNIGBALGHGLDALSBGVGAIKKACGAARSRYSEALFGQTR	76		
Db	1218	GAGSGSP-----NTSPGNGGQ-----GQSGSGAGAG--AGGAGGANGTAGNGGQ	1266		
Qy	77	EAVTGYRQYVGFPAADALNKRVEAAHALGNTHEIGRQAEVYIRRGADAVYSGWQVP	136		
Db	1267	GAGGTG-----GAGMASSATMGSGGAGGTGAAGTGA-----GGGVGAGAGNG	1313		
Qy	137	GH-----SGAMETSGGHGIFGSGGLGQ-----GQGNPGLGTP	171		
Db	1314	GHGDDADGCGNAGANNRRSSGSLFLAAGTGGAAADGGGQGGGAGGAGGAGGAGGT	1373		
Qy	172	WVHGYPGN-----SAGSFQMNPOGAPWQGGNGPNNFTNTQ--GAVALPYGTV	220		
Db	1374	GGNG--GNITGTGTAGTAAGNGCAAGKGAAGGQGGTGG-----GTGQGGAGGGDGAAGT	1427		
Qy	221	RASNMQEECTPPPSGSGGSSNNG-----GSGSOSGSSGSGNEDNNNGSS	268		
Db	1428	GGDRTVGGGTYPAASGGCGGNVAGCGGAGCGGADGSGGCGDAGTGGNGNGNRRISGN	1487		
Qy	269	SGSSSGSSSGSSSGSSG--GSSGSGSGNCGSGSHDGSBSBSSWGSSTGSSBGNHGS--	325		
Db	1488	GTGAGAGNGCGGANGAGAGAGSGGGTGTGNCGAGDAGDAGNGNGNGTGNNGGNGNGGI	1547		
Qy	326	-----GNGHNRPCCKPENEARSGESGIIQFRG--QYVSSMRE	363		
Db	1548	AGMGANGAGTSGSNGNGSGGANGNG--MGNSGTGSGDGGAGGANGGAAGTGTGGD	1605		
Qy	364	ISKGNRLLGSGGNYRGQSGSSWGGCGDAVGVTYNNSETSPG	407		
Db	1606	GGLTGTGTGSGS-----GTGGDGGNGGNGGADNTANMTAAG	1645		

	RESULT	11
ID	Q6MWW7_MYCTU	PRELIMINARY; PRT; 1079 AA.
AC	Q6MWW7;	
DT	05-JUL-2004,	integrated into UniProtKB/TrEMBL.
DT	05-JUL-2004,	sequence version 1.
DT	02-MAY-2006,	entry version 10.
DE	PE-PGRS FAMILY PROTEIN (Fragment).	
GN	Name=PE_PGRS56; Ordered locus names=Rv3512;	
OS	Mycobacterium tuberculosis.	
OC	Bacteria; Actinobacteria; Actinomycetales;	
OC	Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;	
OC	Mycobacterium tuberculosis complex.	
OX	NCBI_TaxId=1773;	
RN	[1]	
RC	Nucleotide sequence [large scale genomic DNA].	
CC	STRAIN=H37Rv;	
CC	MEDLINE=98295987; Pubmed=9634230; DOI=10.1038/31159;	
CC	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,	
CC	Harris D.E., Gordon S.V., Eigleier K., Gas S., Barry C.F. III,	
CC	Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,	
CC	Connor R., Davies R.M., Devlin K., Felzelwell T., Gentles S., Hamlin N.,	
CC	Holtroyd S., Hornby T., Jagels K., Krogh A., Mclean J., Moule S.,	
CC	Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,	
CC	Rogers J., Rutter S., Seeger K., Skellern S., Squares S., Squares R.,	
CC	Sulton J.E., Taylor K., Whitehead S., Barrett B.G.;	
CC	"Deciphering the biology of Mycobacterium tuberculosis from the	
CC	complete genome sequence."	
CC	Nature 393:537-544 (1998).	
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DR	EMBL; BX842583; CAB55606.1; -, Genomic_DNA.	
DR	GenomeReviews; ALI23456_GR; RV3512.	
DR	TubercuList; RV3512; -	
DR	InterPro; IPR002202; HMG-CoA red.	
DR	PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1.	
FT	Complete proteome.	
KW	NON_TER	
SO	SEQUENCE	1079 AA; 81162 MW; A79718CDBC74B97D CRC64;
	Query Match	19.1%; Score 450.5; DB 2; Length 1079;
	Best Local Similarity	30.5%; Pred. No. 6.1e-16;
	Matches	139; Conservative 40; Mismatches 181; Indels 95; Gaps 15
QY	17 GSSEKGPLQSSESTGTNIIGELGH-----GLDPALSEGVCALGKEAGGAASRYSE	69
DB	336 GNGGAAGAATAGSNAGAGTSGAGNGCTGRGSGGAGGADGICGVGGKGNGADQEVCG	395
QY	70 ALGGCTRRAVETGVNQVP-----FGAADLGNRVGEAAH-ALGNTGH	111
DB	396 AGGAG----SSGPNTSPGANGGGGGGGGGGAGGAAGAAGAGGAGANTGANGGGGAGG	450
QY	112 EIGHQAEDIVIRHGDAVRGSWGCVFHSAGMETSG-----GHGIFSSQGLG3--QG	161
DB	451 TGAGAGAAASATNNGSGGAGAGTCGDDGSGAGAGTGACGTGCAAGADCGGGGAGAGAGG	510
QY	162 QGNPGCLGTPWHVGYPN-----SAGSFQNNPQAPWVGCGGNGGPPNFNTQ-G	210
DB	511 QGAGAGAGAGTGANG--GNITGCTAGTAGAAGNGAAGKAGAGAGGGGTG---GTGGGQG	564
QY	211 AVADPGYSVAASNQEGCTNPPEGSGGGGSSNSG-----GSSGSSGSSSGS	258
DB	565 AGDGAGAGTGCTDRTVGGGTVPAGSGGGQGANGGGAGAGGGAGDGGSGGDGDACTGANG	624
QY	259 SNGDNNNSSSGSSSSSSSSSSSSSGSSSGS86--GSSGSSGNGSGSRDPSGESWSGSTGS	317
DB	625 GNGCNRRNSGNTGCAGCGNGCGGANGAGAGAGSGCGGTGNGAGAGDADAGNGNGNGTG	684
QY	318 SGNHGSGS-----GGNGHKPCGCEKRGNEARSGSGESGICGFRCQGVSSNMREISKGNRL	372

Db	685	NGCANGNGAGIAGMGN	-----GAGGTGSGNGNGSGGANG-----	CNAGM 722
Qy	373	CGSGDNTRGCGSSWMSGGADAVGVNTYNSERSPG	407	
Db	725	GANSCTGSGDGAAGNGGAAGTGTGCGDGLTGTG	759	
RESULT 12				
Qy	17	GSGEAGPLOSGBESTGTN--IGEALGHGLGALSGEVKATLK-----EKGAGASGV	67	
Db	567	GHGAAGL-----GVNCGVGAGAGHG-GD---PVGAGAGGQSSGSPGANGA.PGMT	615	
Qy	68	SEA--LQGTREAVGTGVRQVPGFADALGNRVE-AAHALGNTGHE--IGFOADV	120	
Db	616	TSGNGNGGAGGADATGPGQTGAAGRGDGLVNGGAGAGGNGSKLPGLGRLGNP-	674	
Qy	121	IRHGADAVRSGWQVPHSGSGWERSGCHGIRGSGGGLGQG-----QGNPG	166	
Db	675	---GLDGGTGNAGGAGSGGAMAENGKGTGAGGTGGVGGTGGSGSDGVNGSSAGADGHHG	731	
Qy	167	GLGTPWVHGVRGNSAGSFGMNPQG-----APWGAGGANGGPPVFGTN-----TQG	210	
Db	732	GTCGAVGTGCGGCGGCGGAAPNGVAGSQGREGAGSDGGTGTGVRGNGRGRLDADGATRG	791	
Qy	211	AVAQPGVGSVRASNONBCTNP-----PSGS-----GGGSSNGGSGSGQSGSGSGSNGD	262	

Db 792 ARGODGAGAGAGCGKGGCTGPGGAGPAGTTGSGAGNGSGGTGDPDGGANGS 851  
 QY 263 --NNNGSSSGSSSSSGSSSGSSG-----GSS-----GSSGNSG----- 298  
 Db 852 VFTNNGIGGNGGNGGNGAGPAGAGTGTGATGSSSSIHVNGGNGGNGDHALSG 911  
 QY 299 -GSRGDSSESSSWGSSSTGSS-SGNGHGSG-----GGNGHKPCCEKPGNEARSGESGI 349  
 Db 912 NGAAGGNGGNGGNGSLRSGSGAGGNGGNGASRGMGGDGTGTGAGGAGGQIGNGAGAGN 971  
 QY 350 QGFRGQGVSSNMREISKEGNNR-----LLGSGSDNTRGQSSSWGSGGDAVGV---NTVNS 402  
 Db 972 GGGGTGSDNPAITGSGGGRGDDGVGGGGSVAAGDAGRGAGGTGTGTRGTTGA 1031  
 QY 403 ETSFGMEN 410  
 Db 1032 TGATGTFD 1039

## RESULT 13

O6MX28 MYCTU

ID O6MX28 MYCTU PRELIMINARY; PRT: 1306 AA.

AC O6MX28; MEDLINE=9829587; Pubmed=9634230; DOI=10.1038/31159;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 02-MAY-2006, entry version 10.

DE PE-PGRS FAMILY PROTEIN

GN Name=PE\_PGRS7; OrderedLocustNames=Rv0578c;

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;

OC Mycobacterium tuberculosis complex.

OX NCBI\_TaxID=1773;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=H37Rv; MEDLINE=9829587; Pubmed=9634230; DOI=10.1038/31159;

RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C.M.,

RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,

RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,

RA Connor R., Davies R.M., Devlin K., Feltham T., Gentles S., Hamlin N.,

RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,

RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,

RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sissons J.E., Taylor K., Whitehead S., Barrett B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence."

RL Nature 393:537-544(1998).

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CC EMBL: BX842573; CA255300.1; -; Genomic DNA.

DR GenomeReviews: AL123456 GR; Rv0578c.

DR Tuberculist: Rv0578c; -;

DR InterPro: IPR002952; Eggshell.

DR InterPro: IPR000084; PE\_region\_N.

DR Pfam: PF00934; PE; 1.

DR PRINTS: PR01228; EGGSHL.

DR ProDom: PD001223; PE\_region\_N.1.

DR PROSITE: PS00138; SUBTILASE\_SER; UNKNOWN\_1.

KW Complete proteome.

SQ SEQUENCE 1306 AA; 105963 MW; 843A30955FFA56B6 CRC64;

Query Match 18.6%; Score 439.5; DB 2; Length 1306;

Best local similarity 30.9%; Pred. No. 2.8e-15;

Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

QY 17 GSGEAGPLQSGESTGTN--IGELIGHGLDALSEGVAKIGK-----BAGAGAGSKV 67  
 Db 567 GHGAMGAL-----GVNGVGAGAGGCG-GD---PGVGAGAGGSGSGSTPGANAPANTP 615

QY 68 SEA--LQGTTEAVGTGVRYPGFADALGNRYGE-AAHALGNTGHE-----IGRQAEV 120  
 Db 616 TSGNGNGGGRGADATGPGQTGTASGGRGDDGLVGNNGAGAGAGNGSKGLPGLRLGNP- 674  
 QY 121 IRHGDADVRSWQGVPPHSGAETSQGHGTFGSGGLGQGG-----QGNPG 166  
 Db 675 --GLDGTGTGNGAGSGSGGMAAGNGTGTGAGGTGVTGTGSSSDVNGSSAGADGHPG 731  
 QY 167 GLGTPWVHYGPNASGSPGNPQG-----APWGGGNGGPNPFGTN-----TOG 210  
 Db 732 GTGAVGTGTGCGGCGGCGGGAAPNVASQGFPGAGDGTGTGCGVNGCRGIDGADGATAG 791  
 QY 211 AVAPGYGVASVNASQNECTNP-----PSGS-----GGSSNSGGGSGSQSSSGSGSNGD 262  
 Db 792 ARGODGAGAGAGCGKGRGTGTGPGGAGPAGTTGSGAGNGSGSGTGTGDPDGGANGS 851  
 QY 263 --NNNGSSSGSSSSSGSSSGSSG-----GSS-----GSSGNSG----- 298  
 Db 852 VFTNNGIGGNGGNGGNGAGPAGAGTGTGATGSSSSIHVNGGNGGNGDHALSG 911  
 QY 299 -GSRGDSSESSSWGSSSTGSS-SGNGHGSG-----GGNGHKPCCEKPGNEARSGESGI 349  
 Db 912 NGAAGGNGGNGGNSLRSGSGAGGNGGNGASRGMGGDGTGTGAGGAGGQIGNGAGAGN 971  
 QY 350 QGFRGQGVSSNMREISKEGNNR-----LLGSGSDNTRGQSSSWGSGGDAVGV---NTVNS 402  
 Db 972 GGGGTGSDNPAITGSGGGRGDDGVGGGGSVAAGDAGRGAGGTGTGTRGTTGA 1031  
 QY 403 ETSFGMEN 410  
 Db 1032 TGATGTFD 1039

## RESULT 14

Q7U1Q7 MYCBO

ID Q7U1Q7 MYCBO PRELIMINARY; PRT: 1306 AA.

AC Q7U1Q7; MEDLINE=22709107; Pubmed=12788972; DOI=10.1073/pnas.1130426100;

DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2003, sequence version 1.

DT 02-MAY-2006, entry version 12.

DE PE-PGRS FAMILY PROTEIN.

GN Name=PE\_PGRS7; OrderedLocustNames=Mb0593c;

OS Mycobacterium bovis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;

OC Mycobacterium tuberculosis complex.

OX NCBI\_TaxID=1765;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=AF2123/97; MEDLINE=22709107; Pubmed=12788972; DOI=10.1073/pnas.1130426100;

RA Gantler T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

RA Pryor M., Dutfoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,

RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

RA Parkhill J., Barrett B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

RT "The complete genome sequence of Mycobacterium bovis."

RT Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

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CC EMBL: BX248336; CA293455.1; -; Genomic DNA.

DR GenomeReviews: BX248333 GR; Mb0593c.

DR InterPro: IPR002952; Eggshell.

DR InterPro: IPR000084; PE\_region\_N.

DR Pfam: PF00934; PE; 1.

DR PRINTS: PR01228; EGGSHL.

DR ProDom: PD001223; PE\_region\_N.1.

DR PROSITE: PS00138; SUBTILASE\_SER; UNKNOWN\_1.

KW Complete proteome.

SQ SEQUENCE 1306 AA; 105993 MW; 65628F8D401F4AD42 CRC64;

Query Match 18.6%; Score 439.5; DB 2; Length 1306;  
 Best Local Similarity 30.9%; Pred. No. 2.8e-15;  
 Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

QY 17 GSGEAGPIQSGEESTGTN--IGELALGHGLDALSEGVAAIK-----EAGGAAGSKV 67  
 DB 567 GHGAAGL-----GVAGGVGAGAGHG-GD---FVGAGAGGQSSGSPRANGAPGNTP 615  
 QY 68 SEA--LGGTRBAVGTGRVQVPGFADALGNRVE-AAHALGNTGHE---IGRQAEV 120  
 DB 616 TSGGNGNGRGADATGFGQTGASGGRGDDGLVNGAGAGAGNGSKGLPELGLRLGNP- 674  
 QY 121 IRRHADAVRSGMOWGVPFHSAMETSGHGIFPSQGLGQG-----QGNPG 166  
 DB 675 ---GLDGGTGAGGAGSGGAGMAAGGCTGAGAGTGAGTGSGSDGVNGSSAGADGHPG 731  
 QY 167 GLGTPWVHYGPONASGFGMNPQ-----APWGQAGNGGPPNFGTN-----TQG 210  
 DB 732 GTGCVGTGKGGKGGDGGDGAAPNVAGSQGPGAGAGDGTGTVGNGRGIDGADGATNG 791  
 QY 211 AVAOPGYGVRAVSNONEGCTNP---PSGS-----GGSSNSGGSGSGSGSGSGSND 262  
 DB 792 ARGQDGGAGAGAGKGGRGGTGGGAGPAGTTGSGAGAGNGSGGTGDDPDGCGANGANG 851  
 QY 263 --NNNGSSSGSSSGSSSGSSSGSSG-----GSS-----GSSGNSG----- 298  
 DB 852 VFTNNGTGGNGGNGNAPSGAGSGGAGSTFGATGSSSSIHVNGNGNGNGNGDHALSG 911  
 QY 299 -GSHGDSSESSWGSSTGS--SSGNHGSAG-----GGNGHKGCEKNGENARSGESGI 349  
 DB 912 NGAAGNGNGNGNGNGSLRSGGAGGGGNGGNGNARMGMDGGTGGAGGAGAGGAGAGN 971  
 QY 350 QGFRGQGVSSNMREISKEGNNR---LIGSGGDNVYRGSSWGSAGGAVGV---NTVNS 402  
 DB 972 GGDGDTGSDGNPAGLTGSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1031  
 QY 403 ETSFGMPN 410  
 DB 1032 TGATGTG 1039

RESULT 15  
 Q7SEP7 NEUCR PRELIMINARY; PRT; 725 AA.  
 AC Q7SEP7;  
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
 DT 15-DEC-2003, sequence version 1.  
 DT 30-MAY-2006, entry version 12.  
 DE Predicted protein.  
 GN Name=NCU02170.1;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OC NCBI\_TaxID=5141;  
 RN NP  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=OR74A.  
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 Jaffe D., Fitzhugh W., Ma L.-U., Smirnov S., Purcell S., Reiman B.,  
 Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
 Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
 Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
 Kamal M., Kamysselellis M., Mauceli E., Bielke C., Rudd S., Frisman D.,  
 Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
 Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,  
 Desouza C.C., Glass L., Orbach M.J., Berglund J.A., Voelker R.,  
 Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,  
 Natvig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Freitag M.,  
 Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,  
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa,"  
 RL Nature 0:0(2003).

RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=74-OR23-1A / FGSC 987;  
 RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;  
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 Jaffe D., Fitzhugh W., Ma L.-U., Smirnov S., Purcell S., Reiman B.,  
 Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
 Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
 Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
 Kamal M., Kamysselellis M., Mauceli E., Bielke C., Rudd S., Frisman D.,  
 Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
 Cogoni C., Macino G., Catchside D.E.A., Li W., Pratt R.J., Osmani S.A.,  
 Desouza C.C., Glass L., Orbach M.J., Berglund J.A., Voelker R.,  
 Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,  
 Natvig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Freitag M.,  
 Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,  
 RT "The genome sequence of the filamentous fungus Neurospora crassa,"  
 RL Nature 422:859-868(2003).  
 CC -! CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
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 CC Distributed under the Creative Commons Attribution-NonCommercial-ShareAlike license  
 CC EMBL, AABX0100029; EAA35293.1; -; Genomic\_DNA.  
 DR UniGene: Ncr.3814; -;  
 DR InterPro: IPR02952; Eggshell.  
 DR PRINTS: PR01228; EGSSHELL.  
 SQ SEQUENCE 725 AA; 63929 MW; 60F0003860219B9C CRC64;

Query Match 18.3%; Score 433; DB 2; Length 725;  
 Best Local Similarity 29.8%; Pred. No. 3.6e-15;  
 Matches 137; Conservative 46; Mismatches 173; Indels 104; Gaps 20;

QY 17 GSGEAGPIQSGEESTGTNIGELALGHGLDALSEGVAAIK-----EAGGAAGSKV 76  
 DB 185 GSG-LGGFGAGAGAGYVNGAGNGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243  
 QY 77 EAVGTGRVQVPGF-----AADALGNRVGEAAHALGNTGHEIGRQAEVIRHGDV 128  
 DB 244 N--GLGVNIGTGLNSAGGLDGSAGYVNGAG--AGNGAGNG--LG----- 284  
 QY 129 RGSNGV--PGHSAMETSGHG--IFSGGGLGQGGQGNPGLGTPWVHYGPGNSAGSFGM 186  
 DB 285 NGSNGGLANGSGANNNGNGMDGSGMGAGAGGPG--GAGGLGNG--ASGPGNGVGLGN 341  
 QY 187 NPGAPMGQGGNGPPNFGTITQCAVAPGYGVRAVSNONEGCTN-----PPSGSG 238  
 DB 342 GAGGLGYSSGGPGGDTSGNGNIGASNNNGNSAGNGNNGNGSGNGAGAGCAPCGNG 401  
 QY 239 GGSNSG 276  
 DB 402 NGNGN--GNGNGNGNGNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAG 460  
 QY 277 -----SSGSSSG 325  
 DB 461 IGTSPREALIVGSGAGNGCGNGNGNGSGSGSGSGSGSGSGAGNGNGN--GSGNGAGAGNGCG 519  
 QY 326 GGNHKGCEKPGNEARGSGSTIQG---FRGGVSSNM-----REISKE--- 367  
 DB 520 NGNGN-----GNDG--GAGNGGAPAPTPCTGSGPSFLVITITVPPARVVEKKQYWN 571  
 QY 368 GNRLLGSGGDNVYRGSG 407  
 DB 572 ANVAVYGGPDD--GAGAAPSGSGSGSVAPGNGNGSGSGSAPG 609

Search completed: March 28, 2007, 21:09:49  
 Job time : 411 secs



GenCore version 6.2  
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OM protein - protein search, using sw model

Run on: March 28, 2007, 20:52:45 ; Search time 83 seconds  
(without alignments)  
2455.597 Million cell updates/sec

Perfect score: 2363  
Sequence: 1 MKFGPIACILALCLSGSE.....KLGFINMDAINKDQSRNP 440

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :

Published Applications\_AA\_Main:  
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2: /EMC\_Celettera\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celettera\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celettera\_SIDS3/prodata/2/pubppaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celettera\_SIDS3/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celettera\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
146	2363	100.0	440	4	US-10-066-269-1066
516	2363	100.0	440	4	US-10-223-085-1506
522	2363	100.0	440	4	US-10-219-065-1506
565	2363	100.0	440	4	US-10-223-084-1506
566	2363	100.0	440	4	US-10-223-088-1506
573	2363	100.0	440	4	US-10-223-090-1506
586	2363	100.0	440	4	US-10-223-087-1506
592	2363	100.0	440	4	US-10-223-083-1506
618	2363	100.0	440	4	US-10-223-089-1506
688	2363	100.0	440	4	US-10-174-587-2022
688	2363	100.0	440	4	US-10-063-742-522
764	2363	100.0	440	4	US-10-013-909A-522
769	2363	100.0	440	4	US-10-223-081-1506
807	2363	100.0	440	4	US-10-223-082-1506
839	2363	100.0	440	4	US-10-305-654-1506
848	2363	100.0	440	4	US-10-081-056-1506
860	2363	100.0	440	5	US-10-972-317-522
874	2363	100.0	440	6	US-11-025-607-522
875	2363	100.0	440	6	US-11-102-240-522
876	2363	100.0	440	6	US-11-103-195-522
877	2030	85.9	386	4	US-10-050-704-100
878	2030	85.9	386	4	US-10-798-512-100
879	875.5	37.1	186	5	US-10-986-405-266
880	450.5	19.1	1079	3	US-09-820-843A-20
881	450.5	19.1	1079	6	US-11-052-554A-145
882	439.5	18.6	1306	4	US-10-282-122A-64405
883	439.5	18.6	1306	6	US-11-052-554A-139
884	421	17.8	384	4	US-10-479-638-19

885	415.5	17.6	1381	4	US-10-282-122A-64895	Sequence 64895, A
886	415.5	17.6	1381	6	US-11-052-554A-138	Sequence 138, App
887	412.5	17.5	484	3	US-09-820-843A-19	Sequence 19, App
888	412.5	17.5	484	4	US-10-282-122A-64867	Sequence 64867, A
889	412.5	17.5	484	6	US-11-052-554A-170	Sequence 170, App
890	406.5	17.2	357	3	US-09-864-761-35807	Sequence 35807, A
891	406	17.2	1901	6	US-11-052-554A-135	Sequence 135, App
892	404.5	17.1	532	4	US-10-282-122A-64658	Sequence 64658, A
893	402.5	17.0	1136	2	US-08-806-029-9	Sequence 9, App
894	402.5	17.0	1137	4	US-10-096-986-64	Sequence 64, App
895	400.5	16.9	1538	6	US-11-052-554A-146	Sequence 146, App
896	399.5	16.9	853	6	US-11-052-554A-149	Sequence 149, App
897	399	16.9	1059	2	US-08-806-029-10	Sequence 10, App
898	399	16.9	1101	4	US-10-096-986-83	Sequence 83, App
899	395	16.7	1660	6	US-11-052-554A-137	Sequence 137, App
900	392.5	16.6	923	4	US-10-282-122A-64474	Sequence 64474, A
901	392.5	16.6	923	6	US-11-052-554A-147	Sequence 147, App
902	392	16.6	731	6	US-11-052-554A-155	Sequence 155, App
903	392	16.6	1329	6	US-11-052-554A-136	Sequence 136, App
904	392	16.6	1329	6	US-11-087-099-882	Sequence 882, App
905	392	16.6	1408	6	US-11-087-099-8482	Sequence 8482, App
906	386	16.3	778	4	US-10-282-122A-64751	Sequence 64751, A
907	386	16.3	778	6	US-11-052-554A-144	Sequence 144, App
908	383.5	16.2	767	6	US-11-052-554A-154	Sequence 154, App
909	383	16.2	641	4	US-10-138-098-52	Sequence 52, App
910	383	16.2	641	4	US-10-294-804-4	Sequence 4, App
911	383	16.2	641	4	US-10-225-838B-22	Sequence 22, App
912	383	16.2	641	4	US-10-732-694-11	Sequence 11, App
913	383	16.2	641	5	US-10-194-046-4	Sequence 4, App
914	383	16.2	641	5	US-10-476-615-52	Sequence 52, App
915	383	16.2	641	5	US-10-978-696A-22	Sequence 22, App
916	383	16.2	641	5	US-10-848-976-1	Sequence 1, App
917	381.5	16.1	741	6	US-11-052-554A-161	Sequence 161, App
918	380.5	16.1	837	4	US-10-282-122A-64362	Sequence 64362, A
919	380.5	16.1	837	6	US-11-052-554A-159	Sequence 159, App
920	379	16.0	465	6	US-11-087-099-9344	Sequence 9344, App
921	378	16.0	588	4	US-10-282-122A-64869	Sequence 64869, A
922	378	16.0	588	5	US-10-481-563A-4	Sequence 4, App
923	378	16.0	646	4	US-10-406-832-27	Sequence 27, App
924	378	16.0	646	5	US-10-893-588-27	Sequence 27, App
925	376.5	15.9	749	6	US-11-052-554A-148	Sequence 148, App
926	375	15.9	914	4	US-10-282-122A-64606	Sequence 64606, A
927	375	15.9	914	6	US-11-052-554A-160	Sequence 160, App
928	373.5	15.8	520	4	US-10-479-638-21	Sequence 21, App
929	373.5	15.8	584	4	US-10-282-122A-64903	Sequence 64903, A
930	373.5	15.8	667	4	US-10-282-122A-64494	Sequence 64494, A
931	372	15.7	694	4	US-10-282-122A-64726	Sequence 64726, A
932	372	15.7	694	6	US-11-052-554A-158	Sequence 158, App
933	371	15.7	400	6	US-11-087-099-11207	Sequence 11207, A
934	371	15.7	615	4	US-10-282-122A-64786	Sequence 64786, A
935	371	15.7	615	6	US-11-052-554A-152	Sequence 152, App
936	371	15.7	651	3	US-09-861-597-1	Sequence 1, App
937	371	15.7	651	4	US-10-414-760-1	Sequence 1, App
938	371	15.7	651	5	US-10-887-100-1	Sequence 1, App
939	370.5	15.7	491	4	US-10-282-122A-64558	Sequence 64558, A
940	368	15.6	420	4	US-10-437-965-201378	Sequence 201378, A
941	367	15.5	1011	4	US-10-096-986-94	Sequence 94, App
942	366	15.5	408	6	US-11-087-099-1332	Sequence 1332, App
943	366	15.5	610	6	US-11-097-143-30480	Sequence 30480, App
944	366	15.5	691	5	US-10-488-056-48	Sequence 48, App
945	366	15.5	766	4	US-10-096-986-88	Sequence 88, App
946	366	15.5	979	4	US-10-096-986-89	Sequence 89, App
947	365	15.4	576	4	US-10-282-122A-64547	Sequence 64547, A
948	365	15.4	576	6	US-11-052-554A-164	Sequence 164, App
949	365	15.4	591	4	US-10-282-122A-64363	Sequence 64363, A
950	364.5	15.4	801	6	US-11-052-554A-166	Sequence 166, App
951	364.5	15.4	2018	4	US-10-096-986-80	Sequence 80, App
952	364	15.4	606	4	US-10-282-122A-64464	Sequence 64464, A
953	364	15.4	606	6	US-11-052-554A-163	Sequence 163, App
954	363.5	15.4	2304	4	US-10-479-638-53	Sequence 53, App
955	363	15.4	639	4	US-10-282-122A-64609	Sequence 64609, A
956	363	15.4	639	6	US-11-052-554A-165	Sequence 165, App
957	360	15.2	562	4	US-10-282-122A-64514	Sequence 64514, A



958	359.5	15.2	1011	4	US-10-282-122A-64589	Sequence 64589, A	1031	320	13.5	620	6	US-11-097-143-39294	Sequence 39294, A
959	359	15.2	525	5	US-10-479-638-16	Sequence 16, Appl	1032	320	13.5	1953	5	US-10-488-056-42	Sequence 42, Appl
960	359	15.2	525	5	US-10-488-056-54	Sequence 54, Appl	1033	319.5	13.5	318	4	US-10-258-678-727	Sequence 727, App
961	359	15.2	854	5	US-10-488-056-47	Sequence 47, Appl	1034	319.5	13.5	318	5	US-10-802-796-727	Sequence 727, App
962	358.5	15.2	466	4	US-10-437-963-117435	Sequence 117435,	1035	319.5	13.5	318	6	US-11-221-284-127	Sequence 127, App
963	358.5	15.2	486	6	US-11-087-099-9792	Sequence 9792, Ap	1036	318	13.5	884	5	US-10-800-179-25	Sequence 25, Appl
964	358.5	15.2	2055	4	US-10-096-986-81	Sequence 81, Appl	1037	318	13.5	884	5	US-10-845-775A-25	Sequence 25, Appl
965	358	15.2	606	3	US-09-861-597-4	Sequence 4, Appli	1038	318	13.5	884	5	US-10-845-936A-25	Sequence 25, Appl
966	358	15.2	606	3	US-09-861-597-6	Sequence 6, Appli	1039	318	13.5	884	5	US-10-939-036-25	Sequence 25, Appl
967	358	15.2	606	3	US-09-861-597-8	Sequence 8, Appli	1039	317.5	13.5	888	5	US-08-806-029-28	Sequence 28, Appl
968	358	15.2	606	5	US-10-887-100-4	Sequence 4, Appli	1041	315.5	13.4	965	4	US-10-800-179-31	Sequence 31, Appl
969	358	15.2	606	5	US-10-887-100-6	Sequence 6, Appli	1042	315.5	13.4	965	5	US-10-845-775A-31	Sequence 31, Appl
970	358	15.2	606	5	US-10-887-100-8	Sequence 8, Appli	1043	315.5	13.4	965	5	US-10-845-936A-31	Sequence 31, Appl
971	358	15.2	809	4	US-10-414-760-13	Sequence 13, Appl	1044	315.5	13.4	965	5	US-10-939-036-31	Sequence 31, Appl
972	358	15.2	818	4	US-10-414-760-22	Sequence 22, Appl	1045	314.5	13.3	965	5	US-11-053-554A-162	Sequence 162, App
973	358	15.2	1617	4	US-10-414-760-14	Sequence 14, Appl	1046	314.5	13.3	1968	4	US-10-123-155-163	Sequence 163, App
974	358	15.2	1626	4	US-10-414-760-24	Sequence 24, Appl	1058	314	13.3	304	6	US-09-764-891-2877	Sequence 2877, Ap
975	357	15.1	761	4	US-10-479-638-18	Sequence 18, Appl	1059	314	13.3	304	6	US-11-188-298-16460	Sequence 16460, A
976	355	15.0	291	6	US-11-087-099-3763	Sequence 3763, Ap	1060	312.5	13.2	252	6	US-11-087-039-8418	Sequence 8418, Ap
977	355	15.0	291	6	US-11-188-298-14514	Sequence 14514, A	1061	312	13.2	242	4	US-10-425-114-61520	Sequence 61520, A
978	353	14.9	505	4	US-10-282-122A-62341	Sequence 62341, A	1062	309.5	13.1	200	3	US-09-798-584-18	Sequence 18, Appl
979	352	14.9	505	4	US-10-282-122A-62341	Sequence 64537, A	1063	309.5	13.1	200	3	US-09-967-624-19	Sequence 19, Appl
980	351.5	14.9	1056	2	US-08-806-029-29	Sequence 29, Appl	1064	309.5	13.1	200	3	US-09-968-657-18	Sequence 18, Appl
981	351	14.9	957	4	US-10-282-122A-64361	Sequence 64361, A	1065	309.5	13.1	200	3	US-09-921-159-34	Sequence 34, Appl
982	350.5	14.8	461	4	US-10-282-122A-64750	Sequence 64750, A	1066	309.5	13.1	200	3	US-09-990-940-21	Sequence 21, Appl
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986	349	14.8	618	6	US-11-052-554A-150	Sequence 150, App	1070	309.5	13.1	200	4	US-10-026-021B-21	Sequence 21, Appl
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988	346	14.6	648	5	US-10-488-056-30	Sequence 30, Appl	1072	309.5	13.1	200	4	US-10-161-165-3	Sequence 3, Appli
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991	344	14.6	651	5	US-10-488-056-45	Sequence 45, Appl	1075	309.5	13.1	200	4	US-10-094-417-25	Sequence 25, Appl
992	344	14.6	783	6	US-11-052-554A-157	Sequence 157, App	1076	309.5	13.1	200	4	US-10-188-405-13	Sequence 13, Appl
993	343	14.5	681	5	US-10-426-124-6	Sequence 6, Appli	1077	309.5	13.1	200	4	US-10-273-575-29	Sequence 29, Appl
994	343	14.5	691	5	US-10-426-124-6	Sequence 6, Appli	1078	309.5	13.1	200	4	US-10-233-098-5	Sequence 5, Appli
995	342.5	14.5	629	4	US-10-406-832-29	Sequence 29, Appl	1079	309.5	13.1	200	4	US-10-245-850-3	Sequence 3, Appli
996	342.5	14.5	629	5	US-10-893-588-29	Sequence 29, Appl	1080	309.5	13.1	200	4	US-10-293-582-27	Sequence 27, Appl
997	342	14.5	515	4	US-10-282-122A-64613	Sequence 64613, A	1081	309.5	13.1	200	4	US-10-100-818-14	Sequence 14, Appl
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1000	337	14.3	1002	5	US-10-488-056-46	Sequence 46, Appl	1084	309.5	13.1	200	4	US-10-179-766-12	Sequence 12, Appl
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1002	336	14.2	1169	2	US-08-806-029-33	Sequence 33, Appl	1086	309.5	13.1	200	4	US-10-123-731-10	Sequence 10, Appl
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1004	335	14.2	1123	5	US-10-287-436A-285	Sequence 285, App	1088	309.5	13.1	200	4	US-10-352-924-5	Sequence 5, Appli
1005	334	14.1	488	4	US-10-225-838B-21	Sequence 21, Appl	1089	309.5	13.1	200	4	US-10-328-916-57	Sequence 57, Appl
1006	334	14.1	488	4	US-10-282-122A-64610	Sequence 64610, A	1090	309.5	13.1	200	4	US-10-452-015-3	Sequence 3, Appli
1007	334	14.1	488	5	US-10-976-699A-21	Sequence 21, Appl	1091	309.5	13.1	200	4	US-10-364-861-94	Sequence 94, Appl
1008	332.5	14.1	342	6	US-11-037-143-33645	Sequence 33645, A	1092	309.5	13.1	200	4	US-10-231-956A-521	Sequence 521, App
1009	330	14.0	447	5	US-10-488-056-29	Sequence 29, Appl	1093	309.5	13.1	200	4	US-10-255-775-3	Sequence 3, Appli
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1011	329	13.9	780	4	US-10-441-965-19	Sequence 19, Appl	1095	309.5	13.1	200	4	US-10-339-744-4	Sequence 4, Appli
1012	329	13.9	780	4	US-10-800-179-19	Sequence 19, Appl	1096	309.5	13.1	200	4	US-10-648-400-7	Sequence 7, Appli
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1014	329	13.9	780	5	US-10-845-936A-19	Sequence 19, Appl	1098	309.5	13.1	200	5	US-10-794-897-9	Sequence 9, Appli
1015	327.5	13.9	334	4	US-10-259-678-128	Sequence 78, App	1099	309.5	13.1	200	5	US-10-616-403-7	Sequence 7, Appli
1016	327.5	13.9	334	4	US-10-802-796-728	Sequence 728, App	1100	309.5	13.1	200	5	US-10-679-102-32	Sequence 32, Appl
1017	327.5	13.9	334	6	US-11-221-284-728	Sequence 728, App	1101	309.5	13.1	200	5	US-10-696-909A-72	Sequence 72, Appl
1018	327.5	13.9	334	6	US-11-221-284-728	Sequence 728, App	1102	309.5	13.1	200	5	US-10-491-545A-96	Sequence 96, Appl
1019	326	13.8	422	4	US-10-437-963-121579	Sequence 121579,	1103	309.5	13.1	200	5	US-10-805-075-10	Sequence 10, Appl
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1023	324	13.7	1038	5	US-10-845-936A-30	Sequence 30, Appl	1107	309.5	13.1	200	5	US-10-510-903-39	Sequence 39, Appl
1024	324	13.7	1038	5	US-10-939-036-30	Sequence 30, Appl	1108	309.5	13.1	200	5	US-10-513-269-8	Sequence 8, Appli
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1027	322.5	13.6	972	2	US-08-806-029-30	Sequence 30, Appl	1111	309.5	13.1	200	6	US-11-086-846-25	Sequence 25, Appl
1028	320.5	13.6	263	4	US-10-425-114-49960	Sequence 49960, A	1112	309.5	13.1	200	6	US-11-036-643-27	Sequence 27, Appl
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1116	309	13.1	201	3	US-09-760-364-14	Sequence 14, Appl	1200	280	11.8	1466	4	US-10-474-794-226	Sequence 226, App
1117	309	13.1	201	3	US-09-754-947-5	Sequence 5, Appl	1201	280	11.8	1466	5	US-10-852-335A-159	Sequence 159, App
1118	309	13.1	201	4	US-10-339-744-5	Sequence 5, Appl	1202	280	11.8	1466	5	US-10-979-159-226	Sequence 226, App
1119	309	13.1	201	4	US-10-488-806-8	Sequence 8, Appl	1203	280	11.8	1466	5	US-10-287-436A-451	Sequence 451, App
1120	309	13.1	201	5	US-10-513-269-9	Sequence 9, Appl	1204	280	11.8	1466	5	US-10-287-436A-494	Sequence 494, App
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1134	305.5	12.9	2016	4	US-10-479-638-52	Sequence 52, Appl	1207	280	11.8	1466	6	US-11-186-284-33	Sequence 33, Appl
1135	305	12.9	242	4	US-10-471-587A-1	Sequence 1, Appl	1208	280	11.8	1469	5	US-10-450-763-45550	Sequence 45550, A
1136	305	12.9	242	6	US-11-197-315-18	Sequence 18, Appl	1209	279	11.8	1096	5	US-10-741-849-7179	Sequence 7179, App
1137	304.5	12.9	889	2	US-08-806-029-19	Sequence 19, Appl	1210	278.5	11.8	526	5	US-10-469-469-178	Sequence 178, App
1138	302	12.8	592	4	US-10-369-423-17534	Sequence 17534, A	1211	278.5	11.8	2280	6	US-11-097-143-11742	Sequence 11742, A
1139	302	12.8	592	6	US-11-087-039-1770	Sequence 1770, App	1212	278	11.8	220	6	US-11-087-039-11133	Sequence 11133, A
1140	302	12.8	714	3	US-09-861-597-10	Sequence 10, Appl	1213	277.5	11.7	230	4	US-10-437-963-122258	Sequence 122258, A
1141	302	12.8	714	5	US-10-887-100-10	Sequence 10, Appl	1214	277.5	11.7	332	4	US-10-437-963-137550	Sequence 137550, A
1142	301.5	12.8	285	4	US-10-437-963-187773	Sequence 187773, A	1215	277	11.7	237	4	US-10-482-112A-60804	Sequence 60804, A
1143	300.5	12.7	768	2	US-08-806-029-35	Sequence 35, Appl	1216	277	11.7	256	4	US-10-282-115-801334	Sequence 801334, A
1144	300.5	12.7	884	4	US-10-117-931-15	Sequence 15, Appl	1217	276	11.7	1040	4	US-10-104-889-30	Sequence 30, Appl
1145	300.5	12.7	884	6	US-11-201-606-15	Sequence 15, Appl	1218	276	11.7	1040	4	US-10-104-889-32	Sequence 32, Appl
1146	300.5	12.7	983	5	US-10-845-936A-37	Sequence 37, Appl	1219	276	11.7	1040	5	US-10-104-793-32	Sequence 30, Appl
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1148	300.5	12.7	1105	5	US-10-845-936A-33	Sequence 33, Appl	1221	276	11.7	1078	4	US-10-058-124-21	Sequence 21, Appl
1149	300.5	12.7	1125	5	US-10-845-936A-34	Sequence 34, Appl	1222	276	11.7	1366	3	US-09-918-715-214	Sequence 214, App
1150	299	12.7	373	5	US-10-488-056-40	Sequence 40, Appl	1223	276	11.7	1366	3	US-09-918-715-234	Sequence 234, App
1151	298.5	12.6	284	6	US-11-188-298-10638	Sequence 10638, A	1224	276	11.7	1366	3	US-09-918-715-265	Sequence 265, App
1152	297.5	12.6	270	4	US-10-437-963-122263	Sequence 122263, A	1225	276	11.7	1366	4	US-10-171-311-38	Sequence 38, Appl
1153	297	12.6	156	5	US-10-506-651-28	Sequence 28, Appl	1226	276	11.7	1366	4	US-10-301-822-31	Sequence 31, Appl
1154	296.5	12.5	1024	2	US-08-806-029-31	Sequence 31, Appl	1227	276	11.7	1366	4	US-10-610-049-24	Sequence 24, Appl
1155	296	12.5	624	4	US-10-479-638-12	Sequence 12, Appl	1228	276	11.7	1366	4	US-10-734-564-95	Sequence 95, Appl
1156	294.5	12.5	612	6	US-11-087-039-3677	Sequence 3677, App	1229	276	11.7	1366	4	US-10-474-794-214	Sequence 214, App
1157	294.5	12.5	832	2	US-08-806-029-27	Sequence 27, Appl	1230	276	11.7	1366	4	US-10-474-794-234	Sequence 234, App
1158	294	12.4	529	3	US-09-861-597-2	Sequence 2, Appl	1231	276	11.7	1366	4	US-10-474-794-265	Sequence 265, App
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1160	294	12.4	821	4	US-10-292-798-1370	Sequence 1370, App	1233	276	11.7	1366	5	US-10-979-159-234	Sequence 234, App
1161	293.5	12.4	586	6	US-11-097-143-15258	Sequence 15258, A	1234	276	11.7	1366	5	US-10-979-159-265	Sequence 265, App
1162	293.5	12.4	586	6	US-11-097-143-18014	Sequence 18014, A	1235	276	11.7	1366	5	US-10-821-224-1431	Sequence 1431, App
1163	293.5	12.4	611	4	US-10-066-510-4	Sequence 4, Appl	1236	276	11.7	1366	6	US-11-166-284-31	Sequence 31, Appl
1164	293.5	12.4	611	6	US-11-049-348-4	Sequence 4, Appl	1237	275	11.6	208	4	US-10-029-386-33055	Sequence 33055, A
1165	293	12.4	236	3	US-09-820-843A-18	Sequence 18, Appl	1238	275	11.6	525	4	US-10-755-889-650	Sequence 650, App
1166	292	12.4	912	5	US-10-488-056-50	Sequence 50, Appl	1239	275	11.6	944	6	US-10-469-469-184	Sequence 184, App
1167	291.5	12.3	257	5	US-10-739-930-8532	Sequence 8532, App	1240	275	11.6	944	6	US-11-097-143-12192	Sequence 12192, A
1168	290.5	12.3	406	4	US-10-156-761-14828	Sequence 14828, A	1241	274.5	11.6	1536	4	US-10-479-638-54	Sequence 54, Appl
1169	290.5	12.3	805	4	US-10-029-386-34042	Sequence 34042, A	1242	274	11.6	593	4	US-10-435-696-50	Sequence 50, Appl
1170	289	12.2	295	3	US-09-855-604-902	Sequence 902, App	1243	273.5	11.6	160	5	US-10-797-606-27	Sequence 27, Appl
1171	289	12.2	295	3	US-09-855-604-902	Sequence 902, App	1244	272	11.5	696	4	US-10-441-965-23	Sequence 23, Appl
1172	289	12.2	627	5	US-10-406-832-28	Sequence 28, Appl	1245	272	11.5	291	5	US-10-426-124-2	Sequence 2, Appl
1173	289	12.2	627	5	US-10-893-588-28	Sequence 28, Appl	1246	272	11.5	671	5	US-10-450-763-50945	Sequence 50945, A
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1178	287	12.1	258	4	US-10-425-115-300390	Sequence 300390, A	1251	271.5	11.5	594	6	US-11-087-039-1758	Sequence 1758, App
1179	286	12.1	454	4	US-10-767-701-45105	Sequence 45105, A	1252	271	11.5	681	6	US-11-087-039-2744	Sequence 2744, App
1180	286	12.1	563	5	US-10-488-056-43	Sequence 43, Appl	1253	271	11.5	2338	4	US-10-029-386-31982	Sequence 31982, A
1181	286	12.1	2112	6	US-11-097-143-8001	Sequence 8001, App	1254	270.5	11.4	1268	4	US-10-437-963-108730	Sequence 108730, A
1182	285.5	12.1	234	4	US-10-767-701-45603	Sequence 45603, A	1255	270.5	11.4	1366	4	US-10-764-425-119	Sequence 119, App
1183	285	12.1	450	6	US-11-087-039-1260	Sequence 1260, App	1256	270.5	11.4	1366	4	US-10-357-851-2	Sequence 2, Appl
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1185	283.5	12.0	599	5	US-10-672-040-22	Sequence 22, Appl	1258	270.5	11.4	1366	4	US-10-768-792-153	Sequence 153, App
1186	283.5	12.0	599	5	US-10-672-040-23	Sequence 23, Appl	1259	270	11.4	920	4	US-10-768-798-1514	Sequence 1514, App
1187	283	12.0	764	4	US-10-424-599-143917	Sequence 143917, A	1260	270	11.4	1466	4	US-10-402-089-12	Sequence 12, Appl
1188	281.5	11.9	185	4	US-10-437-963-126075	Sequence 126075, A	1261	270	11.4	1466	4	US-10-402-072A-12	Sequence 12, Appl
1189	281.5	11.9	185	5	US-10-928-992-76	Sequence 76, Appl	1262	269.5	11.4	360	5	US-10-488-056-11	Sequence 31, Appl
1190	281	11.9	223	4	US-10-424-599-244310	Sequence 244310, A	1263	269	11.4	272	6	US-11-097-143-73366	Sequence 73366, A
1191	280.5	11.9	223	6	US-11-197-315-33	Sequence 33, Appl	1264	269	11.4	361	6	US-11-052-554A-169	Sequence 169, App
1192	280	11.8	444	5	US-10-488-056-37	Sequence 37, Appl	1265	268.5	11.4	278	4	US-10-425-114-54522	Sequence 54522, A
1193	280	11.8	1466	3	US-09-918-715-226	Sequence 226, App	1266	268.5	11.4	287	4	US-10-437-963-161543	Sequence 161543, A
1194	280	11.8	1466	4	US-10-177-293-68	Sequence 68, Appl	1267	268.5	11.4	900	6	US-11-098-666-10288	Sequence 10288, A
1195	280	11.8	1466	4	US-10-301-822-33	Sequence 33, Appl	1268	267.5	11.3	1027	4	US-10-360-101-221	Sequence 221, App
1196	280	11.8	1466	4	US-10-257-021-72	Sequence 72, Appl	1269	267.5	11.3	1366	4	US-10-058-124-19	Sequence 19, App
1197	280	11.8	1466	4	US-10-357-851-3	Sequence 3, Appl	1270	267.5	11.3	1366	4	US-10-257-021-76	Sequence 76, Appl
1198	280	11.8	1466	4	US-10-358-024-3	Sequence 3, Appl	1271	267.5	11.3	1366	5	US-10-852-335A-158	Sequence 158, App

1272	266	11.3	243	6	US-11-087-099-7914	Sequence 7914, Ap	1356	250	10.6	597	3	US-09-793-306-146	Sequence 146, App
1273	266	11.3	317	6	US-11-097-143-19458	Sequence 19458, A	1357	249.5	10.6	410	5	US-10-984-482-17	Sequence 17, Appl
1274	265	11.3	1088	4	US-10-437-963-158455	Sequence 158455,	1358	249.5	10.6	669	4	US-10-282-122A-53462	Sequence 53462, A
1275	265.5	11.2	265	4	US-10-437-963-154907	Sequence 154907,	1359	249	10.5	1190	6	US-11-097-143-8322	Sequence 8340, Ap
1276	265.5	11.2	568	4	US-10-086-510-5	Sequence 5, Appli	1360	247.5	10.5	399	6	US-11-097-143-8822	Sequence 6822, App
1277	265.5	11.2	568	6	US-11-049-348-5	Sequence 5, Appli	1361	247.5	10.5	943	3	US-09-996-634-131	Sequence 131, App
1278	265.5	11.2	1366	4	US-10-402-089-10	Sequence 10, Appl	1362	247.5	10.5	943	3	US-09-997-182-131	Sequence 131, App
1279	265.5	11.2	1366	4	US-10-402-072A-10	Sequence 21, Appl	1363	247.5	10.5	943	3	US-09-997-181-131	Sequence 131, App
1280	265	11.2	343	4	US-10-148-306-21	Sequence 27, Appl	1364	247.5	10.5	1739	3	US-09-795-061-2	Sequence 2, Appli
1281	264.5	11.2	132	5	US-10-506-651-27	Sequence 27, Appl	1365	247.5	10.5	3300	4	US-10-282-122A-64369	Sequence 64369, A
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1284	264.5	11.2	578	4	US-10-437-963-164510	Sequence 164510,	1368	246.5	10.4	595	4	US-10-342-331-50	Sequence 50, Appl
1285	264.5	11.2	1008	4	US-10-342-331-8	Sequence 8, Appli	1369	246.5	10.4	822	4	US-10-342-331-19	Sequence 19, Appl
1286	264.5	11.2	1008	4	US-10-441-965-22	Sequence 22, Appl	1370	246.5	10.4	1341	4	US-10-058-124-18	Sequence 26, Appl
1287	264.5	11.2	1063	4	US-10-800-179-29	Sequence 29, Appl	1371	246.5	10.4	1453	4	US-10-468-031-26	Sequence 48, Appl
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1291	264.5	11.2	1063	5	US-10-939-036-34	Sequence 34, Appl	1375	245.5	10.4	1449	4	US-10-784-004-428	Sequence 428, App
1292	264.5	11.2	1065	4	US-10-117-931-16	Sequence 16, Appl	1376	245.5	10.4	1014	4	US-10-194-441A-48	Sequence 48, Appl
1293	264.5	11.2	1065	6	US-11-201-606-16	Sequence 16, Appl	1377	245.5	10.4	1449	4	US-10-402-089-8	Sequence 8, Appli
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1297	262.5	11.1	1466	4	US-10-402-089-6	Sequence 6, Appli	1381	245	10.4	894	5	US-10-723-860-3614	Sequence 3614, Ap
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1301	260.5	11.1	828	6	US-11-097-143-16215	Sequence 16215, A	1385	244.5	10.3	660	5	US-10-901-816A-4	Sequence 4, Appli
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1315	259.5	11.0	399	5	US-10-488-056-41	Sequence 41, Appl	1388	244.5	10.3	1014	5	US-10-901-816A-5	Sequence 5, Appli
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1323	257	10.9	208	6	US-11-188-298-17429	Sequence 17429, A	1396	244.5	10.3	1107	4	US-10-104-889-11	Sequence 11, Appl
1324	257	10.9	385	6	US-11-097-143-42156	Sequence 42156, A	1397	244.5	10.3	1107	5	US-10-104-889-11	Sequence 11, Appl
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1331	254	10.7	1040	2	US-08-806-029-32	Sequence 32, Appl	1404	244.5	10.3	1464	4	US-10-291-265-243	Sequence 243, App
1332	254	10.7	1487	5	US-10-756-149-4739	Sequence 4739, Ap	1405	244.5	10.3	1464	4	US-10-764-425-114	Sequence 114, App
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1334	254	10.7	1487	6	US-11-202-057-5	Sequence 5, Appli	1407	244.5	10.3	1464	4	US-10-358-024-1	Sequence 1, Appli
1335	254	10.7	1745	3	US-09-795-061-4	Sequence 4, Appli	1408	244.5	10.3	1464	4	US-10-788-792-150	Sequence 150, App
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1338	253	10.7	1014	4	US-10-194-441A-1	Sequence 1, Appli	1411	244	10.3	266	4	US-10-148-306-20	Sequence 20, Appl
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1340	253	10.7	1418	4	US-10-058-124-20	Sequence 20, Appl	1413	244	10.3	591	4	US-10-233-553-33	Sequence 23, Appl
1341	253	10.7	1418	4	US-10-468-091-5	Sequence 5, Appli	1414	243.5	10.3	492	4	US-11-087-099-3343	Sequence 3343, Ap
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1345	252	10.7	1227	4	US-10-479-638-22	Sequence 22, Appl	1420	243	10.3	714	4	US-10-231-581-64	Sequence 44, Appl
1346	252	10.7	1497	4	US-10-468-091-23	Sequence 23, Appl	1421	243	10.3	714	4	US-10-326-508A-15	Sequence 15, Appl
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1350	251	10.6	1453	5	US-10-784-004-434	Sequence 434, App	1425	242.5	10.3	940	4	US-10-221-172-363	Sequence 363, App
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1352	251	10.6	1453	5	US-10-784-004-918	Sequence 950, App	1427	242.5	10.3	1014	5	US-10-901-816A-9	Sequence 9, Appli
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1455	241.5	10.2	968	4	US-10-221-278-739	Sequence 739, App
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1461	240.5	10.2	943	4	US-10-193-002-199	Sequence 199, App
1462	240.5	10.2	943	4	US-10-084-843-204	Sequence 204, App
1463	240.5	10.2	943	6	US-11-028-898-204	Sequence 204, App
1464	240.5	10.2	943	6	US-11-082-005-199	Sequence 199, App
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1477	239.5	10.1	1057	4	US-10-104-889-16	Sequence 16, Appl
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1482	239.5	10.1	1464	4	US-10-149-352-2	Sequence 2, Appl
1483	239.5	10.1	1464	4	US-10-177-293-65	Sequence 65, Appl
1484	239.5	10.1	1464	4	US-10-301-822-28	Sequence 28, Appl
1485	239.5	10.1	1464	4	US-10-734-564-79	Sequence 79, Appl
1486	239.5	10.1	1464	4	US-10-474-794-261	Sequence 261, App
1487	239.5	10.1	1464	5	US-10-723-860-2289	Sequence 2289, Ap
1488	239.5	10.1	1464	5	US-10-852-335A-157	Sequence 157, App
1489	239.5	10.1	1464	5	US-10-979-159-261	Sequence 261, App
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1494	239.5	10.1	1464	6	US-11-021-603-2	Sequence 2, Appl
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1496	239.5	10.1	1629	5	US-10-287-436A-443	Sequence 443, App
1497	239.5	10.1	1629	5	US-10-287-436A-1144	Sequence 1144, Ap
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# SUMMARIES

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7	2363	100.0	440	7	US-11-102-284-52
8	2266.5	95.9	555	6	US-10-835-904-3
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21	423	17.9	396	7	US-11-241-607-1550
22	423	17.9	396	7	US-11-241-607-42820
23	420.5	17.8	1384	7	US-11-330-403-2821
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25	412.5	17.5	484	7	US-11-330-403-11800
26	412.5	17.5	1360	7	US-11-330-403-10138
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28	406	17.2	1901	7	US-11-330-403-13083

29	404.5	17.1	532	7	US-11-330-403-1154	Sequence 1154, Ap
30	403	17.1	1489	7	US-11-330-403-13106	Sequence 13106, A
31	400.5	16.9	992	7	US-11-330-403-10143	Sequence 10143, A
32	400.5	16.9	1538	7	US-11-330-403-11802	Sequence 11802, A
33	399.5	16.9	853	7	US-11-330-403-5068	Sequence 5068, Ap
34	398	16.8	850	7	US-11-330-403-2447	Sequence 2447, Ap
35	397.5	16.8	763	7	US-11-330-403-2359	Sequence 2359, Ap
36	397.5	16.8	1217	7	US-11-330-403-2513	Sequence 2513, Ap
37	397.5	16.8	1460	7	US-11-330-403-10139	Sequence 10139, A
38	397.5	16.8	1507	7	US-11-330-403-5475	Sequence 5475, Ap
39	396.5	16.8	1715	7	US-11-330-403-2837	Sequence 2837, Ap
40	395	16.7	714	7	US-11-330-403-13087	Sequence 13087, A
41	395	16.7	749	7	US-11-330-403-9435	Sequence 9435, Ap
42	395	16.7	1660	7	US-11-330-403-10317	Sequence 10317, A
43	395	16.7	1665	7	US-11-330-403-18623	Sequence 18623, A
44	393	16.6	626	7	US-11-330-403-9413	Sequence 9413, Ap
45	392.5	16.6	923	7	US-11-330-403-4339	Sequence 4339, Ap
46	392	16.6	731	7	US-11-330-403-12386	Sequence 12386, A
47	392	16.6	775	7	US-11-330-403-5553	Sequence 5553, Ap
48	392	16.6	1329	7	US-11-330-403-7129	Sequence 7129, Ap
49	392	16.6	1408	7	US-11-330-403-551	Sequence 551, Ap
50	391.5	16.6	306	7	US-11-056-3558-81494	Sequence 81494, A
51	391.5	16.6	306	7	US-11-241-607-1551	Sequence 1551, Ap
52	391.5	16.6	1003	7	US-11-330-403-10079	Sequence 10079, A
53	391.5	16.5	635	7	US-11-330-403-16986	Sequence 16986, A
54	390.5	16.5	1408	7	US-11-330-403-4893	Sequence 4893, Ap
55	389.5	16.5	788	7	US-11-330-403-457	Sequence 457, Ap
56	388	16.4	1150	7	US-11-330-403-7484	Sequence 7484, Ap
57	388	16.4	518	6	US-10-449-902-54389	Sequence 54389, A
58	386.5	16.4	778	7	US-11-330-403-10028	Sequence 11028, A
59	386	16.2	767	7	US-11-330-403-5052	Sequence 5052, Ap
60	383.5	16.2	641	6	US-10-511-937-2524	Sequence 2524, Ap
61	383	16.2	838	7	US-11-330-403-15569	Sequence 15569, A
62	382.5	16.2	738	7	US-11-330-403-562	Sequence 562, Ap
63	381.5	16.1	741	7	US-11-330-403-7140	Sequence 7140, Ap
64	381.5	16.1	774	7	US-11-330-403-2433	Sequence 2433, Ap
65	381.5	16.1	749	7	US-11-330-403-15068	Sequence 15068, A
66	380.5	16.1	837	7	US-11-330-403-1825	Sequence 1825, Ap
67	380.5	16.1	628	7	US-11-330-403-5511	Sequence 5511, Ap
68	379.5	16.1	465	7	US-11-330-403-13492	Sequence 13492, A
69	379	16.0	470	7	US-11-241-607-55209	Sequence 55209, A
70	378.5	16.0	490	7	US-11-330-403-5380	Sequence 5380, A
71	378.5	16.0	588	7	US-11-330-403-12346	Sequence 12346, A
72	378	16.0	749	7	US-11-330-403-7219	Sequence 7219, Ap
73	376.5	15.9	820	7	US-11-330-403-6822	Sequence 6822, Ap
74	375	15.9	914	7	US-11-330-403-9236	Sequence 9236, Ap
75	375	15.9	1255	6	US-10-297-389-313	Sequence 313, Ap
76	374	15.8	831	7	US-11-330-403-1189	Sequence 1189, Ap
77	374	15.8	1880	6	US-10-297-389-35	Sequence 35, Ap
78	374	15.8	584	7	US-11-330-403-3413	Sequence 3413, Ap
79	373.5	15.8	667	7	US-11-330-403-5016	Sequence 5016, Ap
80	373.5	15.8	667	7	US-11-330-403-16913	Sequence 16913, A
81	373.5	15.8	189	6	US-10-294-433-664	Sequence 364, Ap
82	373	15.8	694	7	US-11-330-403-18622	Sequence 18622, A
83	372	15.7	909	7	US-11-330-403-4305	Sequence 4305, Ap
84	372	15.7	671	7	US-11-330-403-2398	Sequence 2398, Ap
85	371.5	15.7	615	7	US-11-330-403-5859	Sequence 5859, Ap
86	371	15.7	615	7	US-11-330-403-12394	Sequence 12394, A
87	371	15.7	491	7	US-11-330-403-7107	Sequence 7107, Ap
88	370.5	15.6	491	7	US-11-330-403-4874	Sequence 4874, Ap
89	369.5	15.6	795	7	US-11-330-403-4896	Sequence 4896, Ap
90	369.5	15.6	989	6	US-10-297-389-54	Sequence 34, Ap
91	369.5	15.6	682	7	US-11-330-403-15032	Sequence 15032, A
92	369	15.6	606	7	US-11-330-403-1241	Sequence 8187, Ap
93	368	15.6	686	7	US-11-330-403-11817	Sequence 11817, Ap
94	367.5	15.6	608	7	US-11-330-403-1085	Sequence 1085, Ap
95	367.5	15.6	877	7	US-11-330-403-1187	Sequence 1187, Ap
96	366.5	15.5	496	7	US-11-330-403-2669	Sequence 2669, Ap
97	365.5	15.5	496	7	US-11-330-403-18838	Sequence 18838, A
98	365.5	15.5	533	7	US-11-330-403-13787	Sequence 13787, A
99	365.5	15.5	630	6	US-10-297-389-38	Sequence 38, Ap
100	365.5	15.5	785	7	US-11-330-403-14489	Sequence 14489, A
101	365.5	15.5				

102	365	15.4	576	7	US-11-330-403-7001	Sequence 7001, Ap	175	323	13.7	7362	7	US-11-330-403-9773	Sequence 9773, Ap
103	365	15.4	591	7	US-11-330-403-3845	Sequence 3845, Ap	176	322.5	13.6	355	7	US-11-330-403-5931	Sequence 5931, Ap
104	365	15.4	663	7	US-11-330-403-1856	Sequence 1845, Ap	177	320.5	13.6	257	6	US-10-953-349-58261	Sequence 58261, A
105	364.5	15.4	801	7	US-11-330-403-6548	Sequence 6548, Ap	178	320.5	13.6	257	7	US-11-241-607-9793	Sequence 9793, Ap
106	364	15.4	606	7	US-11-330-403-3712	Sequence 3712, Ap	179	320.5	13.6	263	7	US-11-520-715-49960	Sequence 49960, A
107	364	15.4	609	7	US-11-330-403-15134	Sequence 15134, A	180	320.5	13.6	271	6	US-10-953-349-38260	Sequence 38260, A
108	364	15.4	1086	7	US-11-330-403-3535	Sequence 3535, Ap	181	320.5	13.6	271	7	US-11-241-607-9792	Sequence 9792, Ap
109	363.5	15.4	349	7	US-11-241-607-47268	Sequence 47268, A	182	320.5	13.6	756	7	US-11-330-403-9344	Sequence 9344, Ap
110	363	15.4	639	7	US-11-330-403-9873	Sequence 9873, Ap	183	320	13.5	594	7	US-11-330-403-5230	Sequence 5230, Ap
111	362.5	15.3	561	7	US-11-330-403-14266	Sequence 14266, A	184	318	13.5	884	7	US-11-351-712-325	Sequence 25, Ap
112	361	15.3	540	7	US-11-330-403-6917	Sequence 6917, Ap	185	316	13.4	546	7	US-11-330-403-8081	Sequence 8081, Ap
113	360	15.2	562	7	US-11-330-403-5727	Sequence 5727, Ap	186	315.5	13.4	965	7	US-11-351-712-11	Sequence 31, Ap
114	360	15.2	586	7	US-11-330-403-17736	Sequence 17736, A	187	314.5	13.3	505	7	US-11-330-403-19235	Sequence 19235, A
115	359.5	15.2	773	7	US-11-330-403-1018	Sequence 1018, Ap	188	314.5	13.3	543	7	US-11-330-403-10935	Sequence 10935, A
116	359.5	15.2	1011	7	US-11-330-403-8415	Sequence 8415, Ap	189	312.5	13.2	252	7	US-11-330-403-13490	Sequence 13490, A
117	359.5	15.2	1011	7	US-11-330-403-16807	Sequence 16807, A	190	312	13.2	242	7	US-11-520-715-61520	Sequence 61520, A
118	359.5	15.2	1018	7	US-11-330-403-6127	Sequence 6127, Ap	191	311.5	13.2	405	7	US-11-330-403-17531	Sequence 17531, A
119	359	15.2	463	7	US-11-241-607-5017	Sequence 5017, Ap	192	309.5	13.1	200	6	US-10-516-032-15	Sequence 15, Ap
120	358.5	15.2	338	7	US-11-241-607-47269	Sequence 47269, A	193	309.5	13.1	200	6	US-10-515-8922A-14	Sequence 14, Ap
121	356	15.1	603	7	US-11-330-403-4179	Sequence 4179, Ap	194	309.5	13.1	200	6	US-10-531-492-27	Sequence 27, Ap
122	355	15.0	831	7	US-11-330-403-1018	Sequence 1019, Ap	195	309.5	13.1	200	6	US-10-516-803-36	Sequence 36, Ap
123	355	15.0	868	7	US-11-330-403-1186	Sequence 1186, Ap	196	309.5	13.1	200	6	US-10-516-803-36	Sequence 46, Ap
124	354.5	15.0	840	7	US-11-330-403-1186	Sequence 16605, A	197	309.5	13.1	200	6	US-10-525-573-525	Sequence 525, Ap
125	353	14.9	624	7	US-11-330-403-6837	Sequence 6837, Ap	198	309.5	13.1	200	6	US-10-533-593-42	Sequence 42, Ap
126	352	14.9	603	7	US-11-330-403-6405	Sequence 6405, Ap	199	309.5	13.1	200	6	US-10-516-229-16	Sequence 16, Ap
127	351	14.9	957	7	US-11-330-403-3816	Sequence 3816, Ap	200	309.5	13.1	200	7	US-11-239-308-62	Sequence 62, Ap
128	350.5	14.8	461	7	US-11-330-403-10983	Sequence 10983, A	201	309.5	13.1	200	7	US-11-325-764-34	Sequence 34, Ap
129	350.5	14.8	476	7	US-11-330-403-424	Sequence 424, Ap	202	309.5	13.1	200	7	US-11-367-182-24	Sequence 24, Ap
130	350.5	14.8	879	7	US-11-330-403-15071	Sequence 15071, A	203	309.5	13.1	200	7	US-11-282-262-12	Sequence 12, Ap
131	349	14.8	819	7	US-11-330-403-9789	Sequence 9789, Ap	204	309.5	13.1	200	7	US-11-452-213-25	Sequence 25, Ap
132	349	14.8	882	7	US-11-330-403-7222	Sequence 7222, Ap	205	309.5	13.1	200	7	US-11-488-338-18	Sequence 8, Ap
133	347.5	14.7	464	7	US-11-330-403-8624	Sequence 8624, Ap	206	309.5	13.1	200	7	US-11-512-788-19	Sequence 19, Ap
134	347	14.7	535	7	US-11-330-403-18340	Sequence 18340, A	207	309.5	13.1	200	7	US-11-471-464-3	Sequence 3, Ap
135	344.5	14.6	797	7	US-11-330-403-4304	Sequence 4304, Ap	208	309.5	13.1	200	7	US-11-450-656-9	Sequence 9, Ap
136	344.5	14.6	905	7	US-11-330-403-14996	Sequence 14996, A	209	309.5	13.1	200	7	US-11-591-992-53	Sequence 53, Ap
137	344	14.6	525	7	US-11-330-403-11652	Sequence 11652, A	210	309.5	13.1	265	6	US-10-449-902-37490	Sequence 37490, A
138	344	14.6	783	7	US-11-330-403-6547	Sequence 6547, A	211	309.5	13.1	454	7	US-11-330-403-7500	Sequence 7500, Ap
139	344	14.6	783	7	US-11-330-403-14473	Sequence 14473, A	212	309	13.0	572	7	US-11-330-403-11982	Sequence 11982, A
140	343	14.5	538	7	US-11-330-403-450	Sequence 450, Ap	213	306.5	12.9	418	7	US-11-506-611-10	Sequence 10, Ap
141	342.5	14.5	773	6	US-10-297-389-49	Sequence 49, Ap	214	304.5	12.9	280	6	US-10-449-902-55551	Sequence 55551, A
142	342.5	14.5	717	6	US-10-297-389-51	Sequence 51, Ap	215	304	12.9	1670	6	US-11-174-307B-1006	Sequence 1006, Ap
143	342	14.5	515	7	US-11-330-403-18098	Sequence 18098, A	216	303.5	12.8	276	6	US-10-703-033-115948	Sequence 115948
144	340.5	14.4	482	7	US-11-330-403-4306	Sequence 4306, Ap	217	302.5	12.8	393	7	US-11-506-611-12	Sequence 12, Ap
145	339.5	14.4	487	7	US-11-330-403-2686	Sequence 2686, Ap	218	301	12.7	622	7	US-11-471-740-10	Sequence 10, Ap
146	337.5	14.3	2804	7	US-11-330-403-12380	Sequence 12380, A	219	300.5	12.7	983	7	US-11-351-712-37	Sequence 37, Ap
147	337	14.3	290	7	US-11-241-607-3619	Sequence 3619, Ap	220	300.5	12.7	1027	7	US-11-351-712-32	Sequence 32, Ap
148	337	14.3	296	7	US-11-241-607-3618	Sequence 3618, Ap	221	300.5	12.7	1105	7	US-11-351-712-33	Sequence 33, Ap
149	336.5	14.2	338	7	US-11-330-403-5456	Sequence 5456, Ap	222	300.5	12.7	1125	7	US-11-351-712-34	Sequence 34, Ap
150	336	14.2	255	6	US-10-449-902-40495	Sequence 40495, A	223	300.5	12.7	1125	7	US-11-056-355B-16346	Sequence 16346, A
151	335	14.2	434	7	US-11-330-403-7608	Sequence 7608, Ap	224	300	12.7	231	7	US-11-241-607-8643	Sequence 8643, Ap
152	335	14.2	581	7	US-11-330-403-3052	Sequence 3052, Ap	225	300	12.7	231	7	US-11-056-355B-16345	Sequence 16345, A
153	334	14.1	255	7	US-11-056-355B-89548	Sequence 89548, A	226	300	12.7	249	7	US-11-241-607-8642	Sequence 8642, Ap
154	334	14.1	255	7	US-11-056-355B-93304	Sequence 93304, A	227	300	12.7	280	6	US-10-449-902-35399	Sequence 35399, A
155	334	14.1	255	7	US-11-241-607-2368	Sequence 2368, Ap	228	299	12.7	280	6	US-11-330-403-18778	Sequence 18778, A
156	334	14.1	488	7	US-11-330-403-7523	Sequence 7523, Ap	229	299	12.7	1292	7	US-11-330-403-18540	Sequence 18540, A
157	334	14.1	488	7	US-11-330-403-9896	Sequence 9896, Ap	230	298.5	12.6	210	7	US-11-056-355B-76468	Sequence 76468, A
158	333.5	14.1	501	7	US-11-330-403-7880	Sequence 7880, Ap	231	298.5	12.6	210	7	US-11-241-607-6604	Sequence 6604, Ap
159	332.5	14.1	491	7	US-11-330-403-599	Sequence 599, Ap	232	298.5	12.6	210	7	US-11-241-607-31899	Sequence 31899, A
160	332.5	14.1	501	7	US-11-330-403-3428	Sequence 3428, Ap	233	297	12.6	222	6	US-10-449-902-32123	Sequence 32123, A
161	331.5	14.0	364	6	US-10-297-389-39	Sequence 39, Ap	234	296.5	12.5	429	7	US-11-330-403-5736	Sequence 5736, Ap
162	331.5	14.0	493	7	US-11-330-403-10638	Sequence 10638, A	235	296.5	12.5	1047	7	US-11-330-403-18778	Sequence 18778, A
163	331.5	14.0	622	7	US-11-330-403-16834	Sequence 16834, A	236	294.5	12.5	614	7	US-11-330-403-7995	Sequence 7995, Ap
164	331	14.0	1029	7	US-11-174-307B-1924	Sequence 1924, Ap	237	294	12.4	271	7	US-11-241-607-31899	Sequence 31899, A
165	329.5	13.9	295	7	US-11-241-607-54773	Sequence 54773, A	238	294	12.4	273	7	US-11-241-607-31899	Sequence 31899, A
166	329.5	13.9	504	7	US-11-330-403-17618	Sequence 17618, A	239	294	12.4	282	7	US-11-241-607-31897	Sequence 31897, A
167	329.5	13.9	504	7	US-11-330-403-9455	Sequence 9455, Ap	240	294	12.4	821	7	US-11-214-063A-1370	Sequence 1370, Ap
168	329.5	13.9	780	7	US-11-330-403-1606	Sequence 1606, Ap	241	293.5	12.4	586	6	US-10-527-571A-117	Sequence 317, Ap
169	329	13.9	780	7	US-11-351-712-19	Sequence 19, Ap	242	293	12.4	256	7	US-11-330-403-7663	Sequence 7663, Ap
170	325.5	13.8	439	7	US-11-330-403-13663	Sequence 13663, A	243	293	12.4	257	7	US-11-330-403-11153	Sequence 11153, A
171	325.5	13.8	452	7	US-11-241-607-42429	Sequence 42429, A	244	293	12.4	245	7	US-11-330-403-11586	Sequence 11586, A
172	324	13.7	1038	7	US-11-351-712-30	Sequence 30, Ap	245	290	12.3	489	6	US-10-953-349-7613	Sequence 7613, Ap
173	323.5	13.7	436	7	US-11-330-403-3416	Sequence 3416, Ap	246	290	12.3	543	6	US-10-953-349-7612	Sequence 7612, Ap
174	323	13.7	268	7	US-11-241-607-6220	Sequence 6220, Ap	247	290	12.3	549	6	US-10-953-349-7611	Sequence 7611, Ap

248	290	12.3	1055	7	US-11-174-307B-3194	Sequence 3194, Ap	321	269	11.4	945	7	US-11-174-307B-2018	Sequence 2018, Ap
249	289	12.2	295	7	US-11-329-260-902	Sequence 902, App	322	269	11.4	1025	7	US-11-330-403-16057	Sequence 16057, A
250	288.5	12.2	1255	7	US-11-174-307B-1594	Sequence 1594, Ap	323	268.5	11.4	278	7	US-11-520-715-54522	Sequence 54522, A
251	287.5	12.2	916	7	US-11-174-307B-948	Sequence 948, App	324	268.5	11.4	2430	7	US-11-174-307B-86	Sequence 96, App1
252	286	12.1	876	7	US-11-174-307B-1902	Sequence 1902, Ap	325	267.5	11.3	1366	6	US-10-985-570-3	Sequence 7532, Ap
253	286	12.1	1246	7	US-11-174-307B-2518	Sequence 2518, Ap	326	266.5	11.3	987	7	US-11-330-403-7532	Sequence 10902, A
254	286	12.1	1248	7	US-11-174-307B-458	Sequence 458, App	327	266	11.3	243	7	US-11-174-307B-253	Sequence 2532, Ap
255	285	12.1	1227	6	US-10-449-902-41618	Sequence 41618, A	328	266	11.3	1169	7	US-11-330-403-10902	Sequence 1584, Ap
256	285	12.1	1250	7	US-11-330-403-16515	Sequence 16515, A	329	266	11.3	1545	7	US-11-174-307B-1584	Sequence 106846, A
257	285	12.1	536	7	US-11-218-141-1018	Sequence 1018, Ap	330	265.5	11.2	175	7	US-11-056-335B-118085	Sequence 118085, A
258	283.5	12.0	271	6	US-10-297-389-40	Sequence 40, App1	331	265.5	11.2	175	7	US-11-056-335B-118085	Sequence 5084, Ap
259	283	12.0	831	7	US-11-174-307B-1974	Sequence 1974, Ap	332	265.5	11.2	1058	7	US-11-174-307B-5084	Sequence 29, App1
260	283	12.0	1061	7	US-11-174-307B-1894	Sequence 1894, Ap	333	264.5	11.2	1063	7	US-11-351-712-29	Sequence 100540, A
261	281.5	11.9	185	6	US-10-449-902-35393	Sequence 35393, A	334	264	11.2	227	7	US-11-056-335B-1100540	Sequence 111779, A
262	281.5	11.9	185	6	US-10-449-902-35641	Sequence 35641, A	335	264	11.2	227	7	US-11-056-335B-1100539	Sequence 100539, A
263	281	11.9	223	7	US-11-330-403-18289	Sequence 18289, A	336	264	11.2	246	7	US-11-056-335B-1100539	Sequence 111778, A
264	280.5	11.9	906	7	US-11-174-307B-1482	Sequence 1482, Ap	337	264	11.2	246	7	US-11-056-335B-111778	Sequence 56361, A
265	280.5	11.9	954	7	US-11-174-307B-1922	Sequence 1922, Ap	338	264	11.2	1163	7	US-11-371-354-56961	Sequence 9976, Ap
266	280	11.8	1028	6	US-10-529-708-2	Sequence 2, App11	339	261.5	11.1	690	6	US-10-276-817B-9976	Sequence 738, App
267	280	11.8	1313	6	US-10-529-708-1	Sequence 1, App11	340	260	11.0	1403	7	US-11-174-307B-738	Sequence 6128, Ap
268	280	11.8	1380	6	US-10-219-051B-7400	Sequence 7400, Ap	341	259.5	11.0	261	7	US-11-330-403-6128	Sequence 6128, Ap
269	280	11.8	1466	6	US-10-985-570-1	Sequence 1, App1	342	259	11.0	441	7	US-11-506-611-14	Sequence 3094, Ap
270	280	11.8	1466	6	US-10-700-439-140	Sequence 140, App	343	259	11.0	1212	7	US-11-174-307B-3094	Sequence 1432, Ap
271	280	11.8	1466	7	US-11-105-233-44	Sequence 44, App1	344	259	11.0	1553	7	US-11-174-307B-1432	Sequence 1970, Ap
272	280	11.8	1466	7	US-11-105-233-167	Sequence 167, App1	345	259	11.0	1780	7	US-11-174-307B-1970	Sequence 1816, A
273	280	11.8	1572	6	US-10-554-068-27	Sequence 27, App1	346	259	11.0	4659	7	US-11-174-307B-1816	Sequence 58912, A
274	280	11.8	1604	6	US-10-554-068-14	Sequence 14, App1	347	258.5	10.9	478	7	US-11-520-715-61022	Sequence 61022, A
275	280	11.8	1950	6	US-10-554-068-10	Sequence 10, App1	348	258.5	10.9	480	7	US-11-520-715-61022	Sequence 504, App
276	278.5	11.8	526	7	US-11-371-354-1637	Sequence 1637, A	349	258	10.9	208	7	US-11-330-403-504	Sequence 234, Ap
277	278.5	11.8	526	7	US-11-218-141-1017	Sequence 1017, Ap	350	258	10.9	1532	7	US-11-174-307B-2324	Sequence 6957, Ap
278	278.5	11.7	1067	7	US-11-174-307B-2718	Sequence 2718, Ap	351	257.5	10.9	440	7	US-11-330-403-6957	Sequence 308, App
279	277.5	11.7	230	6	US-10-449-902-56230	Sequence 56230, A	352	257.5	10.9	1081	7	US-11-174-307B-308	Sequence 1892, Ap
280	277	11.7	1707	7	US-11-174-307B-2636	Sequence 2636, Ap	353	256.5	10.9	894	7	US-11-174-307B-1976	Sequence 1976, Ap
281	277	11.7	1708	7	US-11-174-307B-2076	Sequence 2076, Ap	354	256.5	10.9	957	7	US-11-351-712-36	Sequence 36, App1
282	276.5	11.7	1372	6	US-10-219-051B-5579	Sequence 5579, Ap	355	256.5	10.9	1016	7	US-11-174-307B-1356	Sequence 1356, Ap
283	276.5	11.7	1372	6	US-10-219-051B-5583	Sequence 5583, Ap	356	256.5	10.9	1094	7	US-11-174-307B-1016	Sequence 1016, Ap
284	276.5	11.7	1372	6	US-10-219-051B-10581	Sequence 10581, A	357	256.5	10.9	1168	7	US-11-174-307B-1016	Sequence 1926, A
285	276.5	11.7	1372	6	US-10-219-051B-11370	Sequence 11370, A	358	256.5	10.8	1572	7	US-11-174-307B-1926	Sequence 7211, Ap
286	276	11.7	1372	6	US-10-219-051B-113225	Sequence 113225, A	359	255.5	10.8	230	6	US-10-297-389-11	Sequence 67419, A
287	276	11.7	231	6	US-10-603-113-14281	Sequence 14281, A	360	255.5	10.8	501	7	US-11-371-354-67419	Sequence 71399, A
288	276	11.7	1040	7	US-11-048-197-30	Sequence 30, App1	361	255.5	10.8	592	7	US-11-371-354-11399	Sequence 35, App1
289	276	11.7	1040	7	US-11-048-197-32	Sequence 32, App1	362	255.5	10.8	1043	7	US-11-351-712-35	Sequence 1634, Ap
290	276	11.7	1227	6	US-10-405-027-3917	Sequence 3917, Ap	363	255.5	10.8	1474	7	US-10-953-349-1211	Sequence 18828, A
291	276	11.7	1366	6	US-10-700-439-1316	Sequence 1316, App	364	255	10.8	279	6	US-10-953-349-1211	Sequence 2766, Ap
292	276	11.7	1366	7	US-11-105-233-159	Sequence 159, App	365	254.5	10.8	273	7	US-11-330-403-18828	Sequence 1513, Ap
293	276	11.7	1366	7	US-11-510-530-38	Sequence 38, App1	366	254	10.7	1431	7	US-11-174-307B-2766	Sequence 124, App
294	275	11.6	202	6	US-10-703-032-115964	Sequence 115964, A	367	254	10.7	1487	5	US-09-976-858-124	Sequence 124, App
295	274.5	11.6	1566	7	US-11-174-307B-1406	Sequence 1406, Ap	368	254	10.7	1487	5	US-11-212-799-124	Sequence 10, App1
296	274	11.6	234	7	US-11-056-355B-17479	Sequence 17479, A	369	254	10.7	818	7	US-11-415-063-10	Sequence 490, App
297	274	11.6	234	7	US-11-241-607-9232	Sequence 9232, Ap	370	253	10.7	1217	7	US-11-523-343-2	Sequence 490, App
298	274	11.6	240	7	US-11-056-355B-17478	Sequence 17478, A	371	253	10.7	1306	7	US-11-174-307B-490	Sequence 2036, Ap
299	274	11.6	240	7	US-11-241-607-9231	Sequence 9231, Ap	372	253	10.7	1516	7	US-11-174-307B-2358	Sequence 19092, Ap
300	274	11.6	1313	6	US-10-529-708-3	Sequence 3, App11	373	253	10.7	1533	7	US-11-174-307B-2056	Sequence 49077, A
301	274	11.6	1366	6	US-10-574-398-195	Sequence 195, App	374	253	10.7	455	7	US-11-520-715-65134	Sequence 49076, A
302	274	11.6	1366	6	US-10-574-398-309	Sequence 309, App	375	252.5	10.7	529	7	US-11-520-715-49406	Sequence 10489, A
303	274	11.6	3016	7	US-11-330-403-7222	Sequence 7229, Ap	376	252.5	10.7	529	7	US-11-520-715-49406	Sequence 10485, A
304	272.5	11.5	619	6	US-10-419-128-26352	Sequence 26352, A	377	252.5	10.7	1308	7	US-11-174-307B-1850	Sequence 14037, A
305	272.5	11.5	972	7	US-11-174-307B-1318	Sequence 1318, Ap	378	252.5	10.6	1474	7	US-11-174-307B-2220	Sequence 14041, A
306	271.5	11.5	370	7	US-11-330-403-7660	Sequence 7660, Ap	379	251.5	10.6	343	7	US-11-330-403-19092	Sequence 14045
307	271.5	11.5	375	7	US-11-330-403-596	Sequence 596, App	380	251.5	10.6	452	7	US-11-241-607-49077	Sequence 14045
308	271.5	11.5	569	7	US-11-218-141-2985	Sequence 2985, Ap	381	251.5	10.6	480	7	US-11-241-607-49077	Sequence 14045
309	271.5	11.5	569	7	US-11-218-141-2986	Sequence 2986, Ap	382	251.5	10.6	490	7	US-11-241-607-49077	Sequence 14045
310	271.5	11.5	544	7	US-11-330-403-6136	Sequence 6136, Ap	383	251	10.6	1453	6	US-10-219-051B-10485	Sequence 14045
311	271	11.5	112695	7	US-10-703-032-112695	Sequence 112695, A	384	251	10.6	1453	6	US-10-219-051B-10485	Sequence 14045
312	271	11.5	681	7	US-11-330-403-16365	Sequence 16365, A	385	251	10.6	1453	6	US-10-219-051B-14037	Sequence 14045
313	271	11.5	1037	7	US-11-174-307B-1268	Sequence 1268, Ap	386	251	10.6	1453	6	US-10-219-051B-14037	Sequence 14045
314	271	11.5	2499	6	US-10-276-817B-9905	Sequence 9905, App	387	251	10.6	1453	6	US-10-219-051B-14045	Sequence 14045
315	270.5	11.4	360	7	US-11-330-403-6766	Sequence 6766, App	388	251	10.6	1453	6	US-10-219-051B-14045	Sequence 14045
316	270	11.4	920	7	US-11-214-063A-1514	Sequence 1514, Ap	389	250.5	10.6	219	6	US-10-297-389-36	Sequence 36, App1
317	270	11.4	1407	7	US-11-174-307B-1498	Sequence 1498, Ap	390	250.5	10.6	540	7	US-11-330-403-41121	Sequence 41121, Ap
318	269.5	11.4	845	7	US-11-174-307B-1232	Sequence 1232, Ap	391	250.5	10.6	585	6	US-10-805-394-6032	Sequence 6032, Ap
319	269	11.4	361	7	US-11-330-403-9698	Sequence 9698, App	392	250.5	10.6	585	6	US-11-097-052-1960	Sequence 1960, App
320	269	11.4	382	7	US-11-330-403-3032	Sequence 3032, App	393	250.5	10.6	585	7	US-11-507-088A-1960	Sequence 1960, App



394	250	10.6	274	6	US-10-953-349-7212	Sequence 7212, Ap	467	238	10.1	1806	7	US-11-050-875-634	Sequence 634, App
395	250	10.6	597	7	US-11-476-254-146	Sequence 146, App	468	237.5	10.1	207	7	US-11-056-355B-3487	Sequence 3487, Ap
396	249.5	10.6	567	6	US-10-553-436-358	Sequence 358, App	469	237.5	10.1	207	7	US-11-241-607-7736	Sequence 7736, Ap
397	249.5	10.6	660	6	US-10-553-836-357	Sequence 357, App	470	237.5	10.1	218	7	US-11-056-355B-3486	Sequence 3486, Ap
398	249.5	10.6	702	6	US-10-523-834-288	Sequence 288, App	471	237.5	10.1	218	7	US-11-241-607-7735	Sequence 7735, Ap
399	249.5	10.6	328	6	US-10-449-902-40129	Sequence 40129, A	472	237	10.0	273	7	US-11-056-355B-98265	Sequence 98265, A
400	249	10.5	384	6	US-10-533-520-1837	Sequence 1837, A	473	237	10.0	273	7	US-11-056-355B-109504	Sequence 109504, A
401	249	10.5	710	6	US-10-449-902-41319	Sequence 41319, A	474	237	10.0	309	7	US-11-056-355B-98264	Sequence 98264, A
402	248.5	10.5	271	7	US-11-056-355B-10851	Sequence 10851, A	475	237	10.0	309	7	US-11-056-355B-109503	Sequence 109503, A
403	248.5	10.5	271	7	US-11-241-607-8910	Sequence 8910, A	476	237	10.0	1445	7	US-11-174-307B-3368	Sequence 3368, Ap
404	248.5	10.5	1253	7	US-11-174-307B-2590	Sequence 2590, Ap	477	236	10.0	887	7	US-11-520-715-88923	Sequence 88923, A
405	248	10.5	1254	7	US-11-174-307B-840	Sequence 840, App	478	236	10.0	1365	7	US-11-174-307B-2318	Sequence 2318, Ap
406	247	10.5	386	7	US-11-330-403-15574	Sequence 15574, A	479	235.5	10.0	1337	7	US-11-174-307B-2450	Sequence 2450, Ap
407	247	10.5	1155	7	US-11-174-307B-1546	Sequence 1546, A	480	235.5	10.0	1783	7	US-11-174-307B-1440	Sequence 1440, Ap
408	246.5	10.4	448	6	US-10-603-113-19135	Sequence 19135, A	481	235	9.9	1703	7	US-11-174-307B-2576	Sequence 2576, Ap
409	246.5	10.4	556	6	US-10-603-113-22338	Sequence 22338, A	482	234.5	9.9	818	7	US-11-174-307B-1448	Sequence 1448, Ap
410	246.5	10.4	1614	7	US-11-174-307B-1770	Sequence 1770, Ap	483	234	9.9	301	7	US-11-330-403-18823	Sequence 18823, A
411	246	10.4	1510	7	US-10-703-032-139668	Sequence 139668, A	484	233.5	9.9	263	7	US-11-056-355B-98266	Sequence 98266, A
412	246	10.4	1509	7	US-11-174-307B-1838	Sequence 1838, Ap	485	233.5	9.9	263	7	US-11-056-355B-109505	Sequence 109505, A
413	246	10.4	1610	7	US-11-174-307B-838	Sequence 838, App	486	233.5	9.9	336	6	US-10-449-902-53338	Sequence 53338, A
414	245.5	10.4	1610	7	US-11-174-307B-1688	Sequence 1688, App	487	233.5	9.9	1459	7	US-11-174-307B-1332	Sequence 1332, Ap
415	245.5	10.4	2445	7	US-11-174-307B-2052	Sequence 2052, App	488	233	9.9	783	7	US-11-330-403-15564	Sequence 15564, A
416	245	10.4	894	6	US-10-532-050-3	Sequence 3, App1	489	233	9.9	864	6	US-10-219-051B-254	Sequence 2524, Ap
417	244.5	10.3	1057	7	US-11-048-197-20	Sequence 20, App1	490	233	9.9	1335	7	US-11-174-307B-388	Sequence 388, App
418	244.5	10.3	1107	7	US-11-048-197-11	Sequence 11, App1	491	232.5	9.8	418	6	US-10-449-902-38356	Sequence 38356, A
419	244.5	10.3	1171	7	US-11-048-197-8	Sequence 8, App1	492	232.5	9.8	515	7	US-11-330-403-14952	Sequence 14952, A
420	244.5	10.3	1286	7	US-11-174-307B-2482	Sequence 2482, Ap	493	232.5	9.8	1337	7	US-11-174-307B-304	Sequence 304, App
421	244.5	10.3	1388	7	US-11-048-197-10	Sequence 10, App1	494	232.5	9.8	1703	7	US-11-174-307B-2214	Sequence 2214, Ap
422	244.5	10.3	1464	6	US-10-985-570-2	Sequence 2, App1	495	232	9.8	391	7	US-11-520-715-56860	Sequence 56860, A
423	244.5	10.3	1464	6	US-10-219-051B-10483	Sequence 10483, A	496	232	9.8	491	7	US-11-056-355B-75851	Sequence 75851, A
424	244.5	10.3	1464	6	US-10-219-051B-10487	Sequence 10487, A	497	232	9.8	491	7	US-11-056-355B-1100995	Sequence 1100995, A
425	244.5	10.3	1464	6	US-10-219-051B-10491	Sequence 10491, A	498	232	9.8	491	7	US-11-056-355B-112234	Sequence 112234, A
426	244.5	10.3	1464	6	US-10-566-878-1	Sequence 1, App1	499	232	9.8	581	7	US-11-056-355B-1100994	Sequence 1100994, A
427	244.5	10.3	2037	7	US-11-174-307B-148	Sequence 148, App	500	232	9.8	581	7	US-11-056-355B-112233	Sequence 112233, A
428	244.5	10.3	2740	7	US-11-330-403-5490	Sequence 5490, App	501	232	9.8	587	7	US-11-056-355B-100993	Sequence 100993, A
429	243.5	10.3	413	7	US-11-330-403-7999	Sequence 7999, App	502	232	9.8	587	7	US-11-056-355B-112232	Sequence 112232, A
430	243	10.3	237	7	US-11-330-403-11239	Sequence 11239, A	503	232	9.8	614	7	US-11-056-355B-75850	Sequence 75850, A
431	242.5	10.3	205	7	US-11-330-403-17000	Sequence 17000, A	504	232	9.8	850	7	US-11-174-307B-534	Sequence 534, App
432	242.5	10.3	243	6	US-10-449-902-35284	Sequence 35284, A	505	232	9.8	1506	7	US-11-174-307B-1870	Sequence 1870, Ap
433	242.5	10.3	345	7	US-11-520-715-42660	Sequence 42660, A	506	232	9.8	1959	7	US-11-174-307B-1428	Sequence 1428, Ap
434	242.5	10.3	1496	6	US-10-700-439-104	Sequence 104, App	507	231	9.8	373	6	US-10-449-902-62371	Sequence 42371, A
435	242.5	10.3	1496	6	US-10-219-051B-7098	Sequence 7098, App	508	231	9.8	373	6	US-11-330-403-12018	Sequence 5018, Ap
436	242	10.2	193	6	US-10-449-902-51303	Sequence 51303, A	509	230.5	9.8	1242	7	US-11-174-307B-1616	Sequence 1616, Ap
437	242	10.2	220	7	US-11-330-403-15395	Sequence 15395, A	510	230.5	9.8	1244	7	US-11-174-307B-488	Sequence 488, App
438	242	10.2	1282	7	US-11-174-307B-564	Sequence 564, App	511	230	9.7	1340	7	US-11-174-307B-2412	Sequence 2412, Ap
439	242	10.2	1765	7	US-11-174-307B-2282	Sequence 2282, App	512	229.5	9.7	539	7	US-11-330-403-3358	Sequence 9358, Ap
440	241.5	10.2	1057	7	US-11-174-307B-2602	Sequence 2602, Ap	513	229	9.7	201	6	US-10-276-817B-14460	Sequence 14460, A
441	241.5	10.2	1065	7	US-11-174-307B-370	Sequence 370, App	514	229	9.7	391	6	US-10-703-032-142270	Sequence 142270, A
442	241	10.2	1056	7	US-11-174-307B-342	Sequence 342, App	515	229	9.7	570	7	US-11-330-403-12944	Sequence 12944, A
443	241	10.2	1056	7	US-11-174-307B-1808	Sequence 1808, Ap	516	229	9.7	625	6	US-10-550-786-3	Sequence 3, App1
444	240.5	10.2	185	6	US-10-449-902-34633	Sequence 34633, A	517	229	9.7	1192	7	US-11-174-307B-2814	Sequence 2814, Ap
445	240.5	10.2	250	6	US-10-603-113-22487	Sequence 22487, A	518	229	9.7	1502	7	US-11-174-307B-5302	Sequence 5302, Ap
446	240.5	10.2	266	6	US-10-449-902-37278	Sequence 37278, A	519	228.5	9.7	197	7	US-11-158-863-914	Sequence 6764, Ap
447	240.5	10.2	1080	6	US-10-574-398-48	Sequence 48, App1	520	228.5	9.7	430	7	US-11-330-403-3764	Sequence 314, App
448	240.5	10.2	1169	7	US-11-048-197-6	Sequence 6, App1	521	228.5	9.7	1270	7	US-11-174-307B-2730	Sequence 2730, Ap
449	240	10.2	1092	7	US-11-174-307B-2680	Sequence 2680, Ap	522	228.5	9.7	1299	7	US-11-174-307B-1640	Sequence 1640, Ap
450	240	10.2	1108	7	US-11-174-307B-5006	Sequence 5006, App	523	228.5	9.7	1500	7	US-11-174-307B-1522	Sequence 1522, Ap
451	239.5	10.1	644	7	US-11-174-307B-4730	Sequence 4730, Ap	524	228.5	9.7	1542	7	US-11-174-307B-50	Sequence 50, App1
452	239.5	10.1	1057	7	US-11-048-197-16	Sequence 16, App1	525	228.5	9.7	1685	7	US-11-174-307B-2212	Sequence 2212, Ap
453	239.5	10.1	1464	6	US-10-700-439-125	Sequence 125, App	526	228.5	9.7	1686	7	US-11-174-307B-1802	Sequence 1802, Ap
454	239.5	10.1	1464	7	US-11-105-233-143	Sequence 143, App	527	228	9.6	178	6	US-10-953-349-5149	Sequence 35149, A
455	239.5	10.1	1464	7	US-11-389-543-199	Sequence 199, App	528	228	9.6	192	6	US-10-953-349-5148	Sequence 35148, A
456	239.5	10.1	1464	7	US-11-510-530-36	Sequence 36, App1	529	228	9.6	690	6	US-10-934-893-5270	Sequence 5270, Ap
457	239	10.1	1611	7	US-11-174-307B-2234	Sequence 2234, Ap	530	228	9.6	690	6	US-11-330-403-3347	Sequence 4347, Ap
458	239	10.1	1611	7	US-11-174-307B-2552	Sequence 2552, Ap	531	227.5	9.6	180	7	US-11-330-403-14749	Sequence 14749, A
459	239	10.1	1806	6	US-10-245-882-202	Sequence 202, App	532	227	9.6	873	7	US-11-174-307B-1646	Sequence 1646, Ap
460	238.5	10.1	1430	6	US-10-534-538A-3	Sequence 3, App1	533	227	9.6	1152	7	US-11-174-307B-2712	Sequence 2712, Ap
461	238.5	10.1	1802	7	US-11-174-307B-1932	Sequence 1932, App	534	227	9.6	1181	6	US-10-533-519-62	Sequence 62, App1
462	238.5	10.1	1942	7	US-11-174-307B-2732	Sequence 2732, App	535	227	9.6	1382	7	US-11-174-307B-2402	Sequence 2402, Ap
463	238	10.1	584	7	US-11-121-154-181	Sequence 181, App	536	226.5	9.6	264	6	US-10-703-032-116126	Sequence 116126, A
464	238	10.1	1806	7	US-11-043-842-348	Sequence 348, App	537	226.5	9.6	469	6	US-10-703-032-111478	Sequence 111478, A
465	238	10.1	1806	7	US-11-043-842-349	Sequence 349, App	538	226	9.6	379	6	US-10-219-051B-7077	Sequence 7077, App
466	238	10.1	1806	7	US-11-050-875-633	Sequence 633, App	539	226	9.6	1382	7	US-11-174-307B-828	Sequence 828, App



540	226	9.6	2309	7	US-11-174-307B-1562	Sequence 1562, Ap	613	216.5	9.2	445	7	US-11-056-355B-75852	Sequence 75852, A
541	226	9.6	2633	7	US-11-174-307B-1414	Sequence 1414, Ap	614	216.5	9.2	684	7	US-11-090-997-1994	Sequence 1954, Ap
542	225.5	9.5	1420	7	US-11-174-307B-2516	Sequence 2516, Ap	615	216.5	9.2	693	7	US-11-090-997-1994	Sequence 1946, Ap
543	225.5	9.5	1566	7	US-11-174-307B-2208	Sequence 2208, Ap	616	216.5	9.2	828	6	US-10-796-280-1335	Sequence 1335, Ap
544	225	9.5	153	6	US-10-703-032-107145	Sequence 107145, A	617	216.5	9.2	918	6	US-10-796-280-1333	Sequence 1333, Ap
545	225	9.5	434	6	US-10-703-032-111479	Sequence 111479, A	618	216.5	9.2	1019	6	US-10-533-519-1393	Sequence 1393, Ap
546	224.5	9.5	174	7	US-11-056-355B-96118	Sequence 96118, A	619	216.5	9.2	1019	6	US-10-533-519-1393	Sequence 1393, Ap
547	224.5	9.5	184	7	US-11-056-355B-96117	Sequence 96117, A	620	216.5	9.2	1019	6	US-10-796-280-1344	Sequence 1344, Ap
548	224.5	9.5	197	7	US-11-520-715-67750	Sequence 67750, A	621	216.5	9.2	1339	7	US-10-796-280-1348	Sequence 1948, Ap
549	224.5	9.5	378	7	US-11-218-141-1281	Sequence 1281, Ap	622	216.5	9.2	1339	7	US-10-796-280-1348	Sequence 1948, Ap
550	224.5	9.5	1060	7	US-11-174-307B-2474	Sequence 2474, Ap	623	216.5	9.2	2282	7	US-10-556-747-20	Sequence 1952, Ap
551	224.5	9.5	1125	7	US-11-174-307B-2582	Sequence 2582, Ap	624	216.5	9.2	1479	7	US-11-174-307B-722	Sequence 722, Ap
552	224.5	9.5	1126	7	US-11-174-307B-2134	Sequence 2134, Ap	625	216	9.1	1479	7	US-11-174-307B-758	Sequence 758, Ap
553	224	9.5	324	7	US-11-056-355B-47338	Sequence 47338, A	626	216	9.1	1838	6	US-10-574-398-1177	Sequence 177, Ap
554	224	9.5	367	7	US-11-056-355B-47337	Sequence 47337, A	627	216	9.1	1838	6	US-10-574-398-1177	Sequence 177, Ap
555	224	9.5	404	7	US-11-056-355B-47336	Sequence 47336, A	628	216	9.1	1838	6	US-10-574-398-1177	Sequence 177, Ap
556	223.5	9.5	238	7	US-11-241-607-56915	Sequence 56915, A	629	215.5	9.1	520	6	US-10-574-398-1177	Sequence 177, Ap
557	223.5	9.5	1362	7	US-11-174-307B-1772	Sequence 1772, Ap	630	215.5	9.1	520	6	US-10-574-398-1177	Sequence 177, Ap
558	223	9.4	218	6	US-10-703-032-110433	Sequence 110433, A	631	215.5	9.1	520	6	US-10-533-519-1095	Sequence 1095, Ap
559	222.5	9.4	200	6	US-10-703-032-115901	Sequence 115901, A	632	215.5	9.1	520	7	US-11-363-149-27	Sequence 27, Ap
560	222.5	9.4	1140	7	US-11-174-307B-2536	Sequence 2536, Ap	633	215.5	9.1	520	7	US-11-363-149-27	Sequence 27, Ap
561	222.5	9.4	1142	7	US-11-174-307B-310	Sequence 310, Ap	634	215.5	9.1	1605	7	US-11-174-307B-1410	Sequence 1410, Ap
562	222.5	9.4	1432	7	US-11-174-307B-2846	Sequence 2846, Ap	635	215.5	9.1	1605	7	US-11-174-307B-1410	Sequence 1410, Ap
563	222	9.4	412	6	US-10-603-113-26345	Sequence 26345, A	636	215.5	9.1	1961	7	US-11-174-307B-1714	Sequence 1714, Ap
564	222	9.4	1022	7	US-11-174-307B-4710	Sequence 4710, Ap	637	215	9.1	155	7	US-11-520-715-4752	Sequence 4752, A
565	222	9.4	1336	7	US-11-174-307B-1036	Sequence 1036, Ap	638	215	9.1	200	7	US-11-330-403-3189	Sequence 3189, Ap
566	222	9.4	2433	7	US-11-174-307B-1618	Sequence 1618, Ap	639	215	9.1	535	7	US-11-056-355B-71789	Sequence 71789, A
567	221.5	9.4	950	7	US-11-174-307B-2002	Sequence 2002, Ap	640	215	9.1	541	7	US-11-056-355B-71788	Sequence 71788, A
568	221.5	9.4	1637	7	US-11-174-307B-2178	Sequence 2178, Ap	641	215	9.1	571	7	US-11-056-355B-36660	Sequence 36660, A
569	221.5	9.4	1637	7	US-11-174-307B-2562	Sequence 2562, Ap	642	215	9.1	577	7	US-11-056-355B-36660	Sequence 36660, A
570	221.5	9.4	1809	7	US-11-174-307B-2054	Sequence 2054, Ap	643	215	9.1	1122	7	US-11-174-307B-2524	Sequence 2524, Ap
571	221.5	9.4	1831	7	US-11-174-307B-1034	Sequence 1034, Ap	644	215	9.1	1233	7	US-11-174-307B-734	Sequence 734, Ap
572	221	9.4	1081	7	US-11-043-842-350	Sequence 350, Ap	645	214.5	9.1	466	7	US-11-174-307B-1342	Sequence 1342, Ap
573	221	9.4	1081	7	US-11-050-875-576	Sequence 576, Ap	646	214.5	9.1	780	7	US-11-174-307B-1866	Sequence 1866, Ap
574	221	9.4	1865	7	US-11-174-307B-2174	Sequence 2174, Ap	647	214.5	9.1	985	7	US-11-174-307B-1840	Sequence 1840, Ap
575	220.5	9.3	645	6	US-10-529-348-703	Sequence 703, Ap	648	214.5	9.1	1126	7	US-11-174-307B-568	Sequence 568, Ap
576	220.5	9.3	879	7	US-11-174-307B-1938	Sequence 1938, Ap	649	214.5	9.1	1266	7	US-11-174-307B-2348	Sequence 2348, Ap
577	220	9.3	214	6	US-10-449-902-54526	Sequence 54526, A	650	214.5	9.1	1600	7	US-11-174-307B-2584	Sequence 2584, Ap
578	219.5	9.3	214	6	US-10-449-902-55835	Sequence 55835, A	651	214.5	9.1	1636	7	US-11-174-307B-2242	Sequence 2242, Ap
579	219.5	9.3	214	6	US-10-449-902-55835	Sequence 55835, A	652	214.5	9.1	1636	7	US-11-174-307B-2242	Sequence 2242, Ap
580	219.5	9.3	617	6	US-10-540-167A-1	Sequence 1, Appl	653	214	9.1	133	7	US-11-486-448-77313	Sequence 77313, A
581	219.5	9.3	684	7	US-11-371-354-57949	Sequence 57949, A	654	214	9.1	188	7	US-11-241-607-55699	Sequence 55699, A
582	219.5	9.3	791	7	US-11-121-154-24	Sequence 24, Appl	655	214	9.1	399	7	US-11-330-403-2175	Sequence 2175, Ap
583	219.5	9.3	1743	7	US-11-174-307B-1614	Sequence 1614, Ap	656	214	9.1	1154	7	US-11-174-307B-1508	Sequence 1508, Ap
584	219	9.3	154	6	US-11-486-448-61579	Sequence 61579, A	657	214	9.1	1156	7	US-11-174-307B-1018	Sequence 1018, Ap
585	219	9.3	170	6	US-10-297-389-37	Sequence 37, Appl	658	214	9.1	1332	7	US-11-174-307B-1336	Sequence 1336, Ap
586	219	9.3	193	6	US-10-219-051B-7075	Sequence 7075, Ap	659	214	9.1	566	7	US-11-241-607-26850	Sequence 26850, A
587	219	9.3	1132	7	US-11-174-307B-892	Sequence 892, Ap	660	213.5	9.0	601	7	US-11-241-607-26849	Sequence 26849, A
588	219	9.3	1238	7	US-11-174-307B-1082	Sequence 1082, Ap	661	213.5	9.0	1263	7	US-11-090-997-1950	Sequence 1950, Ap
589	219	9.3	1736	7	US-11-174-307B-664	Sequence 664, Ap	662	213.5	9.0	1326	7	US-11-090-997-1950	Sequence 1950, Ap
590	219	9.3	2616	7	US-11-174-307B-1680	Sequence 1680, Ap	663	213.5	9.0	1326	7	US-11-090-997-1950	Sequence 1950, Ap
591	218.5	9.2	389	7	US-11-218-141-3249	Sequence 3249, Ap	664	213.5	9.0	1337	7	US-11-174-307B-376	Sequence 376, Ap
592	218.5	9.2	1303	7	US-11-174-307B-430	Sequence 430, Ap	665	213.5	9.0	1424	7	US-11-188-417A-23	Sequence 23, Appl
593	218.5	9.2	1630	7	US-11-174-307B-2222	Sequence 2222, Ap	666	213.5	9.0	1670	6	US-10-219-051B-12751	Sequence 12751, A
594	218.5	9.2	215	7	US-11-520-715-68305	Sequence 68305, A	667	213.5	9.0	1736	7	US-11-174-307B-2668	Sequence 2668, Ap
595	218	9.2	360	6	US-10-449-902-31341	Sequence 31341, A	668	213.5	9.0	1840	6	US-10-743-643-1001	Sequence 1001, Ap
596	218	9.2	647	7	US-11-174-307B-714	Sequence 714, Ap	669	213	9.0	218	6	US-10-449-902-30343	Sequence 30343, A
597	218	9.2	1581	7	US-11-174-307B-1314	Sequence 1314, Ap	670	213	9.0	218	6	US-10-449-902-30343	Sequence 30343, A
598	218	9.2	1656	7	US-11-174-307B-3004	Sequence 3004, Ap	671	213	9.0	367	6	US-10-449-902-34733	Sequence 34733, A
599	217.5	9.2	1663	7	US-11-174-307B-1028	Sequence 1028, Ap	672	213	9.0	529	6	US-10-529-348-620	Sequence 620, Ap
600	217.5	9.2	270	6	US-10-449-902-37505	Sequence 37505, A	673	213	9.0	529	6	US-10-529-348-620	Sequence 620, Ap
601	217.5	9.2	1485	7	US-11-174-307B-2206	Sequence 2206, Ap	674	213	9.0	1683	7	US-11-214-062A-1190	Sequence 1190, Ap
602	217.5	9.2	1673	7	US-11-174-307B-1178	Sequence 1178, Ap	675	212.5	9.0	1762	7	US-11-174-307B-1156	Sequence 1156, Ap
603	217.5	9.2	2412	7	US-11-174-307B-136	Sequence 136, Ap	676	212.5	9.0	1763	7	US-11-174-307B-2674	Sequence 2674, Ap
604	217.5	9.2	2658	7	US-11-174-307B-2464	Sequence 2464, Ap	677	212.5	9.0	2628	7	US-11-174-307B-2692	Sequence 2692, Ap
605	217.5	9.2	2841	7	US-11-174-307B-2530	Sequence 2530, Ap	678	212	9.0	635	7	US-11-218-141-1460	Sequence 1460, Ap
606	217	9.2	295	6	US-10-603-113-25715	Sequence 25715, A	679	212	9.0	644	7	US-11-218-141-1460	Sequence 1460, Ap
607	217	9.2	376	6	US-10-953-349-29760	Sequence 29760, A	680	212	9.0	899	7	US-11-174-307B-1264	Sequence 1264, Ap
608	217	9.2	376	6	US-10-953-349-29760	Sequence 29760, A	681	212	9.0	899	7	US-11-174-307B-1264	Sequence 1264, Ap
609	217	9.2	1452	7	US-11-174-307B-4154	Sequence 4154, Ap	682	212	9.0	1486	7	US-11-174-307B-1772	Sequence 1772, Ap
610	217	9.2	1527	7	US-11-174-307B-1326	Sequence 1326, Ap	683	212	9.0	1662	7	US-11-174-307B-1966	Sequence 1966, Ap
611	217	9.2	1861	7	US-11-174-307B-1744	Sequence 1744, Ap	684	212	9.0	2325	7	US-11-174-307B-5472	Sequence 5472, Ap
612	217	9.2	1873	7	US-11-174-307B-846	Sequence 846, Ap	685	211.5	9.0	187	6	US-10-703-032-11559	Sequence 11559, A
							686	211.5	9.0	301	6	US-10-449-902-43990	Sequence 43990, A
							687	211.5	9.0	442	6	US-10-467-478-1390	Sequence 1390, Ap

688	211.5	9.0	1322	7	US-11-174-307B-2724	Sequence 2724, Ap	761	206	8.7	898	7	US-11-090-997-1960	Sequence 1960, Ap
689	211.5	9.0	1792	7	US-11-174-307B-1192	Sequence 1192, Ap	762	206	8.7	1248	7	US-11-174-307B-2506	Sequence 2506, Ap
690	211	8.9	188	6	US-10-703-032-108776	Sequence 108776, Ap	763	206	8.7	1309	7	US-11-174-307B-2670	Sequence 2670, Ap
691	211	8.9	327	6	US-10-523-834-287	Sequence 287, App	764	206	8.7	1464	7	US-11-174-307B-2038	Sequence 2038, Ap
692	211	8.9	1050	7	US-11-174-307B-2634	Sequence 2634, Ap	765	206	8.7	1516	6	US-10-533-520-2157	Sequence 2157, Ap
693	211	8.9	1155	7	US-11-174-307B-2122	Sequence 2122, Ap	766	206	8.7	1516	6	US-11-431-526-8	Sequence 8, Appl1
694	211	8.9	1437	7	US-11-174-307B-2302	Sequence 2302, Ap	767	206	8.7	1516	7	US-11-431-663-8	Sequence 8, Appl1
695	211	8.9	1521	7	US-11-174-307B-1002	Sequence 1002, Ap	768	206	8.7	1516	7	US-11-521-715-3	Sequence 3, Appl1
696	211	8.9	1553	7	US-11-174-307B-1430	Sequence 1430, Ap	769	206	8.7	1712	6	US-10-796-307-777	Sequence 777, App
697	210.5	8.9	134	6	US-10-276-817B-14459	Sequence 14459, A	770	206	8.7	1914	7	US-10-796-307-20	Sequence 20, Appl
698	210.5	8.9	1238	7	US-11-214-063A-1142	Sequence 1142, Ap	771	206	8.7	2110	7	US-11-174-307B-2010	Sequence 2010, Ap
699	210.5	8.9	506	7	US-11-092-052-778	Sequence 778, App	772	206	8.7	2128	7	US-11-174-307B-1364	Sequence 1364, Ap
700	210.5	8.9	506	7	US-11-507-098A-778	Sequence 778, App	773	205.5	8.7	331	7	US-11-056-355B-82301	Sequence 82302, A
701	210.5	8.9	910	7	US-11-214-063A-1192	Sequence 1192, Ap	774	205.5	8.7	374	7	US-11-056-355B-82301	Sequence 82300, A
702	210.5	8.9	910	7	US-11-174-307B-1536	Sequence 1536, Ap	775	205.5	8.7	411	7	US-11-056-355B-82300	Sequence 1944, Ap
703	210.5	8.9	1387	7	US-11-174-307B-3992	Sequence 3992, Ap	776	205.5	8.7	1767	7	US-11-174-307B-1944	Sequence 1071, Ap
704	210.5	8.9	1488	6	US-10-805-394-5495	Sequence 5495, Ap	777	205.5	8.7	2205	6	US-10-767-471-1071	Sequence 1133, Ap
705	210.5	8.9	1488	6	US-11-092-052-772	Sequence 772, App	778	205.5	8.7	2205	6	US-10-767-471-1072	Sequence 1072, Ap
706	210.5	8.9	1488	7	US-11-507-098A-772	Sequence 772, App	779	205.5	8.7	2210	6	US-10-796-280-1134	Sequence 1134, Ap
707	210.5	8.9	2971	6	US-10-767-471-1075	Sequence 1075, Ap	780	205.5	8.7	2211	6	US-10-796-280-1134	Sequence 1077, Ap
708	210.5	8.9	2971	6	US-10-796-280-1137	Sequence 1137, Ap	781	205.5	8.7	2211	6	US-10-767-471-1077	Sequence 1139, Ap
709	210.5	8.9	2977	6	US-10-767-471-1076	Sequence 1076, Ap	782	205.5	8.7	2244	6	US-10-767-471-1070	Sequence 1070, Ap
710	210.5	8.9	2977	6	US-10-796-280-1138	Sequence 1138, Ap	783	205.5	8.7	2244	6	US-10-796-280-1133	Sequence 1133, Ap
711	210.5	8.9	3177	6	US-10-767-471-1074	Sequence 1074, Ap	784	205.5	8.7	2244	6	US-10-767-471-1073	Sequence 1132, Ap
712	210.5	8.9	3177	6	US-10-796-280-1136	Sequence 1136, Ap	785	205.5	8.7	2411	6	US-10-767-471-1073	Sequence 1135, Ap
713	210	8.9	183	7	US-11-056-355B-10291	Sequence 10291, A	786	205.5	8.7	2411	6	US-10-796-280-1135	Sequence 1135, Ap
714	210	8.9	192	6	US-10-449-902-40198	Sequence 40198, A	787	205	8.7	652	7	US-11-090-997-1944	Sequence 1944, Ap
715	210	8.9	244	6	US-11-056-355B-10290	Sequence 10290, A	788	205	8.7	999	7	US-11-174-307B-1422	Sequence 1422, Ap
716	210	8.9	272	7	US-11-056-355B-10289	Sequence 10289, A	789	205	8.7	1248	7	US-11-174-307B-1262	Sequence 1262, Ap
717	210	8.9	1806	7	US-11-174-307B-872	Sequence 872, App	790	205	8.7	1376	7	US-11-174-307B-378	Sequence 378, App
718	210	8.9	2762	7	US-11-174-307B-2672	Sequence 2672, A	791	205	8.7	1379	7	US-11-174-307B-1738	Sequence 1738, Ap
719	209.5	8.9	203	7	US-11-520-715-50832	Sequence 50832, A	792	205	8.7	1415	6	US-10-419-128-26438	Sequence 26438, A
720	209.5	8.9	1034	6	US-10-419-128-26658	Sequence 26658, A	793	205	8.7	2068	7	US-11-174-307B-2652	Sequence 2652, Ap
721	209.5	8.9	1139	7	US-11-174-307B-2368	Sequence 2368, A	794	205	8.7	2077	7	US-11-174-307B-324	Sequence 324, App
722	209	8.8	150	7	US-11-520-715-67746	Sequence 67746, A	795	205	8.7	2117	7	US-11-174-307B-2836	Sequence 2836, Ap
723	209	8.8	288	7	US-11-377-336-31	Sequence 31, Appl	796	205	8.7	3392	7	US-11-174-307B-1654	Sequence 1654, Ap
724	209	8.8	288	7	US-11-377-338-31	Sequence 31, Appl	797	205	8.7	5109	7	US-11-174-307B-1520	Sequence 1520, Ap
725	209	8.8	433	6	US-10-533-520-2469	Sequence 2469, Ap	798	204.5	8.7	611	6	US-10-449-902-38432	Sequence 38432, A
726	209	8.8	457	7	US-11-330-403-1822	Sequence 1822, Ap	799	204.5	8.7	1206	7	US-11-174-307B-916	Sequence 916, App
727	209	8.8	651	7	US-11-174-307B-3918	Sequence 3918, Ap	800	204.5	8.7	1296	7	US-11-174-307B-2080	Sequence 2080, Ap
728	209	8.8	1066	7	US-11-174-307B-1396	Sequence 1396, Ap	801	204	8.6	1485	7	US-10-703-032-134839	Sequence 13839, A
729	209	8.8	1197	7	US-11-174-307B-1796	Sequence 1796, Ap	802	204	8.6	1485	7	US-11-174-307B-1180	Sequence 1180, Ap
730	209	8.8	2175	7	US-11-174-307B-2008	Sequence 2008, Ap	803	204	8.6	1713	7	US-11-174-307B-1752	Sequence 1752, Ap
731	208.5	8.8	171	6	US-10-953-349-35445	Sequence 35445, A	804	203.5	8.6	192	6	US-10-449-902-11740	Sequence 41740, A
732	208.5	8.8	1434	7	US-11-174-307B-1194	Sequence 1194, A	805	203	8.6	196	7	US-11-330-403-10617	Sequence 10617, A
733	208	8.8	181	7	US-11-056-355B-39799	Sequence 39799, A	806	203	8.6	300	6	US-10-449-902-14151	Sequence 4151, A
734	208	8.8	188	7	US-11-520-715-52710	Sequence 52710, A	807	203	8.6	1245	7	US-11-174-307B-3982	Sequence 3982, Ap
735	208	8.8	457	7	US-11-056-355B-97438	Sequence 97438, A	808	203	8.6	1413	7	US-11-174-307B-1954	Sequence 1954, Ap
736	208	8.8	457	7	US-11-330-403-4358	Sequence 4358, Ap	809	203	8.6	1828	7	US-11-174-307B-698	Sequence 698, App
737	208	8.8	535	6	US-10-796-280-714	Sequence 714, App	810	202.5	8.6	234	6	US-10-703-032-105759	Sequence 105759, A
738	208	8.8	535	6	US-10-796-280-715	Sequence 715, App	811	202.5	8.6	236	6	US-10-953-349-19440	Sequence 39440, A
739	208	8.8	535	6	US-10-796-280-717	Sequence 717, App	812	202.5	8.6	250	6	US-10-953-349-19439	Sequence 39439, A
740	208	8.8	595	6	US-10-796-280-718	Sequence 718, App	813	202.5	8.6	515	6	US-10-449-902-36868	Sequence 36868, A
741	208	8.8	689	6	US-10-796-280-720	Sequence 720, App	814	202.5	8.6	983	7	US-11-174-307B-2434	Sequence 2434, Ap
742	208	8.8	689	6	US-10-796-280-719	Sequence 719, App	815	202.5	8.6	1028	6	US-10-533-519-1651	Sequence 1651, Ap
743	207.5	8.8	476	7	US-11-330-403-16200	Sequence 16200, A	816	202.5	8.6	1448	7	US-11-174-307B-2194	Sequence 2194, Ap
744	207.5	8.8	824	7	US-11-174-307B-1042	Sequence 1042, A	817	202.5	8.6	1448	7	US-11-174-307B-134	Sequence 134, App
745	207.5	8.8	1703	7	US-11-174-307B-558	Sequence 558, App	818	202.5	8.6	1449	7	US-11-174-307B-336	Sequence 336, App
746	207.5	8.8	2047	7	US-11-174-307B-680	Sequence 680, App	819	202.5	8.6	1521	7	US-11-174-307B-1956	Sequence 1956, Ap
747	207.5	8.8	2459	7	US-11-174-307B-268	Sequence 268, App	820	202.5	8.6	1737	7	US-11-174-307B-2046	Sequence 2046, Ap
748	207.5	8.8	2740	7	US-11-174-307B-1234	Sequence 1234, Ap	821	202.5	8.6	3176	6	US-10-533-520-148	Sequence 448, App
749	207	8.8	660	6	US-10-219-051B-11603	Sequence 11603, A	822	202.5	8.6	3176	7	US-11-105-223-155	Sequence 155, App
750	207	8.8	660	7	US-11-226-554-83	Sequence 83, Appl	823	202	8.5	184	6	US-10-703-032-109702	Sequence 109702, A
751	207	8.8	680	7	US-11-248-718-83	Sequence 83, Appl	824	202	8.5	480	7	US-11-520-715-67988	Sequence 67988, A
752	207	8.8	680	7	US-11-538-552-83	Sequence 83, Appl	825	202	8.5	1248	7	US-11-174-307B-934	Sequence 934, App
753	207	8.8	680	7	US-11-538-764-118	Sequence 118, App	826	202	8.5	1641	7	US-11-174-307B-760	Sequence 760, App
754	207	8.8	1838	7	US-11-174-307B-586	Sequence 586, App	827	202	8.5	1737	7	US-11-174-307B-674	Sequence 674, App
755	207	8.8	2062	7	US-11-174-307B-1454	Sequence 1454, App	828	202	8.5	3204	6	US-10-276-817B-10759	Sequence 10759, A
756	206.5	8.7	466	6	US-10-467-478-1391	Sequence 1391, Ap	829	201.5	8.5	174	6	US-10-703-032-113962	Sequence 113962, A
757	206.5	8.7	621	7	US-11-121-154-8	Sequence 8, Appl1	830	201.5	8.5	197	6	US-10-703-032-157713	Sequence 157713, A
758	206.5	8.7	1074	7	US-11-330-403-10732	Sequence 10732, A	831	201.5	8.5	416	6	US-10-703-032-115576	Sequence 115576, A
759	206	8.7	76	6	US-10-631-441-2146	Sequence 2146, Ap	832	201.5	8.5	444	7	US-11-056-355B-52640	Sequence 52640, A
760	206	8.7	447	7	US-11-056-355B-43241	Sequence 43241, A	833	201.5	8.5	467	6	US-10-449-902-36860	Sequence 36860, A

834	201.5	8.5	467	6	US-10-449-902-48607	Sequence 48607, A	907	197.5	8.4	744	7	US-11-510-530-40	Sequence 40, App1
835	201.5	8.5	478	7	US-11-056-355B-36662	Sequence 36662, A	908	197.5	8.4	1050	7	US-11-174-307B-2020	Sequence 2020, Ap
836	201.5	8.5	478	7	US-11-056-355B-71790	Sequence 71790, A	909	197.5	8.4	1108	7	US-11-174-307B-1122	Sequence 1122, Ap
837	201.5	8.5	555	6	US-10-777-288A-3233	Sequence 3233, Ap	910	197.5	8.4	1224	7	US-11-174-307B-1958	Sequence 1958, Ap
838	201.5	8.5	1168	7	US-11-174-307B-700	Sequence 700, App	911	197.5	8.4	1403	7	US-11-174-307B-1448	Sequence 1448, App
839	201.5	8.5	1335	7	US-11-174-307B-3964	Sequence 3964, App	912	197.5	8.4	1416	7	US-11-174-307B-1684	Sequence 1684, App
840	201.5	8.5	1452	7	US-11-174-307B-926	Sequence 926, App	913	197.5	8.4	1633	7	US-11-174-307B-2406	Sequence 2406, Ap
841	201.5	8.5	1730	7	US-11-174-307B-2288	Sequence 2288, Ap	914	197.5	8.4	1668	7	US-11-174-307B-730	Sequence 730, App
842	201.5	8.5	1746	7	US-11-174-307B-2742	Sequence 2742, Ap	915	197.5	8.4	2001	7	US-11-174-307B-1780	Sequence 1780, Ap
843	201.5	8.5	1753	7	US-11-174-307B-1070	Sequence 1070, Ap	916	197	8.3	455	7	US-11-293-697-4328	Sequence 4328, Ap
844	201.5	8.5	1933	7	US-11-174-307B-2226	Sequence 2226, Ap	917	197	8.3	493	7	US-11-520-715-66940	Sequence 66940, A
845	201	8.5	206	7	US-11-241-607-64295	Sequence 64295, A	918	197	8.3	494	7	US-11-520-715-66603	Sequence 66603, A
846	201	8.5	445	6	US-10-527-571A-321	Sequence 321, App	919	197	8.3	717	6	US-10-505-928-438	Sequence 438, App
847	201	8.5	561	7	US-11-121-154-145	Sequence 145, App	920	197	8.3	864	7	US-11-174-307B-1674	Sequence 1674, Ap
848	201	8.5	798	6	US-10-527-571A-369	Sequence 369, App	921	197	8.3	1034	6	US-10-669-920-1271	Sequence 1271, Ap
849	201	8.5	1347	7	US-11-174-307B-844	Sequence 844, App	922	197	8.3	1138	6	US-10-669-920-1273	Sequence 1273, Ap
850	201	8.5	1588	7	US-11-090-987-1786	Sequence 1786, App	923	197	8.3	1537	7	US-11-174-307B-2432	Sequence 2432, Ap
851	201	8.5	1595	7	US-11-174-307B-4562	Sequence 4562, Ap	924	197	8.3	1539	7	US-11-174-307B-2180	Sequence 2180, Ap
852	200.5	8.5	140	6	US-10-703-032-11613	Sequence 11613, A	925	196.5	8.3	541	7	US-11-330-403-3638	Sequence 3638, Ap
853	200.5	8.5	419	6	US-10-276-817B-11037	Sequence 11037, A	926	196.5	8.3	978	7	US-11-174-307B-1692	Sequence 1692, Ap
854	200.5	8.5	1067	7	US-11-174-307B-1718	Sequence 1718, Ap	927	196.5	8.3	1063	7	US-11-174-307B-344	Sequence 344, App
855	200.5	8.5	1227	7	US-11-174-307B-2644	Sequence 2644, Ap	928	196.5	8.3	1089	7	US-11-174-307B-1910	Sequence 1910, Ap
856	200.5	8.5	1245	7	US-11-174-307B-1602	Sequence 1602, Ap	929	196.5	8.3	1433	7	US-11-174-307B-1260	Sequence 1260, Ap
857	200.5	8.5	1252	7	US-11-174-307B-806	Sequence 806, App	930	196.5	8.3	1421	7	US-11-174-307B-870	Sequence 870, App
858	200.5	8.5	1883	7	US-11-174-307B-708	Sequence 708, App	931	196.5	8.3	1443	7	US-11-174-307B-8596	Sequence 8596, Ap
859	200.5	8.5	2148	7	US-11-174-307B-2000	Sequence 2000, A	932	196	8.3	267	6	US-10-953-349-27949	Sequence 27949, A
860	200	8.5	125	6	US-10-449-902-39722	Sequence 39722, A	933	196	8.3	267	6	US-11-056-355B-65580	Sequence 65580, A
861	200	8.5	148	7	US-11-056-355B-15077	Sequence 15077, A	934	196	8.3	320	6	US-10-953-349-27948	Sequence 27948, A
862	200	8.5	148	7	US-11-241-607-10419	Sequence 10419, A	935	196	8.3	320	7	US-11-056-355B-65579	Sequence 65579, A
863	200	8.5	720	7	US-11-174-307B-1550	Sequence 1550, Ap	936	196	8.3	359	6	US-10-953-349-27947	Sequence 27947, A
864	200	8.5	858	7	US-11-174-307B-1934	Sequence 1934, Ap	937	196	8.3	359	7	US-11-056-355B-65578	Sequence 65578, A
865	200	8.5	1378	7	US-11-174-307B-432	Sequence 432, App	938	196	8.3	409	6	US-10-276-817B-11038	Sequence 11038, A
866	200	8.5	1649	7	US-11-174-307B-860	Sequence 860, App	939	196	8.3	1396	7	US-11-174-307B-166	Sequence 166, App
867	200	8.5	1657	7	US-11-174-307B-642	Sequence 642, App	940	196	8.3	1722	7	US-11-174-307B-350	Sequence 350, App
868	200	8.5	1712	7	US-11-174-307B-1086	Sequence 1086, App	941	196	8.3	1723	6	US-10-743-643-176	Sequence 176, App
869	200	8.5	1825	7	US-11-174-307B-882	Sequence 882, App1	942	196	8.3	1723	7	US-11-218-141-1257	Sequence 1257, Ap
870	200	8.5	3303	6	US-10-547-530-49	Sequence 49, App1	943	196	8.3	1727	6	US-10-521-748-11	Sequence 11, App1
871	200	8.5	7697	7	US-11-262-235A-14	Sequence 14, App1	944	196	8.3	1727	6	US-10-533-520-2892	Sequence 2892, Ap
872	199.5	8.4	212	7	US-11-330-403-253	Sequence 253, App	945	196	8.3	1864	7	US-11-174-307B-1994	Sequence 1994, Ap
873	199.5	8.4	232	6	US-10-703-032-124310	Sequence 124310, A	946	196.5	8.3	314	6	US-10-533-519-1692	Sequence 1692, Ap
874	199.5	8.4	356	7	US-11-293-697-3565	Sequence 3565, Ap	947	196.5	8.3	314	6	US-10-528-260B-227	Sequence 227, App
875	199.5	8.4	933	7	US-11-121-154-178	Sequence 178, App	948	196.5	8.3	314	6	US-10-533-520-2737	Sequence 2737, Ap
876	199.5	8.4	1320	7	US-11-174-307B-2270	Sequence 2270, Ap	949	196.5	8.3	923	7	US-11-174-307B-1314	Sequence 1314, Ap
877	199.5	8.4	1512	7	US-11-174-307B-550	Sequence 550, App	950	196.5	8.3	1220	7	US-11-174-307B-1116	Sequence 1116, Ap
878	199.5	8.4	1557	7	US-11-174-307B-1244	Sequence 1244, App	951	196.5	8.3	1272	7	US-11-174-307B-1706	Sequence 1706, Ap
879	199	8.4	303	7	US-11-520-715-42081	Sequence 42081, A	952	196.5	8.3	1655	7	US-11-174-307B-962	Sequence 962, App
880	199	8.4	341	6	US-10-603-113-26119	Sequence 26119, A	953	196.5	8.3	1663	7	US-11-174-307B-938	Sequence 938, App
881	199	8.4	960	7	US-11-090-997-1962	Sequence 1962, App	954	196.5	8.3	1782	7	US-11-174-307B-1652	Sequence 1652, Ap
882	199	8.4	1566	7	US-11-174-307B-222	Sequence 222, App	955	196.5	8.3	1914	7	US-11-174-307B-1256	Sequence 1256, Ap
883	199	8.4	1729	7	US-11-174-307B-540	Sequence 540, App	956	195	8.3	242	7	US-11-056-355B-61074	Sequence 61074, A
884	199	8.4	1855	7	US-11-174-307B-2478	Sequence 2478, App	957	195	8.3	329	7	US-11-214-063A-1438	Sequence 1438, App
885	199	8.4	1856	7	US-11-174-307B-322	Sequence 322, App	958	195	8.3	895	7	US-11-174-307B-1408	Sequence 1408, Ap
886	199	8.4	2016	7	US-11-174-307B-2188	Sequence 2188, Ap	959	195	8.3	1035	7	US-11-174-307B-250	Sequence 250, App
887	198.5	8.4	191	7	US-11-330-403-6050	Sequence 6050, Ap	960	195	8.3	1373	7	US-11-174-307B-1270	Sequence 1270, Ap
888	198.5	8.4	496	7	US-11-090-997-1958	Sequence 1958, Ap	961	195	8.3	1486	7	US-11-174-307B-2522	Sequence 2522, Ap
889	198.5	8.4	1150	6	US-10-669-920-1266	Sequence 1266, App	962	195	8.3	1732	7	US-11-174-307B-2832	Sequence 2832, Ap
890	198.5	8.4	1510	7	US-11-174-307B-584	Sequence 584, App	963	195	8.3	1785	7	US-11-174-307B-2744	Sequence 2744, Ap
891	198.5	8.4	1551	6	US-10-449-902-41326	Sequence 41326, A	964	195	8.3	1859	7	US-11-174-307B-940	Sequence 940, App
892	198.5	8.4	1691	6	US-11-371-354-69607	Sequence 69607, A	965	195	8.3	2238	7	US-11-174-307B-1670	Sequence 1670, Ap
893	198.5	8.4	1884	7	US-11-174-307B-234	Sequence 234, App	966	194.5	8.2	133	6	US-10-703-032-137021	Sequence 137021, A
894	198	8.4	235	6	US-10-953-349-14791	Sequence 14791, A	967	194.5	8.2	139	6	US-10-953-349-21684	Sequence 21684, A
895	198	8.4	235	6	US-10-953-349-25810	Sequence 25810, A	968	194.5	8.2	246	7	US-11-351-712-28	Sequence 28, App1
896	198	8.4	235	7	US-11-056-355B-51294	Sequence 51294, A	969	194.5	8.2	320	6	US-10-703-032-133061	Sequence 133061, A
897	198	8.4	235	7	US-11-056-355B-68107	Sequence 68107, A	970	194.5	8.2	442	6	US-10-603-113-21400	Sequence 12400, A
898	198	8.4	315	7	US-11-241-607-63695	Sequence 63695, A	971	194.5	8.2	1020	7	US-11-174-307B-1624	Sequence 1624, App
899	198	8.4	235	6	US-10-953-349-29761	Sequence 29761, A	972	194.5	8.2	1065	7	US-11-174-307B-118	Sequence 118, App
900	198	8.4	453	7	US-11-174-307B-260	Sequence 260, App	973	194.5	8.2	1359	7	US-11-174-307B-2154	Sequence 2154, App
901	198	8.4	1002	7	US-11-174-307B-1828	Sequence 1828, App	974	194.5	8.2	1370	7	US-11-174-307B-2490	Sequence 2490, App
902	198	8.4	1168	7	US-11-174-307B-316	Sequence 316, App	975	194.5	8.2	1566	7	US-11-174-307B-1548	Sequence 1548, App
903	198	8.4	1181	7	US-11-174-307B-1288	Sequence 1288, App	976	194.5	8.2	1673	7	US-11-174-307B-812	Sequence 812, App
904	198	8.4	1940	7	US-11-174-307B-728	Sequence 728, App	977	194.5	8.2	1689	7	US-11-174-307B-2456	Sequence 2456, App
905	197.5	8.4	196	7	US-11-520-715-67942	Sequence 67942, A	978	194.5	8.2	2124	7	US-11-174-307B-3446	Sequence 3446, App
906	197.5	8.4	464	6	US-10-419-128-24883	Sequence 24883, A	979	194.5	8.2	2247	7	US-11-174-307B-5510	Sequence 5510, App

980	194.5	8.2	2252	US-11-174-307B-1008	Sequence 1008, Ap	1055	189.5	8.0	312	7	US-11-056-355B-42211	Sequence 42211, A
981	194	8.2	2255	US-11-056-355B-2201	Sequence 2201, Ap	1056	189.5	8.0	383	6	US-10-444-902-40221	Sequence 40221, A
982	194	8.2	2255	US-11-241-607-8056	Sequence 8056, Ap	1057	189.5	8.0	1225	7	US-11-174-307B-788	Sequence 788, App
983	194	8.2	715	US-10-669-920-1269	Sequence 1269, Ap	1058	189.5	8.0	1231	7	US-11-174-307B-1168	Sequence 1168, Ap
984	194	8.2	1049	US-11-174-307B-624	Sequence 624, App	1059	189.5	8.0	1260	7	US-11-174-307B-1794	Sequence 1794, Ap
985	194	8.2	1192	US-11-174-307B-694	Sequence 694, App	1060	189.5	8.0	1355	7	US-11-174-307B-2278	Sequence 2278, Ap
986	194	8.2	1478	US-11-174-307B-1442	Sequence 1442, Ap	1061	189.5	8.0	1385	7	US-11-174-307B-1266	Sequence 1266, Ap
987	193.5	8.2	1713	US-11-486-448-74990	Sequence 74990, A	1062	189.5	8.0	1617	7	US-11-174-307B-2448	Sequence 2448, Ap
988	193.5	8.2	769	US-11-121-154-88	Sequence 88, App1	1063	189.5	8.0	1667	6	US-10-934-893-4177	Sequence 4177, A
989	193.5	8.2	1222	US-11-520-715-63118	Sequence 63118, A	1064	189.5	8.0	1836	7	US-11-174-307B-890	Sequence 890, App
990	193.5	8.2	1562	US-11-174-307B-1098	Sequence 998, App	1065	189.5	8.0	4709	7	US-11-174-307B-2292	Sequence 2292, A
991	193	8.2	1559	US-11-174-307B-1050	Sequence 1050, Ap	1066	189.5	8.0	205	6	US-10-703-032-162732	Sequence 162732, A
992	193	8.2	3436	US-11-174-307B-1552	Sequence 1552, Ap	1067	189	8.0	219	7	US-11-056-355B-12769	Sequence 12769, A
993	192.5	8.1	1244	US-11-351-712-27	Sequence 27, App1	1068	189	8.0	222	7	US-11-056-355B-12768	Sequence 12768, A
994	192.5	8.1	1032	US-11-174-307B-2066	Sequence 2066, Ap	1070	189	8.0	236	7	US-11-056-355B-12767	Sequence 12767, A
995	192.5	8.1	1201	US-11-174-307B-2186	Sequence 2186, Ap	1072	189	8.0	445	7	US-11-520-715-45559	Sequence 45559, A
996	192.5	8.1	1215	US-11-174-307B-1632	Sequence 1632, Ap	1073	189	8.0	1105	7	US-11-174-307B-1054	Sequence 1054, Ap
997	192.5	8.1	1374	US-11-174-307B-474	Sequence 474, App	1074	189	8.0	1484	7	US-11-174-307B-1368	Sequence 368, App
998	192.5	8.1	1453	US-11-174-307B-2526	Sequence 2526, Ap	1075	189	8.0	1785	7	US-11-174-307B-4242	Sequence 4242, Ap
999	192.5	8.1	1495	US-11-174-307B-1170	Sequence 1170, Ap	1076	189	8.0	1768	7	US-11-174-307B-1220	Sequence 1220, Ap
999	192.5	8.1	1495	US-11-174-307B-1170	Sequence 1170, Ap	1076	189	8.0	1768	7	US-11-174-307B-1220	Sequence 1220, Ap
1000	192.5	8.1	2012	US-11-174-307B-528	Sequence 528, App	1077	188.5	8.0	203	6	US-10-953-349-5905	Sequence 5905, Ap
1001	192.5	8.1	2017	US-11-174-307B-2682	Sequence 2682, Ap	1078	188.5	8.0	203	6	US-10-374-780A-2096	Sequence 2096, Ap
1002	192	8.1	137	US-10-297-389-32	Sequence 32, App1	1079	188.5	8.0	203	6	US-10-666-642-1436	Sequence 1436, Ap
1003	192	8.1	744	US-10-505-388-493	Sequence 493, App	1080	188.5	8.0	203	6	US-10-412-699B-860	Sequence 860, App
1004	192	8.1	1388	US-11-174-307B-1842	Sequence 1842, App	1081	188.5	8.0	203	7	US-11-036-355B-26302	Sequence 26302, A
1005	192	8.1	1331	US-11-174-307B-566	Sequence 566, App	1082	188.5	8.0	203	7	US-11-056-355B-87042	Sequence 87042, A
1006	192	8.1	1437	US-11-174-307B-1060	Sequence 1060, Ap	1083	188.5	8.0	203	7	US-11-056-355B-103697	Sequence 103697, A
1007	192	8.1	1573	US-11-174-307B-770	Sequence 770, App	1084	188.5	8.0	203	7	US-11-056-355B-114936	Sequence 114936, A
1008	192	8.1	1614	US-11-174-307B-2476	Sequence 2476, App	1085	188.5	8.0	203	7	US-11-433-388-952	Sequence 952, App
1009	192	8.1	1618	US-11-174-307B-484	Sequence 484, App	1086	188.5	8.0	203	7	US-11-479-226-1700	Sequence 1700, App
1010	192	8.1	2205	US-10-547-530-47	Sequence 47, App1	1087	188.5	8.0	203	7	US-11-241-607-27044	Sequence 27044, A
1011	192	8.1	3399	US-10-547-530-47	Sequence 47, App1	1088	188.5	8.0	208	7	US-11-520-715-40715	Sequence 40715, A
1012	192	8.1	3399	US-10-547-530-47	Sequence 47, App1	1088	188.5	8.0	208	7	US-11-520-715-40715	Sequence 40715, A
1013	192	8.1	3399	US-10-547-530-47	Sequence 47, App1	1088	188.5	8.0	208	7	US-11-520-715-40715	Sequence 40715, A
1014	191.5	8.1	147	US-11-241-607-25915	Sequence 25915, A	1089	188.5	8.0	214	7	US-11-330-403-7421	Sequence 7421, App
1015	191.5	8.1	147	US-11-241-607-25915	Sequence 25915, A	1089	188.5	8.0	214	7	US-11-330-403-7421	Sequence 7421, App
1016	191.5	8.1	246	US-11-351-712-26	Sequence 26, App1	1090	188.5	8.0	455	7	US-11-056-355B-95692	Sequence 95692, A
1017	191.5	8.1	270	US-10-703-032-141110	Sequence 141110, A	1091	188.5	8.0	455	7	US-11-241-607-20569	Sequence 20569, A
1018	191.5	8.1	644	US-11-472-437-4	Sequence 4, App1	1092	188.5	8.0	455	7	US-11-241-607-47307	Sequence 47307, A
1019	191.5	8.1	856	US-10-219-051B-14404	Sequence 14404, A	1093	188.5	8.0	455	7	US-11-241-607-47307	Sequence 47307, A
1020	191.5	8.1	1159	US-11-174-307B-1666	Sequence 1666, Ap	1094	188.5	8.0	460	7	US-11-056-355B-95691	Sequence 95691, A
1021	191.5	8.1	1610	US-11-174-307B-1472	Sequence 1472, App	1095	188.5	8.0	460	7	US-11-241-607-20568	Sequence 20568, A
1022	191.5	8.1	1747	US-11-174-307B-2700	Sequence 2700, App	1096	188.5	8.0	460	7	US-11-241-607-47306	Sequence 47306, A
1023	191.5	8.1	1919	US-11-174-307B-978	Sequence 978, App	1097	188.5	8.0	517	7	US-11-056-355B-45764	Sequence 45764, A
1024	191.5	8.1	1991	US-11-174-307B-2144	Sequence 2144, App	1098	188.5	8.0	569	7	US-11-056-355B-45763	Sequence 45763, A
1025	191.5	8.1	1991	US-11-174-307B-2570	Sequence 2570, Ap	1099	188.5	8.0	610	7	US-11-056-355B-95690	Sequence 95690, A
1026	191.5	8.1	2124	US-11-174-307B-2768	Sequence 2768, Ap	1100	188.5	8.0	610	7	US-11-241-607-47305	Sequence 47305, A
1027	191	8.1	305	US-11-371-354-13380	Sequence 13380, A	1101	188.5	8.0	632	7	US-11-056-355B-45762	Sequence 45762, A
1028	191	8.1	305	US-11-371-354-13380	Sequence 13380, A	1102	188.5	8.0	632	7	US-11-056-355B-45762	Sequence 45762, A
1029	191	8.1	305	US-11-371-354-13380	Sequence 13380, A	1103	188.5	8.0	1050	7	US-11-174-307B-724	Sequence 724, App
1030	191	8.1	305	US-11-371-354-13380	Sequence 13380, A	1104	188.5	8.0	1209	7	US-11-174-307B-1884	Sequence 1884, App
1031	191	8.1	305	US-11-371-354-13380	Sequence 13380, A	1105	188.5	8.0	1254	7	US-11-174-307B-1038	Sequence 1038, App
1032	191	8.1	305	US-11-371-354-13380	Sequence 13380, A	1106	188.5	8.0	1574	7	US-11-174-307B-3200	Sequence 3200, App
1033	191	8.1	305	US-11-371-354-13380	Sequence 13380, A	1107	188	8.0	321	7	US-11-520-715-40990	Sequence 40990, Ap
1034	190.5	8.1	159	US-10-953-349-14792	Sequence 14792, A	1108	188	8.0	867	7	US-11-121-154-30	Sequence 30, App1
1035	190.5	8.1	159	US-10-953-349-14792	Sequence 14792, A	1109	188	8.0	1329	7	US-11-174-307B-1822	Sequence 1822, App
1036	190.5	8.1	159	US-10-953-349-14792	Sequence 14792, A	1110	188	8.0	1440	7	US-11-174-307B-2060	Sequence 2060, App
1037	190.5	8.1	159	US-11-056-355B-51295	Sequence 51295, A	1111	188	8.0	1524	7	US-11-174-307B-880	Sequence 880, App
1038	190.5	8.1	159	US-11-056-355B-68108	Sequence 68108, A	1112	188	8.0	1542	7	US-11-174-307B-2656	Sequence 2656, App
1039	190.5	8.1	1637	US-10-603-113-19134	Sequence 19134, A	1113	188	8.0	1569	7	US-11-174-307B-552	Sequence 552, App
1040	190.5	8.1	1452	US-11-174-307B-2286	Sequence 2286, App	1114	188	8.0	1843	7	US-11-174-307B-988	Sequence 988, App
1041	190.5	8.1	1452	US-11-174-307B-1174	Sequence 1174, App	1115	188	8.0	3723	7	US-11-174-307B-2802	Sequence 2802, App
1042	190	8.0	139	US-11-174-307B-576	Sequence 576, App	1116	187.5	7.9	180	6	US-10-603-113-22352	Sequence 22352, App
1043	190	8.0	185	US-10-703-032-137017	Sequence 3800, A	1117	187.5	7.9	233	7	US-11-330-403-17734	Sequence 17774, A
1044	190	8.0	984	US-11-174-307B-2022	Sequence 2022, App	1118	187.5	7.9	470	6	US-10-760-320A-9655	Sequence 3655, App
1045	190	8.0	1136	US-11-174-307B-2400	Sequence 2400, App	1119	187.5	7.9	481	7	US-11-520-715-59250	Sequence 59250, App
1046	190	8.0	1136	US-11-174-307B-2504	Sequence 2504, App	1120	187.5	7.9	543	7	US-11-174-307B-3406	Sequence 3406, App
1047	190	8.0	1146	US-11-174-307B-2372	Sequence 2372, App	1121	187.5	7.9	1089	7	US-11-174-307B-62	Sequence 62, App1
1048	190	8.0	1147	US-10-669-920-722	Sequence 722, App	1122	187.5	7.9	1174	7	US-11-174-307B-66	Sequence 66, App
1049	190	8.0	1139	US-11-174-307B-2050	Sequence 2050, App	1123	187.5	7.9	1284	7	US-11-174-307B-1980	Sequence 1980, App
1050	190	8.0	1408	US-11-174-307B-2196	Sequence 2196, App	1124	187.5	7.9	1357	7	US-11-174-307B-1946	Sequence 1946, App
1051	190	8.0	1464	US-11-174-307B-2594	Sequence 2594, App	1125	187.5	7.9	1358	7	US-11-174-307B-2238	Sequence 2238, App
1052	190	8.0	1767	US-11-174-307B-1882	Sequence 1882, App	1126	187.5	7.9	1460	7	US-11-174-307B-1282	Sequence 1282, App
1053	189.5	8.0	266	US-11-056-355B-42213	Sequence 42213, A	1127	187.5	7.9	1571	7	US-11-174-307B-2074	Sequence 2074, App
1054	189.5	8.0	266	US-11-056-355B-42213	Sequence 42213, A	1128	187.5	7.9	1684	7	US-11-216-141-3225	Sequence 3225, App
1055	189.5	8.0	289	US-11-056-355B-42212	Sequence 42212, A	1129	187.5	7.9	1948	7	US-11-174-307B-2702	Sequence 2702, App

1130	187	7.9	190	7	US-11-520-715-37815	Sequence 37815, A	1203	183.5	7.8	1845	7	US-11-174-307B-1310	Sequence 1310, Ap
1131	187	7.9	252	6	US-10-550-786-2	Sequence 2, Appl1	1204	183.5	7.8	1942	7	US-11-174-307B-1076	Sequence 1076, Ap
1132	187	7.9	397	6	US-10-449-902-53802	Sequence 53802, A	1205	183.5	7.8	2568	7	US-11-174-307B-90	Sequence 90, Appl
1133	187	7.9	1157	7	US-11-174-307B-348	Sequence 348, App	1206	183	7.7	197	6	US-10-703-032-166905	Sequence 166905,
1134	187	7.9	1161	7	US-11-174-307B-2568	Sequence 2568, Ap	1207	183	7.7	278	7	US-11-377-336-28	Sequence 28, Appl
1135	187	7.9	1217	7	US-11-174-307B-4324	Sequence 4324, Ap	1208	183	7.7	278	7	US-11-377-336-28	Sequence 28, Appl
1136	187	7.9	1635	7	US-11-174-307B-3630	Sequence 3630, Ap	1209	183	7.7	658	7	US-11-371-354-70911	Sequence 70911, A
1137	187	7.9	1714	7	US-11-174-307B-740	Sequence 740, App	1210	183	7.7	972	7	US-11-174-307B-1708	Sequence 1708, A
1138	187	7.9	1990	7	US-11-174-307B-862	Sequence 862, App	1211	183	7.7	1231	7	US-11-174-307B-834	Sequence 834, App
1139	187	7.9	2143	7	US-11-174-307B-1284	Sequence 1284, App	1212	183	7.7	2369	7	US-11-174-307B-2012	Sequence 2012, Ap
1140	186.5	7.9	205	6	US-10-703-032-124309	Sequence 124309, A	1213	182.5	7.7	275	7	US-11-486-448-75105	Sequence 75105, A
1141	186.5	7.9	361	6	US-10-449-902-47434	Sequence 47434, A	1214	182.5	7.7	475	7	US-11-056-355B-91701	Sequence 91701, A
1142	186.5	7.9	361	6	US-10-449-902-50393	Sequence 50393, A	1215	182.5	7.7	475	7	US-11-056-355B-95457	Sequence 95457, A
1143	186.5	7.9	614	7	US-11-472-113-25	Sequence 25, Appl1	1216	182.5	7.7	607	7	US-11-174-307B-4430	Sequence 4430, Ap
1144	186.5	7.9	1370	7	US-11-174-307B-2124	Sequence 2124, Ap	1217	182.5	7.7	876	7	US-11-174-307B-144	Sequence 144, App
1145	186.5	7.9	1709	7	US-11-174-307B-2970	Sequence 2970, Ap	1218	182.5	7.7	1270	7	US-11-174-307B-1252	Sequence 1252, Ap
1146	186.5	7.9	1710	7	US-11-174-307B-1588	Sequence 1588, Ap	1219	182.5	7.7	1278	7	US-11-174-307B-1626	Sequence 1626, Ap
1147	186	7.9	610	6	US-10-527-571A-337	Sequence 337, App	1220	182.5	7.7	1721	7	US-11-174-307B-1148	Sequence 1148, Ap
1148	186	7.9	1109	6	US-10-527-571A-335	Sequence 335, App	1221	182.5	7.7	2337	7	US-11-174-307B-1702	Sequence 1702, Ap
1149	186	7.9	1224	7	US-11-174-307B-1844	Sequence 1844, Ap	1222	182.5	7.7	1915	7	US-11-174-307B-1868	Sequence 1868, Ap
1150	186	7.9	1249	7	US-11-174-307B-2566	Sequence 2566, Ap	1223	182.5	7.7	319	7	US-11-056-355B-91702	Sequence 91702, A
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1152	186	7.9	1277	7	US-11-174-307B-888	Sequence 888, App	1225	182	7.7	2604	7	US-11-174-307B-1636	Sequence 1636, Ap
1153	186	7.9	1287	7	US-11-174-307B-444	Sequence 444, App	1226	182	7.7	138	7	US-11-330-403-15653	Sequence 15653, A
1154	186	7.9	1407	7	US-11-174-307B-648	Sequence 648, App	1227	182	7.7	303	7	US-11-520-715-455016	Sequence 50016, A
1155	186	7.9	1416	7	US-11-174-307B-3262	Sequence 3262, Ap	1228	182	7.7	396	7	US-11-056-355B-91702	Sequence 91702, A
1156	186	7.9	1439	7	US-11-174-307B-3364	Sequence 3364, Ap	1229	182	7.7	396	7	US-11-056-355B-95458	Sequence 95458, A
1157	186	7.9	1517	7	US-11-174-307B-1202	Sequence 1202, Ap	1230	182	7.7	619	7	US-11-121-154-51	Sequence 51, Appl
1158	186	7.9	1581	7	US-11-283-329-162	Sequence 162, App	1231	182	7.7	700	7	US-11-121-154-107	Sequence 107, App
1159	186	7.9	1601	7	US-11-174-307B-2264	Sequence 2264, Ap	1232	182	7.7	1053	7	US-11-174-307B-1230	Sequence 1230, Ap
1160	186	7.9	1713	7	US-11-174-307B-3720	Sequence 3720, Ap	1233	182	7.7	1155	7	US-11-174-307B-186	Sequence 186, App
1161	186	7.9	1865	7	US-11-174-307B-1078	Sequence 1078, Ap	1234	182	7.7	1228	7	US-11-174-307B-388	Sequence 388, Ap
1162	185.5	7.9	291	7	US-11-056-355B-3920	Sequence 3920, Ap	1235	181.5	7.7	133	6	US-10-703-032-118878	Sequence 118878, A
1163	185.5	7.9	298	7	US-11-056-355B-3919	Sequence 3919, Ap	1236	181.5	7.7	154	7	US-11-056-355B-26187	Sequence 26187, A
1164	185.5	7.9	336	7	US-11-520-715-67770	Sequence 67770, A	1237	181.5	7.7	651	6	US-10-486-020-13	Sequence 13, Appl
1165	185.5	7.9	384	7	US-11-056-355B-3918	Sequence 3918, Ap	1238	181.5	7.7	1343	7	US-11-174-307B-1146	Sequence 1146, Ap
1166	185.5	7.9	1167	7	US-11-174-307B-2734	Sequence 2734, Ap	1239	181.5	7.7	1537	7	US-11-174-307B-7736	Sequence 7736, Ap
1167	185.5	7.9	1177	7	US-11-174-307B-884	Sequence 884, App	1240	181.5	7.7	1604	7	US-11-174-307B-2250	Sequence 2250, Ap
1168	185.5	7.9	1281	7	US-11-174-307B-106	Sequence 106, App	1241	181.5	7.7	2384	7	US-11-174-307B-1740	Sequence 1740, Ap
1169	185.5	7.9	1299	7	US-11-174-307B-1524	Sequence 1524, Ap	1242	181.5	7.7	2415	7	US-11-174-307B-1564	Sequence 1564, Ap
1170	185.5	7.9	1498	7	US-11-174-307B-5052	Sequence 5052, Ap	1243	181	7.7	469	7	US-11-520-715-43328	Sequence 43328, A
1171	185.5	7.9	1523	7	US-11-174-307B-2716	Sequence 2716, Ap	1244	181	7.7	496	7	US-11-371-354-68559	Sequence 62859, A
1172	185.5	7.9	1675	7	US-11-174-307B-658	Sequence 658, App	1245	181	7.7	511	7	US-11-121-154-96	Sequence 96, Appl
1173	185.5	7.9	1704	7	US-11-174-307B-1004	Sequence 1004, Ap	1246	181	7.7	1348	7	US-11-174-307B-8882	Sequence 2882, Ap
1174	185.5	7.9	1775	7	US-11-174-307B-1538	Sequence 1538, Ap	1247	181	7.7	1478	7	US-11-174-307B-710	Sequence 710, App
1175	185.5	7.9	1844	7	US-11-174-307B-930	Sequence 930, App	1248	181	7.7	1522	7	US-11-174-307B-3906	Sequence 3906, Ap
1176	185.5	7.9	1955	7	US-11-174-307B-1590	Sequence 1590, Ap	1249	181	7.7	2085	7	US-11-174-307B-954	Sequence 954, App
1177	185.5	7.9	2472	7	US-11-174-307B-1716	Sequence 1716, Ap	1250	181	7.7	2682	7	US-11-174-307B-88	Sequence 88, Appl
1178	185.5	7.9	2574	7	US-11-174-307B-1990	Sequence 1990, Ap	1251	180.5	7.6	505	7	US-11-174-307B-4872	Sequence 4872, Ap
1179	185.5	7.9	4243	7	US-11-174-307B-1722	Sequence 1722, Ap	1252	180.5	7.6	725	7	US-11-121-154-18	Sequence 19, Appl
1180	185	7.8	285	7	US-11-520-715-63343	Sequence 63343, A	1253	180.5	7.6	1153	7	US-11-174-307B-300	Sequence 300, App
1181	185	7.8	905	7	US-11-174-307B-1506	Sequence 1506, App	1254	180.5	7.6	1684	7	US-11-174-307B-402	Sequence 402, App
1182	185	7.8	910	7	US-11-174-307B-2232	Sequence 2232, Ap	1255	180.5	7.6	1684	7	US-11-174-307B-1398	Sequence 1398, Ap
1183	185	7.8	1298	7	US-11-174-307B-5050	Sequence 5050, Ap	1256	180.5	7.6	3159	7	US-11-174-307B-1916	Sequence 1916, Ap
1184	185	7.8	1460	7	US-11-174-307B-5280	Sequence 5280, Ap	1257	180	7.6	126	7	US-11-056-355B-26188	Sequence 26188, A
1185	185	7.8	1849	7	US-11-174-307B-5428	Sequence 5428, Ap	1258	180	7.6	125	6	US-10-703-032-151654	Sequence 151654, A
1186	184.5	7.8	388	7	US-11-506-611-20	Sequence 20, Appl1	1259	180	7.6	490	6	US-10-449-902-47491	Sequence 47491, A
1187	184.5	7.8	358	7	US-11-174-307B-174	Sequence 174, App	1260	180	7.6	1084	6	US-10-449-902-41170	Sequence 41170, A
1188	184.5	7.8	659	7	US-11-174-307B-614	Sequence 614, App	1261	180	7.6	1860	7	US-11-174-307B-612	Sequence 612, App
1189	184.5	7.8	823	7	US-11-174-307B-472	Sequence 472, App	1262	180	7.6	1931	7	US-11-174-307B-5056	Sequence 5056, Ap
1190	184.5	7.8	823	7	US-11-174-307B-2598	Sequence 2598, Ap	1263	180	7.6	1962	7	US-11-174-307B-1748	Sequence 1748, Ap
1191	184.5	7.8	1004	6	US-10-805-384-5676	Sequence 5676, Ap	1264	180	7.6	1962	7	US-11-174-307B-2754	Sequence 2754, Ap
1192	184.5	7.8	1075	7	US-11-174-307B-452	Sequence 452, App	1265	180	7.6	7285	7	US-11-272-521-28	Sequence 28, Appl
1193	184.5	7.8	1287	7	US-11-174-307B-2632	Sequence 2632, Ap	1266	179.5	7.6	492	7	US-11-330-403-10767	Sequence 10767, A
1194	184.5	7.8	1293	7	US-11-174-307B-502	Sequence 502, App	1267	179.5	7.6	1131	7	US-11-174-307B-1604	Sequence 1604, Ap
1195	184.5	7.8	1464	7	US-11-174-307B-1116	Sequence 1116, App	1268	179.5	7.6	1344	7	US-11-174-307B-1940	Sequence 1940, Ap
1196	184	7.8	250	6	US-10-550-786-1	Sequence 1, Appl1	1269	179.5	7.6	1472	7	US-11-174-307B-1344	Sequence 1344, Ap
1197	184	7.8	1093	7	US-11-174-307B-1026	Sequence 1026, App	1270	179.5	7.6	1538	7	US-11-174-307B-2654	Sequence 2654, Ap
1198	184	7.8	1505	7	US-11-174-307B-1622	Sequence 1622, App	1271	179.5	7.6	1597	7	US-11-297-134-61	Sequence 61, Appl
1199	184	7.8	1537	7	US-11-174-307B-716	Sequence 716, App	1272	179.5	7.6	1723	7	US-11-174-307B-908	Sequence 908, App
1200	184	7.8	1735	7	US-11-174-307B-2246	Sequence 2246, App	1273	179.5	7.6	2973	7	US-11-174-307B-1566	Sequence 1566, App
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1202	183.5	7.8	1467	7	US-11-174-307B-1854	Sequence 1854, App	1275	179	7.6	202	7	US-11-377-336-37	Sequence 37, Appl

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

## SUMMARIES

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58	366	15.5	766	1	US-08-707-237A-61	Sequence 61, Appl
59	366	15.5	766	2	US-08-482-085B-88	Sequence 88, Appl
60	366	15.5	766	2	US-09-444-791A-88	Sequence 88, Appl
61	366	15.5	979	1	US-08-477-509B-89	Sequence 89, Appl
62	366	15.5	979	2	US-08-482-085B-89	Sequence 89, Appl
63	366	15.5	979	2	US-09-444-791A-89	Sequence 89, Appl
64	366	15.5	1050	1	US-08-175-155-54	Sequence 54, Appl
65	364.5	15.4	907	1	US-09-010-928B-4	Sequence 4, Appl
66	364.5	15.4	2018	2	US-09-444-791A-80	Sequence 80, Appl
67	364.5	15.4	2100	1	US-08-477-509B-80	Sequence 80, Appl
68	364.5	15.4	2100	2	US-08-482-085B-80	Sequence 80, Appl
69	364	15.4	649	1	US-07-609-716-49	Sequence 49, Appl
70	364	15.4	649	2	US-08-475-411A-49	Sequence 49, Appl
71	364	15.4	649	2	US-08-478-029A-49	Sequence 49, Appl
72	364	15.4	784	1	US-07-609-716-48	Sequence 48, Appl
73	364	15.4	784	2	US-08-475-411A-48	Sequence 48, Appl
74	364	15.4	784	2	US-08-478-029A-48	Sequence 48, Appl
75	364	15.4	1018	1	US-08-089-862-11	Sequence 11, Appl
76	364	15.4	1018	1	US-08-587-333-18	Sequence 18, Appl
77	364	15.4	1018	5	PCT-US94-07776-16	Sequence 16, Appl
78	364	15.4	2107	1	US-08-175-155-45	Sequence 45, Appl
79	364	15.4	2107	1	US-08-707-237A-51	Sequence 51, Appl
80	362	15.3	604	2	US-08-556-978B-63	Sequence 63, Appl
81	362	15.3	1332	1	US-07-609-716-41	Sequence 41, Appl
82	362	15.3	1332	2	US-08-475-411A-41	Sequence 41, Appl
83	362	15.3	1332	2	US-08-478-029A-41	Sequence 41, Appl
84	358.5	15.2	2055	1	US-08-175-155-46	Sequence 46, Appl
85	358.5	15.2	2055	1	US-08-477-509B-81	Sequence 81, Appl
86	358.5	15.2	2055	1	US-08-707-237A-82	Sequence 82, Appl
87	358.5	15.2	2055	2	US-08-482-085B-81	Sequence 81, Appl
88	358.5	15.2	2055	2	US-09-444-791A-81	Sequence 81, Appl
89	358	15.2	606	2	US-08-556-978B-21	Sequence 21, Appl
90	358	15.2	606	2	US-08-556-978B-23	Sequence 23, Appl
91	358	15.2	606	2	US-09-247-806-6	Sequence 6, Appl
92	358	15.2	606	2	US-09-247-806-6	Sequence 6, Appl
93	358	15.2	606	2	US-09-247-806-8	Sequence 8, Appl
94	358	15.2	606	2	US-09-861-597-4	Sequence 4, Appl
95	358	15.2	606	2	US-09-861-597-6	Sequence 6, Appl
96	358	15.2	606	2	US-09-861-597-8	Sequence 8, Appl
97	358	15.2	809	2	US-09-863-859-13	Sequence 13, Appl
98	358	15.2	809	2	US-10-414-760-13	Sequence 13, Appl
99	358	15.2	818	2	US-09-863-859-22	Sequence 22, Appl



100	358	15.2	818	2	US-10-414-760-22	Sequence 22, Appl	173	294	12.4	674	2	US-08-808-599A-3	Sequence 3, Appli
101	358	15.2	1617	2	US-09-863-859-14	Sequence 14, Appl	174	290.5	12.3	749	1	US-08-317-522A-2	Sequence 2, Appli
102	358	15.2	1617	2	US-10-414-760-14	Sequence 14, Appl	175	290.5	12.3	749	1	US-08-439-818A-2	Sequence 2, Appli
103	358	15.2	1626	2	US-09-863-859-24	Sequence 24, Appl	176	290.5	12.3	749	1	US-08-751-965-2	Sequence 2, Appli
104	358	15.2	1626	2	US-10-414-760-24	Sequence 24, Appl	177	290.5	12.3	749	1	US-08-728-975-2	Sequence 2, Appli
105	354	15.0	945	1	US-08-089-862-6	Sequence 6, Appli	178	290.5	12.3	749	1	US-08-728-626-2	Sequence 2, Appli
106	354	15.0	945	1	US-08-587-333-13	Sequence 13, Appl	179	290.5	12.3	749	2	US-08-808-599A-2	Sequence 2, Appli
107	354	15.0	945	5	PCT-US94-07776-11	Sequence 11, Appl	180	288.5	12.2	877	1	US-08-397-633A-54	Sequence 54, Appli
108	351.5	14.9	1056	1	US-08-212-237-6	Sequence 6, Appli	181	288.5	12.2	953	2	US-08-806-029-14	Sequence 14, Appl
109	351.5	14.9	1056	2	US-08-806-029-29	Sequence 29, Appl	182	283.5	12.0	401	2	US-09-219-889-34	Sequence 34, Appl
110	351.5	14.9	1056	5	PCT-US95-02772-6	Sequence 6, Appli	183	283.5	12.0	599	2	US-09-602-459-22	Sequence 22, Appl
111	350.5	14.8	2257	1	US-08-175-155-47	Sequence 47, Appl	184	283.5	12.0	599	2	US-09-602-459-23	Sequence 23, Appl
112	350.5	14.8	2257	1	US-08-477-509B-82	Sequence 82, Appl	185	283	12.0	1160	2	US-08-808-599A-24	Sequence 24, Appl
113	350.5	14.8	2257	1	US-08-707-237A-53	Sequence 53, Appl	186	280	11.8	1057	2	US-08-931-820-4	Sequence 4, Appli
114	350.5	14.8	2257	2	US-08-482-085B-82	Sequence 82, Appl	187	278.5	11.8	526	2	US-09-538-092-1080	Sequence 1080, Ap
115	350.5	14.8	2257	2	US-09-444-791A-82	Sequence 82, Appl	188	276	11.7	231	2	US-09-248-766A-14281	Sequence 14281, A
116	350	14.8	316	2	US-09-538-092-997	Sequence 997, App	189	276	11.7	1040	2	US-10-153-469A-30	Sequence 30, Appl
117	348.5	14.7	528	2	US-09-490-291-8	Sequence 8, Appli	190	276	11.7	1040	2	US-10-153-469A-32	Sequence 32, Appl
118	348	14.7	832	1	US-08-209-747-2	Sequence 2, Appli	191	276	11.7	1040	2	US-10-104-889-30	Sequence 30, Appl
119	348	14.7	832	1	US-08-458-298-2	Sequence 2, Appli	192	276	11.7	1040	2	US-10-104-889-32	Sequence 32, Appl
120	343	14.5	681	2	US-09-490-291-4	Sequence 4, Appli	193	276	11.7	1078	2	US-08-963-825-21	Sequence 21, Appl
121	343	14.5	681	2	US-09-490-291-6	Sequence 6, Appli	194	276	11.7	1078	2	US-09-500-811-21	Sequence 21, Appl
122	336	14.2	1169	2	US-08-806-029-33	Sequence 33, Appl	195	276	11.7	1078	2	US-09-570-573-21	Sequence 21, Appl
123	327.5	13.9	334	2	US-09-060-756-728	Sequence 728, App	196	276	11.7	1078	2	US-09-548-608-21	Sequence 21, Appl
124	327.5	13.9	334	2	US-09-670-314-728	Sequence 728, App	197	276	11.7	1366	2	US-09-585-887-10	Sequence 10, Appl
125	327.5	13.9	334	2	US-10-259-678-728	Sequence 728, App	198	276	11.7	1366	2	US-09-289-578-10	Sequence 10, Appl
126	322.5	13.6	972	1	US-08-212-237-7	Sequence 7, Appli	199	276	11.7	1366	2	US-09-949-016-5882	Sequence 5882, Ap
127	322.5	13.6	972	2	US-08-806-029-30	Sequence 30, Appli	200	275	11.6	482	2	US-09-902-540-14708	Sequence 14708, A
128	322.5	13.6	972	5	PCT-US95-02772-7	Sequence 7, Appli	201	274	11.6	593	2	US-09-538-092-919	Sequence 919, App
129	319.5	13.5	318	2	US-09-060-756-727	Sequence 727, App	202	273	11.6	486	1	US-08-397-633A-77	Sequence 77, Appl
130	319.5	13.5	318	2	US-09-670-314-727	Sequence 727, App	203	272.5	11.5	479	2	US-08-397-633A-84	Sequence 84, Appl
131	319.5	13.5	318	2	US-10-259-678-727	Sequence 727, App	204	272.5	11.5	619	2	US-09-252-991A-26352	Sequence 26352, A
132	317.5	13.4	988	2	US-08-212-237-5	Sequence 5, Appli	205	272	11.5	291	2	US-09-490-291-2	Sequence 2, Appli
133	317.5	13.4	988	2	US-08-806-029-28	Sequence 28, Appl	206	272	11.5	696	2	US-08-806-029-26	Sequence 26, Appl
134	317.5	13.4	988	5	PCT-US95-02772-5	Sequence 5, Appli	207	272	11.5	750	2	US-08-806-029-25	Sequence 25, Appl
135	309.5	13.1	200	2	US-09-889-981A-13	Sequence 13, Appl	208	271	11.5	761	1	US-08-707-227A-84	Sequence 84, Appl
136	309.5	13.1	200	2	US-09-850-948A-29	Sequence 29, Appl	209	271	11.5	762	1	US-08-642-255-114	Sequence 114, App
137	309.5	13.1	200	3	US-10-160-633-3	Sequence 3, Appli	210	271	11.5	762	1	US-08-397-633A-26	Sequence 26, Appl
138	309	13.1	201	2	US-09-052-995-1	Sequence 1, Appli	211	268.5	11.4	1027	2	US-10-360-101-221	Sequence 221, App
139	309	13.1	201	2	US-09-053-003-40	Sequence 40, Appl	212	268	11.3	762	1	US-08-642-255-120	Sequence 120, App
140	309	13.1	201	2	US-09-054-281-22	Sequence 22, Appl	213	268	11.3	762	1	US-08-397-633A-31	Sequence 31, Appli
141	309	13.1	201	2	US-09-478-948-6	Sequence 6, Appli	214	267.5	11.3	1024	2	US-08-931-820-2	Sequence 2, Appli
142	309	13.1	201	2	US-09-818-094-40	Sequence 40, Appl	215	267.5	11.3	1366	2	US-08-963-825-19	Sequence 19, Appl
143	309	13.1	201	2	US-09-754-947-5	Sequence 5, Appli	216	267.5	11.3	1366	2	US-09-500-811-19	Sequence 19, Appl
144	308	13.0	225	1	US-08-529-190B-1	Sequence 1, Appli	217	267.5	11.3	1366	2	US-09-570-573-19	Sequence 19, Appl
145	304.5	12.9	889	2	US-08-806-029-19	Sequence 19, Appl	218	267.5	11.3	1366	2	US-09-548-608-19	Sequence 19, Appl
146	302	12.8	714	2	US-08-556-978B-61	Sequence 61, Appl	219	265	11.2	343	2	US-10-148-306-21	Sequence 21, Appl
147	302	12.8	714	2	US-09-247-806-10	Sequence 10, Appl	220	264.5	11.2	1008	1	US-09-219-849-8	Sequence 8, Appli
148	302	12.8	714	2	US-09-861-597-10	Sequence 10, Appl	221	264.5	11.2	1065	1	US-09-642-255-80	Sequence 80, Appl
149	300.5	12.7	768	2	US-08-806-029-35	Sequence 35, Appl	222	264.5	11.2	1065	2	US-08-642-246-16	Sequence 16, Appl
150	300.5	12.7	884	1	US-08-397-633A-68	Sequence 68, Appl	223	264.5	11.2	1065	2	US-08-642-246-16	Sequence 16, Appl
151	300.5	12.7	884	1	US-08-435-641-15	Sequence 15, Appl	224	264.5	11.2	1065	5	PCT-US96-06229-16	Sequence 16, Appl
152	300.5	12.7	884	2	US-08-707-237A-96	Sequence 96, Appl	225	264	11.2	269	1	US-08-452-531-4	Sequence 4, Appli
153	300.5	12.7	884	2	US-08-642-246-15	Sequence 15, Appl	226	264	11.2	269	1	US-08-460-746A-4	Sequence 4, Appli
154	300.5	12.7	884	2	US-09-451-206-15	Sequence 15, Appl	227	264	11.2	269	1	US-08-460-555-4	Sequence 4, Appli
155	300.5	12.7	884	2	PCT-US96-06229-15	Sequence 15, Appl	228	264	11.2	269	2	US-08-460-066-4	Sequence 6, Appli
156	300	12.7	738	5	US-08-864-038A-3	Sequence 3, Appli	229	257	10.9	633	1	US-08-642-255-73	Sequence 73, Appl
157	296.5	12.5	1024	1	US-08-212-237-8	Sequence 8, Appli	230	257	10.9	1065	1	US-08-642-255-72	Sequence 72, Appl
158	296.5	12.5	1024	5	US-08-806-029-31	Sequence 31, Appl	231	254	10.7	1040	2	US-08-806-029-32	Sequence 32, Appl
159	296.5	12.5	1024	5	PCT-US95-02772-8	Sequence 8, Appli	232	254	10.7	1745	2	US-09-795-061-4	Sequence 4, Appli
160	296	12.5	595	1	US-08-425-069-4	Sequence 4, Appli	233	254	10.7	1745	2	US-09-949-002-105	Sequence 405, App
161	296	12.5	595	1	US-08-317-844B-4	Sequence 4, Appli	234	254	10.7	1771	2	US-09-949-002-492	Sequence 492, App
162	294.5	12.5	832	1	US-08-212-237-4	Sequence 4, Appli	235	253	10.7	1060	2	US-08-931-820-3	Sequence 3, Appli
163	294.5	12.5	832	2	US-08-806-029-27	Sequence 27, Appl	236	253	10.7	1077	1	US-07-972-032-82	Sequence 82, Appl
164	294.5	12.5	832	5	PCT-US95-02772-4	Sequence 4, Appli	237	253	10.7	1077	1	US-08-642-255-95	Sequence 95, Appl
165	294	12.4	493	2	US-08-556-978B-59	Sequence 59, Appl	238	253	10.7	1418	2	US-08-963-825-20	Sequence 20, Appl
166	294	12.4	529	2	US-09-247-806-2	Sequence 2, Appli	239	253	10.7	1418	2	US-09-010-999-1	Sequence 1, Appli
167	294	12.4	529	2	US-09-861-597-2	Sequence 2, Appli	240	253	10.7	1418	2	US-09-500-811-20	Sequence 20, Appl
168	294	12.4	674	1	US-08-317-522A-3	Sequence 3, Appli	241	253	10.7	1418	2	US-09-570-573-20	Sequence 20, Appl
169	294	12.4	674	1	US-08-439-818A-3	Sequence 3, Appli	242	253	10.7	1418	2	US-09-548-608-20	Sequence 20, Appl
170	294	12.4	674	1	US-08-751-965-3	Sequence 3, Appli	243	251.5	10.6	462	2	US-09-919-039-124	Sequence 324, App
171	294	12.4	674	1	US-08-728-975-3	Sequence 3, Appli	244	250.5	10.6	585	2	US-09-605-703B-1960	Sequence 1960, Ap
172	294	12.4	674	1	US-08-728-626-3	Sequence 3, Appli	245	248.5	10.5	1442	1	US-08-316-650-12	Sequence 12, Appl

246	248.5	10.5	1442	5	PCT-US95-02251-12	Sequence 12, Appl	319	231.5	9.8	2088	2	US-09-548-376D-13	Sequence 13, Appl
247	247.5	10.5	419	2	US-09-270-767-41767	Sequence 41767, A	320	231.5	9.8	2088	2	US-09-548-376D-13	Sequence 13, Appl
248	247.5	10.5	943	2	US-09-477-135A-131	Sequence 131, App	321	231.5	9.8	2088	2	US-09-548-376D-13	Sequence 13, Appl
249	247.5	10.5	1739	2	US-09-795-061-2	Sequence 2, Appl	322	231.5	9.8	2088	2	US-09-548-376D-13	Sequence 13, Appl
250	247	10.5	975	2	US-09-328-352-4764	Sequence 4764, Ap	323	230.5	9.8	936	1	US-08-707-237A-108	Sequence 108, App
251	246.5	10.4	448	2	US-09-248-796A-1915	Sequence 19135, A	324	230.5	9.8	936	1	US-08-642-246-30	Sequence 30, Appl
252	246.5	10.4	556	2	US-09-248-796A-22338	Sequence 22338, A	325	230.5	9.8	936	1	US-08-642-246-30	Sequence 30, Appl
253	246.5	10.4	595	2	US-09-219-849-48	Sequence 48, Appl	326	230.5	9.8	936	5	PCT-US96-06229-30	Sequence 30, Appl
254	246.5	10.4	595	2	US-09-219-849-50	Sequence 50, Appl	327	229.5	9.7	857	2	US-09-902-540-13312	Sequence 12312, A
255	246.5	10.4	822	2	US-09-219-849-49	Sequence 49, Appl	328	227.5	9.6	485	1	US-08-749-391-2	Sequence 2, Appl
256	246.5	10.4	1057	2	US-08-931-820-1	Sequence 1, Appl	329	227.5	9.6	485	2	US-09-390-200-2	Sequence 2, Appl
257	246.5	10.4	1341	2	US-08-963-825-18	Sequence 18, Appl	330	224.5	9.5	748	2	US-09-219-849-10	Sequence 10, Appl
258	246.5	10.4	1341	2	US-09-500-811-18	Sequence 18, Appl	331	223	9.4	378	1	US-08-707-237A-104	Sequence 104, App
259	246.5	10.4	1341	2	US-09-570-573-18	Sequence 18, Appl	332	223	9.4	378	2	US-08-642-246-26	Sequence 26, Appl
260	246.5	10.4	1341	2	US-09-548-608-18	Sequence 18, Appl	333	223	9.4	378	2	US-09-451-206-26	Sequence 26, Appl
261	246.5	10.4	1958	1	US-07-945-283-2	Sequence 2, Appl	334	223	9.4	378	5	PCT-US96-06229-26	Sequence 26, Appl
262	245	10.4	907	2	US-09-949-016-9750	Sequence 9750, Ap	335	222.5	9.4	966	2	US-08-642-246-34	Sequence 34, Appl
263	245	10.4	907	2	US-09-949-016-9751	Sequence 9751, Ap	336	222.5	9.4	966	2	US-09-451-206-34	Sequence 34, Appl
264	244.5	10.3	492	2	US-08-468-996-11	Sequence 11, Appl	337	222.5	9.4	966	5	PCT-US96-06229-34	Sequence 34, Appl
265	244.5	10.3	1002	1	US-08-707-237A-103	Sequence 103, App	338	222.5	9.4	1343	2	US-09-949-016-10641	Sequence 10641, A
266	244.5	10.3	1002	2	US-08-642-246-25	Sequence 25, Appl	339	222	9.4	412	2	US-09-248-796A-26345	Sequence 26345, A
267	244.5	10.3	1002	2	US-09-451-206-25	Sequence 25, Appl	340	222	9.4	637	2	US-09-949-016-8152	Sequence 8152, Ap
268	244.5	10.3	1002	5	PCT-US96-06229-25	Sequence 25, Appl	341	222	9.4	1694	1	US-08-494-168-2	Sequence 2, Appl
269	244.5	10.3	1057	2	US-10-153-469A-20	Sequence 20, Appl	342	220.5	9.3	645	2	US-09-915-172-41	Sequence 41, Appl
270	244.5	10.3	1057	2	US-10-104-889-20	Sequence 20, Appl	343	220	9.3	509	2	US-09-996-611D-4	Sequence 4, Appl
271	244.5	10.3	1107	2	US-10-153-469A-11	Sequence 11, Appl	344	220	9.3	954	2	US-09-996-611D-1	Sequence 1, Appl
272	244.5	10.3	1107	2	US-10-104-889-11	Sequence 11, Appl	345	219.5	9.3	168	2	US-09-444-791A-52	Sequence 52, Appl
273	244.5	10.3	1171	2	US-10-153-469A-8	Sequence 8, Appl	346	219.5	9.3	829	1	US-08-642-255-132	Sequence 132, App
274	244.5	10.3	1171	2	US-10-104-889-8	Sequence 8, Appl	347	219.5	9.3	829	1	US-08-397-633A-53	Sequence 53, Appl
275	244.5	10.3	1388	2	US-10-153-469A-10	Sequence 10, Appl	348	219	9.3	274	2	US-09-976-594-417	Sequence 417, App
276	244.5	10.3	1388	2	US-10-104-889-10	Sequence 10, Appl	349	218.5	9.2	378	2	US-10-164-595-2	Sequence 2, Appl
277	244.5	10.3	1464	2	US-09-331-347C-21	Sequence 21, Appl	350	217.5	9.2	495	1	US-08-794-795-2	Sequence 2, Appl
278	244	10.3	266	2	US-10-148-306-20	Sequence 20, Appl	351	217.5	9.2	295	2	US-09-248-200-2	Sequence 2, Appl
279	244	10.3	492	2	US-08-468-996-12	Sequence 12, Appl	352	217	9.2	295	2	US-09-248-796A-25715	Sequence 25715, A
280	243	10.3	1017	2	US-08-468-996-10	Sequence 10, Appl	353	216.5	9.2	595	2	US-09-370-838-187	Sequence 187, App
281	242.5	10.3	955	2	US-09-949-016-8369	Sequence 8369, Ap	354	216.5	9.2	595	2	US-09-854-133-187	Sequence 187, App
282	241.5	10.2	1461	2	US-09-585-887-9	Sequence 9, Appl	355	216.5	9.2	684	1	US-08-555-669-12	Sequence 12, Appl
283	241.5	10.2	1461	2	US-09-289-578-9	Sequence 9, Appl	356	216.5	9.2	684	2	US-09-073-663-182	Sequence 182, Appl
284	240.5	10.2	250	2	US-09-248-796A-22487	Sequence 22487, A	357	216.5	9.2	2090	2	US-09-538-092-1081	Sequence 1081, Ap
285	240.5	10.2	943	2	US-09-056-556-204	Sequence 204, App	358	216.5	9.2	2120	2	US-09-949-016-9768	Sequence 9768, Ap
286	240.5	10.2	943	2	US-09-072-556-199	Sequence 199, App	359	216	9.1	638	2	US-10-001-887-108	Sequence 108, App
287	240.5	10.2	943	2	US-09-072-967-204	Sequence 204, App	360	215.5	9.1	520	1	US-08-794-795-6	Sequence 6, Appl
288	240.5	10.2	943	2	US-10-193-002-199	Sequence 199, App	361	215.5	9.1	520	2	US-09-249-200-6	Sequence 6, Appl
289	240.5	10.2	943	2	US-10-084-843-204	Sequence 204, App	362	215.5	9.1	520	2	US-09-949-002-392	Sequence 392, App
290	240.5	10.2	1169	2	US-10-153-469A-6	Sequence 6, Appl	363	215.5	9.1	520	2	US-09-949-002-553	Sequence 553, App
291	240.5	10.2	1169	2	US-10-104-889-6	Sequence 6, Appl	364	215.5	9.1	520	2	US-09-999-833A-614	Sequence 614, App
292	239.5	10.1	1057	2	US-10-153-469A-16	Sequence 16, Appl	365	215.5	9.1	520	2	US-10-020-445A-614	Sequence 614, App
293	239.5	10.1	1057	2	US-10-104-889-16	Sequence 16, Appl	366	215.5	9.1	520	2	US-09-978-189-614	Sequence 614, App
294	239	10.1	662	2	US-09-710-239-33	Sequence 33, Appl	367	215.5	9.1	520	2	US-10-017-085A-614	Sequence 614, App
295	239	10.1	662	2	US-09-219-849-6	Sequence 6, Appl	368	215.5	9.1	520	3	US-10-145-129A-614	Sequence 614, App
296	239	10.1	1806	2	US-09-919-497-56	Sequence 56, Appl	369	215.5	9.1	520	3	US-10-013-929A-614	Sequence 614, App
297	238	10.1	500	2	US-09-710-239-42	Sequence 42, Appl	370	215.5	9.1	520	3	US-10-013-929A-614	Sequence 614, App
298	237.5	10.1	682	1	US-08-642-255-126	Sequence 126, App	371	215	9.1	390	1	US-08-106-981-4	Sequence 4, Appl
299	237.5	10.1	682	1	US-08-397-633A-36	Sequence 36, Appl	372	215	9.1	479	2	US-09-177-349-3	Sequence 3, Appl
300	236.5	10.0	1413	1	US-08-175-155-39	Sequence 39, Appl	373	215	9.1	479	2	US-09-918-951-3	Sequence 3, Appl
301	236.5	10.0	1413	1	US-08-707-237A-45	Sequence 45, Appl	374	215	9.1	1218	2	US-09-949-016-7065	Sequence 7065, Ap
302	236.5	10.0	1464	1	US-08-477-509B-74	Sequence 74, Appl	375	215	9.1	1319	2	US-09-538-092-1291	Sequence 1291, Ap
303	236.5	10.0	1464	1	US-08-482-085B-74	Sequence 74, Appl	376	215	9.1	1690	2	US-09-949-016-5884	Sequence 5884, Ap
304	236.5	10.0	1465	2	US-09-444-791A-74	Sequence 74, Appl	377	214	9.1	406	2	US-09-949-016-5243	Sequence 9243, Ap
305	236	10.0	508	2	US-09-270-767-46233	Sequence 46233, A	378	213.5	9.0	310	2	US-09-219-849-47	Sequence 47, Appl
306	236	10.0	552	2	US-09-219-849-7	Sequence 7, Appl	379	213.5	9.0	1670	2	US-09-949-016-5883	Sequence 5883, Ap
307	235.5	10.0	643	2	US-09-538-092-844	Sequence 844, App	380	213.5	9.0	2316	2	US-09-949-002-314	Sequence 314, App
308	234.5	9.9	510	2	US-09-710-239-26	Sequence 26, Appl	381	213.5	9.0	2415	2	US-09-949-002-398	Sequence 398, App
309	234.5	9.9	936	2	US-08-212-237-3	Sequence 3, Appl	382	213	9.0	529	2	US-09-381-656-1	Sequence 1, Appl
310	234.5	9.9	936	2	US-08-806-029-26	Sequence 26, Appl	383	212.5	9.0	191	2	US-10-148-306-19	Sequence 19, Appl
311	234.5	9.9	936	5	PCT-US95-02272-3	Sequence 3, Appl	384	212.5	9.0	347	2	US-09-623-497-1	Sequence 1, Appl
312	232.5	9.8	416	2	US-09-710-239-25	Sequence 25, Appl	385	212	9.0	100	2	US-09-411-067C-5	Sequence 5, Appl
313	232.5	9.8	536	2	US-09-270-767-43766	Sequence 43766, A	386	211	8.9	371	2	US-09-538-092-884	Sequence 884, App
314	232	9.8	501	2	US-09-710-239-17	Sequence 17, Appl	387	210.5	8.9	262	1	US-08-397-633A-78	Sequence 78, Appl
315	231.5	9.8	100	2	US-09-411-067C-4	Sequence 4, Appl	388	210.5	8.9	506	2	US-09-605-703B-778	Sequence 778, App
316	231.5	9.8	2088	2	US-09-548-372D-13	Sequence 13, Appl	389	210.5	8.9	1488	2	US-09-605-703B-772	Sequence 772, App
317	231.5	9.8	2088	2	US-09-548-367D-13	Sequence 13, Appl	390	210	8.9	1609	2	US-09-949-016-10910	Sequence 10910, A
318	231.5	9.8	2088	2	US-09-551-853D-13	Sequence 13, Appl	391	209.5	8.9	353	1	US-08-687-702-37	Sequence 37, Appl

392	209.5	8.9	1034	2	US-09-252-991A-26658	Sequence 2658, A	465	194.5	8.2	1268	2	US-09-949-016-7487	Sequence 7487, Ap
393	209.5	8.9	1209	2	US-09-949-002-493	Sequence 493, App	466	193	8.2	359	2	US-09-270-767-33751	Sequence 43751, A
394	209.5	8.9	1209	2	US-09-949-002-494	Sequence 494, App	467	192	8.2	623	2	US-09-029-348-3	Sequence 3, App1
395	208.5	8.8	133	2	US-09-710-239-27	Sequence 27, App1	468	192	8.1	744	2	US-09-949-016-9607	Sequence 9607, Ap
396	208.5	8.8	435	2	US-09-902-540-12731	Sequence 12731, A	469	192	8.1	1345	1	US-08-977-767-3	Sequence 3, App1
397	208	8.8	669	2	US-09-949-016-11276	Sequence 11276, A	470	191.5	8.1	160	2	US-08-542-051-18	Sequence 18, App1
398	207	8.8	1064	2	US-08-642-255-62	Sequence 62, App1	471	191.5	8.1	620	2	US-09-931-009B-1	Sequence 1, App1
399	207	8.8	680	2	US-09-949-001-15	Sequence 15, App1	472	191.5	8.1	644	2	US-09-919-039-121	Sequence 121, App
400	206.5	8.7	680	2	US-09-949-001-20	Sequence 20, App1	473	191.5	8.1	831	2	US-10-360-101-236	Sequence 236, App
401	206.5	8.7	348	2	US-10-830-792A-31	Sequence 31, App1	474	191.5	8.1	847	2	US-09-373-157-4	Sequence 4, App1
402	206.5	8.7	938	2	US-09-949-016-9992	Sequence 9992, Ap	475	191.5	8.1	866	2	US-09-949-002-302	Sequence 302, App
403	206	8.7	417	1	US-08-175-155-69	Sequence 69, App1	476	191.5	8.1	875	2	US-09-949-016-8582	Sequence 8582, Ap
404	206	8.7	417	1	US-08-477-509B-104	Sequence 104, App	477	191.5	8.1	875	2	US-09-949-002-455	Sequence 455, App
405	206	8.7	417	1	US-08-642-255-102	Sequence 102, App	478	190.5	8.1	261	2	US-09-710-239-16	Sequence 16, App1
406	206	8.7	417	1	US-08-707-237A-76	Sequence 76, App1	479	190.5	8.1	637	2	US-09-248-796A-19134	Sequence 19134, A
407	206	8.7	417	2	US-08-482-085B-104	Sequence 104, App	480	190.5	8.1	2870	2	US-09-479-467A-15	Sequence 15, App1
408	206	8.7	417	2	US-09-444-791A-104	Sequence 104, App	481	190.5	8.1	2870	2	US-09-655-160-15	Sequence 15, App1
409	206	8.7	837	1	US-08-175-155-68	Sequence 68, App1	482	190.5	8.1	3178	2	US-09-479-467A-4	Sequence 4, App1
410	206	8.7	837	1	US-08-477-509B-103	Sequence 103, App	483	190.5	8.1	3178	2	US-09-655-160-4	Sequence 26, App1
411	206	8.7	837	1	US-08-642-255-101	Sequence 101, App	484	190	8.0	276	2	US-08-506-553C-26	Sequence 7, App1
412	206	8.7	837	2	US-08-707-237A-75	Sequence 75, App1	485	190	8.0	344	1	US-08-891-254-7	Sequence 7, App1
413	206	8.7	837	2	US-08-482-085B-103	Sequence 103, App	486	190	8.0	344	1	US-08-819-539-7	Sequence 7, App1
414	206	8.7	837	2	US-09-444-791A-103	Sequence 103, App	487	190	8.0	344	1	US-09-030-270A-7	Sequence 7, App1
415	206	8.7	837	1	US-08-397-633A-50	Sequence 50, App1	488	190	8.0	344	2	US-08-984-207-7	Sequence 7, App1
416	206	8.7	1516	2	US-09-949-016-8209	Sequence 8209, Ap	489	190	8.0	344	2	US-09-013-587-7	Sequence 7, App1
417	205.5	8.7	489	1	US-08-794-795-7	Sequence 7, App1	490	190	8.0	344	2	US-09-086-118-27	Sequence 27, App1
418	205.5	8.7	489	2	US-09-249-200-7	Sequence 2, App1	491	190	8.0	344	2	US-09-431-614-15	Sequence 15, App1
419	205.5	8.7	518	1	US-08-352-367B-2	Sequence 2, App1	492	190	8.0	344	2	US-09-412-100-35	Sequence 35, App1
420	205.5	8.7	518	2	US-08-893-467A-2	Sequence 2, App1	493	190	8.0	344	2	US-09-597-840-7	Sequence 7, App1
421	205	8.7	187	2	US-09-680-175-4	Sequence 4, App1	494	190	8.0	344	5	PCT-US96-08619-7	Sequence 7, App1
422	205	8.7	228	2	US-09-219-849-38	Sequence 38, App1	495	190	8.0	626	2	US-09-029-348-2	Sequence 2, App1
423	205	8.7	1415	2	US-09-252-991A-26438	Sequence 26438, A	496	189.5	8.0	549	1	US-08-494-168-8	Sequence 8, App1
424	205	8.7	1639	2	US-09-949-016-6136	Sequence 6136, Ap	497	189.5	8.0	644	1	US-08-206-176-2	Sequence 2, App1
425	204	8.6	593	2	US-10-164-230-61	Sequence 61, App1	498	189	8.0	643	1	US-08-551-356-4	Sequence 4, App1
426	203.5	8.6	688	2	US-09-902-540-10297	Sequence 10297, A	499	189	8.0	643	5	PCT-US93-12687-4	Sequence 4, App1
427	203	8.6	1253	2	US-09-958-617A-18	Sequence 18, App1	500	189	8.0	1336	1	US-08-551-356-6	Sequence 6, App1
428	203	8.6	1259	2	US-09-949-016-10366	Sequence 10366, A	501	189	8.0	1336	5	PCT-US93-12687-6	Sequence 6, App1
429	201.5	8.5	133	2	US-09-072-596-243	Sequence 243, App	502	188	8.0	287	1	US-08-397-633A-76	Sequence 76, App1
430	201.5	8.5	133	2	US-09-072-596-248	Sequence 248, App	503	187.5	7.9	180	2	US-09-248-796A-22352	Sequence 22352, A
431	201.5	8.5	133	2	US-10-193-002-243	Sequence 243, App	504	187	7.9	252	1	US-08-642-255-61	Sequence 61, App1
432	201.5	8.5	132	2	US-10-084-843-248	Sequence 248, App	505	186.5	7.9	532	1	US-08-494-168-9	Sequence 9, App1
433	201.5	8.5	313	2	US-08-806-029-34	Sequence 34, App1	506	186.5	7.9	1566	2	US-09-581-472B-2	Sequence 2, App1
434	201.5	8.5	433	2	US-09-524-101D-20	Sequence 20, App1	507	186	7.9	251	1	US-08-397-633A-74	Sequence 74, App1
435	201.5	8.5	684	2	US-09-949-016-8348	Sequence 8348, Ap	508	186	7.9	336	2	US-09-270-767-44531	Sequence 44531, A
436	201	8.5	1712	2	US-09-961-403-9	Sequence 9, App1	509	186	7.9	605	2	US-09-976-594-616	Sequence 616, App
437	200.5	8.5	341	1	US-08-538-711A-8	Sequence 8, App1	510	186	7.9	1581	2	US-09-110-517-2	Sequence 2, App1
438	200.5	8.5	341	2	US-08-725-027-8	Sequence 8, App1	511	185.5	7.9	673	2	US-09-107-532A-5134	Sequence 5134, Ap
439	200.5	8.5	341	2	US-09-542-552-8	Sequence 8, App1	512	185	7.8	251	2	US-09-710-239-21	Sequence 21, App1
440	200.5	8.5	353	1	US-08-538-711A-7	Sequence 7, App1	513	185	7.8	546	1	US-08-494-168-10	Sequence 10, App1
441	200.5	8.5	353	2	US-08-725-027-7	Sequence 7, App1	514	184.5	7.8	174	2	US-09-270-767-61801	Sequence 61801, A
442	200.5	8.5	353	2	US-09-542-552-7	Sequence 7, App1	515	184.5	7.8	216	2	US-08-506-553C-23	Sequence 23, App1
443	200.5	8.5	353	2	US-09-538-092-989	Sequence 989, App	516	184	7.8	159	1	US-07-609-716-104	Sequence 104, App
444	200.5	8.5	410	2	US-09-949-016-10345	Sequence 10345, A	517	184	7.8	159	2	US-08-475-411A-104	Sequence 104, App
445	200.5	8.5	410	2	US-09-949-016-10346	Sequence 10346, A	518	184	7.8	159	2	US-08-478-029A-104	Sequence 104, App
446	199	8.4	541	2	US-09-248-796A-26119	Sequence 26119, A	519	183	7.7	324	2	US-09-254-032B-7	Sequence 7, App1
447	199	8.4	589	2	US-09-949-016-8890	Sequence 8890, Ap	520	182.5	7.7	472	2	US-09-538-032B-112	Sequence 312, App
448	199	8.4	835	2	US-10-210-428-1	Sequence 1, App1	521	182.5	7.7	700	2	US-09-714-865-6	Sequence 6, App1
449	199	8.4	835	2	US-10-237-551-161	Sequence 161, App	522	181.5	7.7	251	2	US-09-710-239-21	Sequence 31, App1
450	199	8.4	826	2	US-09-894-998A-47	Sequence 47, App1	523	181	7.7	234	2	US-09-895-674A-1	Sequence 1, App1
451	199	8.4	826	2	US-10-237-551-47	Sequence 47, App1	524	180	7.6	730	2	US-09-961-403-8	Sequence 8, App1
452	198.5	8.4	547	1	US-08-494-168-7	Sequence 7, App1	525	180	7.6	731	1	US-08-911-364-1	Sequence 1, App1
453	197.5	8.4	541	2	US-09-538-092-247	Sequence 347, App	526	180	7.6	733	2	US-08-464-700-2	Sequence 2, App1
454	197.5	8.4	464	2	US-09-252-991A-24883	Sequence 24883, A	527	180	7.6	792	1	US-08-678-039A-40	Sequence 40, App1
455	197	8.3	1185	2	US-09-949-016-11185	Sequence 11185, A	528	179.5	7.6	960	2	US-09-219-849-5	Sequence 5, App1
456	197	8.3	1143	2	US-09-949-016-6137	Sequence 6137, Ap	529	179	7.6	345	2	US-09-270-767-45883	Sequence 45883, A
457	195.5	8.3	279	2	US-09-010-999-2	Sequence 2, App1	530	178.5	7.6	216	2	US-09-248-796A-14221	Sequence 14221, A
458	195	8.3	146	1	US-07-609-716-105	Sequence 105, App	531	178	7.5	889	2	US-09-336-447A-15	Sequence 15, App1
459	195	8.3	146	2	US-08-475-411A-105	Sequence 105, App	532	178	7.5	889	2	US-09-952-267B-15	Sequence 15, App1
460	195	8.3	146	2	US-08-478-029A-105	Sequence 105, App	533	177.5	7.5	337	2	US-09-270-767-46550	Sequence 46550, A
461	195	8.3	281	1	US-08-397-633A-75	Sequence 75, App1	534	177	7.5	190	1	US-08-560-358-8	Sequence 8, App1
462	194.5	8.2	166	2	US-09-841-334A-21	Sequence 21, App1	535	177	7.5	731	2	US-09-340-736E-1	Sequence 1, App1
463	194.5	8.2	166	2	US-09-837-969A-21	Sequence 21, App1	536	177	7.5	731	2	US-09-964-662-1	Sequence 1, App1
464	194.5	8.2	442	2	US-09-248-796A-21400	Sequence 21400, A	537	177	7.5	2732	2	US-09-086-436-30	Sequence 30, App1

538	176.5	7.5	571	2	US-09-134-001C-3865	Sequence 3865, Ap	611	168	7.1	111	2	US-08-963-168C-15	Sequence 15, Appl
539	176.5	7.5	1152	2	US-09-303-518D-195	Sequence 195, App	612	168	7.1	131	2	US-08-963-168C-8	Sequence 8, Appl
540	176	7.4	450	2	US-09-812-382-6	Sequence 6, Appl	613	168	7.1	136	2	US-08-963-168C-6	Sequence 6, Appl
541	175	7.4	617	2	US-10-104-047-2915	Sequence 2915, Ap	614	168	7.1	316	2	US-09-248-796A-26455	Sequence 26455, A
542	174.5	7.4	385	1	US-08-891-254-3	Sequence 3, Appl	615	168	7.1	345	2	US-09-657-011-112	Sequence 112, Appl
543	174.5	7.4	385	1	US-08-819-539-3	Sequence 3, Appl	616	168	7.1	646	2	US-09-964-899-53	Sequence 53, Appl
544	174.5	7.4	385	1	PCT-US96-08819-3	Sequence 3, Appl	617	168	7.1	1145	3	US-09-961-403-5	Sequence 5, Appl
545	174.5	7.4	403	1	US-08-200-724A-2	Sequence 2, Appl	618	168	7.1	684	2	US-09-866-557A-5	Sequence 5, Appl
546	174.5	7.4	403	1	US-09-030-270A-3	Sequence 3, Appl	619	168	7.1	1717	3	US-09-958-359-20	Sequence 20, Appl
547	174.5	7.4	403	2	US-08-851-376A-2	Sequence 2, Appl	620	167.5	7.1	357	1	US-07-609-716-66	Sequence 66, Appl
548	174.5	7.4	403	2	US-08-984-207-3	Sequence 3, Appl	621	167.5	7.1	357	1	US-08-642-255-33	Sequence 33, Appl
549	174.5	7.4	403	2	US-09-013-587-3	Sequence 3, Appl	622	167.5	7.1	357	2	US-08-475-411A-66	Sequence 66, Appl
550	174.5	7.4	403	2	US-09-086-118-23	Sequence 23, Appl	623	167.5	7.1	357	2	US-08-478-029A-66	Sequence 66, Appl
551	174.5	7.4	403	2	US-09-431-614-3	Sequence 3, Appl	624	167.5	7.1	551	2	US-09-489-039A-0083	Sequence 9083, Ap
552	174.5	7.4	403	2	US-09-412-100-23	Sequence 23, Appl	625	167.5	7.1	551	2	US-09-071-035-268	Sequence 268, App
553	174.5	7.4	403	2	US-09-597-840-3	Sequence 3, Appl	626	167.5	7.1	558	2	US-10-206-576-268	Sequence 268, App
554	174.5	7.4	1261	2	US-09-208-742-4	Sequence 4, Appl	627	167.5	7.1	1638	2	US-09-071-035-258	Sequence 258, App
555	174.5	7.4	1261	2	US-09-332-295-2	Sequence 2, Appl	628	167.5	7.1	1638	2	US-09-071-035-262	Sequence 262, App
556	174.5	7.4	1261	2	US-09-709-979-2	Sequence 2, Appl	629	167.5	7.1	1638	2	US-09-071-035-266	Sequence 266, App
557	174.5	7.4	1261	2	US-10-147-268-2	Sequence 2, Appl	630	167.5	7.1	1638	2	US-10-206-576-268	Sequence 268, App
558	174	7.4	521	2	US-09-270-767-46291	Sequence 46291, A	631	167.5	7.1	1638	2	US-10-206-576-262	Sequence 262, App
559	173.5	7.3	258	2	US-10-104-047-3034	Sequence 3034, Ap	632	167.5	7.1	1638	2	US-10-206-576-266	Sequence 266, App
560	173.5	7.3	424	2	US-09-884-767A-213	Sequence 213, App	633	167.5	7.1	1747	2	US-09-134-000C-5999	Sequence 5999, Ap
561	173.5	7.3	432	2	US-09-403-089A-1	Sequence 1, Appl	634	167	7.1	1221	3	US-09-130-242-2	Sequence 11, Appl
562	173.5	7.3	432	2	US-09-809-517A-25	Sequence 25, Appl	635	166.5	7.0	1088	2	US-09-130-242-2	Sequence 2, Appl
563	173.5	7.3	434	2	US-09-809-517A-23	Sequence 23, Appl	636	166.5	7.0	1088	2	US-09-583-610D-2	Sequence 6, Appl
564	173.5	7.3	434	2	US-09-809-517A-26	Sequence 26, Appl	637	166.5	7.0	1088	2	US-09-949-016-6335	Sequence 6335, Ap
565	173.5	7.3	482	1	US-08-358-160-5	Sequence 5, Appl	638	166.5	7.0	2504	2	US-09-328-325-5821	Sequence 5821, Ap
566	173.5	7.3	484	1	US-08-358-160-7	Sequence 7, Appl	639	165.5	7.0	1116	2	US-08-963-168C-13	Sequence 13, Appl
567	173.5	7.3	484	1	US-09-781-988A-243	Sequence 243, App	640	165.5	7.0	132	2	US-08-963-168C-9	Sequence 9, Appl
568	173.5	7.3	596	2	US-10-012-231A-243	Sequence 243, App	641	165.5	7.0	416	2	US-09-902-540-11959	Sequence 11959, A
569	173.5	7.3	596	2	US-10-015-389A-243	Sequence 243, App	642	165	7.0	715	2	US-09-902-540-9752	Sequence 9752, Ap
570	173.5	7.3	596	2	US-10-006-768A-243	Sequence 243, App	643	165	7.0	823	2	US-09-538-092-439	Sequence 439, App
571	173.5	7.3	596	2	US-10-015-671A-243	Sequence 243, App	644	164.5	7.0	1112	2	US-08-963-168C-16	Sequence 16, Appl
572	173.5	7.3	596	2	US-10-015-393A-243	Sequence 243, App	645	164.5	7.0	356	2	US-09-252-991A-18206	Sequence 18206, A
573	173.5	7.3	596	2	US-10-011-833A-243	Sequence 243, App	646	164.5	7.0	732	2	US-09-270-767-4652	Sequence 4652, A
574	173.5	7.3	596	2	US-10-006-041A-243	Sequence 243, App	647	163.5	6.9	331	2	US-09-949-016-7015	Sequence 7015, Ap
575	173.5	7.3	596	2	US-10-012-064A-243	Sequence 243, App	648	163.5	6.9	335	2	US-09-949-016-7995	Sequence 7995, Ap
576	173.5	7.3	596	2	US-10-015-392A-243	Sequence 243, App	649	163.5	6.9	414	1	US-08-343-682-1	Sequence 1, Appl
577	173.5	7.3	596	2	US-10-011-795B-243	Sequence 243, App	650	163.5	6.9	414	1	US-08-705-660-26	Sequence 26, Appl
578	173.5	7.3	596	2	US-10-015-386A-243	Sequence 243, App	651	163.5	6.9	414	2	US-08-989-045-26	Sequence 26, Appl
579	173.5	7.3	596	2	US-10-012-121A-243	Sequence 243, App	652	163.5	6.9	414	2	US-09-976-594-373	Sequence 373, Appl
580	173.5	7.3	596	2	US-10-006-485A-243	Sequence 243, App	653	163.5	6.9	414	2	US-09-315-355A-26	Sequence 26, Appl
581	173.5	7.3	596	2	US-10-006-746A-243	Sequence 243, App	654	163.5	6.9	666	1	US-08-737-726-14	Sequence 14, Appl
582	173.5	7.3	596	2	US-10-012-752A-243	Sequence 243, App	655	163	6.9	384	2	US-09-949-016-11034	Sequence 11034, A
583	173.5	7.3	596	2	US-10-017-253A-243	Sequence 243, App	656	163	6.9	417	2	US-10-104-047-2653	Sequence 2653, Ap
584	173.5	7.3	596	2	US-10-015-519A-243	Sequence 243, App	657	163	6.9	535	2	US-09-029-348-1	Sequence 1, Appl
585	173.5	7.3	596	2	US-10-015-715A-243	Sequence 243, App	658	163	6.9	537	2	US-09-029-348-4	Sequence 4, Appl
586	173.5	7.3	596	2	US-10-007-236A-243	Sequence 243, App	659	163	6.9	920	2	US-09-538-092-1197	Sequence 1197, Ap
587	173	7.3	600	2	US-10-094-749-2713	Sequence 2713, Ap	660	163	6.9	1216	2	US-09-134-000C-5130	Sequence 5130, Ap
588	173	7.3	656	1	US-08-343-443B-2	Sequence 2, Appl	661	163	6.9	1709	2	US-09-949-016-11345	Sequence 11345, A
589	173	7.3	656	2	US-09-214-564A-4	Sequence 4, Appl	662	162.5	6.9	878	2	US-09-540-236-3401	Sequence 3401, Ap
590	173	7.3	656	2	US-09-538-092-1250	Sequence 1250, Ap	663	162.5	6.9	1165	3	US-10-016-768A-10	Sequence 10, Appl
591	172.5	7.3	259	2	US-09-436-434-2	Sequence 2, Appl	664	162	6.9	683	2	US-09-620-412C-357	Sequence 357, App
592	172.5	7.3	385	5	PCT-US93-06243-2	Sequence 2, Appl	665	162	6.9	683	2	US-09-598-419-357	Sequence 357, App
593	172	7.3	1268	2	US-09-270-767-45320	Sequence 45320, A	666	162	6.9	717	2	US-09-252-991A-11155	Sequence 31195, A
594	171.5	7.3	361	2	US-09-248-796A-20099	Sequence 20099, A	667	161.5	6.8	319	2	US-09-248-796A-18138	Sequence 18138, A
595	171.5	7.3	1127	2	US-09-150-460B-11	Sequence 11, Appl	668	161.5	6.8	424	2	US-09-120-817-2	Sequence 2, Appl
596	171.5	7.3	2211	2	US-09-738-884-1	Sequence 1, Appl	669	161.5	6.8	424	2	US-09-431-614-14	Sequence 14, Appl
597	171.5	7.3	2211	2	US-10-096-961A-1	Sequence 1, Appl	670	161.5	6.8	424	2	US-09-412-100-34	Sequence 34, Appl
598	171	7.2	641	2	US-09-270-767-41562	Sequence 41562, A	671	161.5	6.8	534	2	US-09-029-348-5	Sequence 5, Appl
599	170.5	7.2	591	2	US-09-949-016-10914	Sequence 10914, A	672	161.5	6.8	557	2	US-09-320-095-10	Sequence 10, Appl
600	170.5	7.2	591	2	US-09-949-016-10915	Sequence 10915, A	673	161.5	6.8	557	2	US-09-523-487-10	Sequence 44, Appl
601	170	7.2	513	2	US-09-248-796A-25078	Sequence 25078, A	674	161	6.8	313	2	US-10-833-792A-44	Sequence 52, Appl
602	170	7.2	519	2	US-09-453-702B-265	Sequence 265, App	675	161	6.8	503	2	US-08-845-258-52	Sequence 52, Appl
603	170	7.2	519	2	US-10-114-170-265	Sequence 265, App	676	161	6.8	503	2	US-08-990-571-52	Sequence 52, Appl
604	169.5	7.2	415	2	US-09-025-769B-280	Sequence 280, App	677	161	6.8	503	2	US-09-528-784A-52	Sequence 52, Appl
605	169.5	7.2	415	2	US-09-450-070A-280	Sequence 280, App	678	161	6.8	503	2	US-09-569-098A-82	Sequence 82, Appl
606	169.5	7.2	415	2	US-09-450-153-280	Sequence 280, App	679	161	6.8	666	2	US-09-569-098A-85	Sequence 85, Appl
607	169.5	7.2	415	2	US-09-490-324-280	Sequence 280, App	680	161	6.8	666	2	US-09-569-098A-85	Sequence 85, Appl
608	168.5	7.1	208	1	US-08-212-237-9	Sequence 9, Appl	681	161	6.8	1091	2	US-09-949-016-8595	Sequence 8595, Ap
609	168.5	7.1	208	5	PCT-US95-02772-9	Sequence 9, Appl	682	161	6.8	1132	2	US-09-528-784A-87	Sequence 87, Appl
610	168.5	7.1	755	2	US-09-919-497-57	Sequence 57, Appl	683	161	6.8	1132	2	US-09-569-098A-87	Sequence 87, Appl

684	161	6.8	1850	2	US-09-620-093A-5	Sequence 5, Appli	757	149	6.3	60	2	US-09-832-297A-12	Sequence 12, Appli
685	160.5	6.8	553	2	US-09-252-991A-17984	Sequence 1984, A	758	149	6.3	124	2	US-09-540-236-1076	Sequence 3076, Ap
686	160	6.8	300	2	US-08-765-856-2	Sequence 2, Appli	759	149	6.3	171	2	US-09-011-735-2	Sequence 2, Appli
687	160	6.8	300	2	US-08-935-009A-2	Sequence 2, Appli	760	149	6.3	171	2	US-09-029-156-2	Sequence 2, Appli
688	160	6.8	334	2	US-09-949-016-10178	Sequence 10178, A	761	149	6.3	171	2	US-10-007-408-2	Sequence 2, Appli
689	160	6.8	336	2	US-09-640-211A-1055	Sequence 1055, Ap	762	149	6.3	351	2	US-09-011-735-1	Sequence 1, Appli
690	160	6.8	671	1	US-08-737-716-13	Sequence 13, Appli	763	149	6.3	351	2	US-09-029-156-1	Sequence 1, Appli
691	160	6.8	720	1	US-09-219-849-4	Sequence 4, Appli	764	149	6.3	351	2	US-10-007-408-1	Sequence 1, Appli
692	160	6.8	777	1	US-08-642-255-53	Sequence 53, Appli	765	149	6.3	601	2	US-09-252-991A-27784	Sequence 27784, A
693	159.5	6.7	2616	2	US-09-303-518D-879	Sequence 879, App	766	148.5	6.3	266	2	US-09-495-880A-26	Sequence 26, Appli
694	159	6.7	3546	2	US-09-252-991A-18637	Sequence 18637, A	767	148.5	6.3	326	2	US-09-252-991A-17002	Sequence 17002, A
695	158	6.7	106	2	US-08-963-168C-14	Sequence 14, Appli	768	148.5	6.3	656	2	US-09-252-991A-30630	Sequence 30630, A
696	158	6.7	126	2	US-08-963-168C-7	Sequence 7, Appli	769	148	6.3	247	2	US-09-248-796A-14517	Sequence 14517, A
697	158	6.7	166	2	US-09-297-269-41	Sequence 41, Appli	770	148	6.3	447	2	US-09-130-927-2	Sequence 6, Appli
698	158	6.7	435	2	US-09-270-767-43092	Sequence 43092, A	771	148	6.3	447	2	US-09-431-614-6	Sequence 6, Appli
699	157.5	6.7	186	2	US-10-830-792A-15	Sequence 15, Appli	772	148	6.3	447	2	US-09-412-100-26	Sequence 26, Appli
700	157.5	6.7	430	1	US-08-945-848-8	Sequence 8, Appli	773	148	6.3	447	3	US-09-536-958A-2	Sequence 2, Appli
701	157.5	6.7	1032	2	US-09-270-767-44433	Sequence 44433, A	774	148	6.3	661	2	US-09-714-865-7	Sequence 7, Appli
702	157	6.6	272	2	US-09-949-016-9966	Sequence 9966, Ap	775	147.5	6.2	1584	2	US-09-457-040B-27	Sequence 27, Appli
703	157	6.6	272	2	US-09-949-016-9967	Sequence 9967, Ap	776	147	6.2	97	1	US-08-175-155-15	Sequence 15, Appli
704	157	6.6	461	1	US-08-463-587A-26	Sequence 26, Appli	777	147	6.2	97	1	US-08-477-509B-50	Sequence 50, Appli
705	157	6.6	461	1	US-08-463-67A-4	Sequence 4, Appli	778	147	6.2	97	2	US-08-482-085B-50	Sequence 50, Appli
706	157	6.6	461	2	US-08-923-854-26	Sequence 26, Appli	779	147	6.2	97	2	US-09-444-791A-50	Sequence 50, Appli
707	157	6.6	461	5	PCT-US91-09133-27	Sequence 27, Appli	780	147	6.2	98	1	US-08-707-237A-22	Sequence 22, Appli
708	156.5	6.6	471	1	US-08-399-889-24	Sequence 24, Appli	781	147	6.2	212	2	US-09-270-767-41907	Sequence 41907, A
709	156.5	6.6	471	2	US-09-167-364-24	Sequence 24, Appli	782	147	6.2	230	2	US-09-248-796A-26509	Sequence 26509, A
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711	156	6.6	238	2	US-09-495-880A-42	Sequence 42, Appli	784	147	6.2	264	2	US-09-128-450-71	Sequence 21, Appli
712	156	6.6	694	2	US-09-949-016-7117	Sequence 7117, Ap	785	147	6.2	264	2	US-09-823-794-21	Sequence 21, Appli
713	155.5	6.6	187	2	US-09-634-238-414	Sequence 414, App	786	147	6.2	264	2	US-09-155-794-2	Sequence 2, Appli
714	155.5	6.6	746	1	US-09-134-001C-3214	Sequence 3214, Ap	787	147	6.2	760	1	US-08-155-152-2	Sequence 2, Appli
715	155	6.6	618	2	US-09-252-991A-27666	Sequence 27666, A	788	147	6.2	760	2	US-08-754-741-8	Sequence 2, Appli
716	154.5	6.5	196	2	US-09-252-991A-23071	Sequence 23071, A	789	147	6.2	908	2	US-08-714-741-4	Sequence 44, Appli
717	154.5	6.5	302	2	US-08-765-856-4	Sequence 4, Appli	790	146.5	6.2	365	2	US-09-270-767-46506	Sequence 46506, A
718	154.5	6.5	302	2	US-08-935-009A-4	Sequence 4, Appli	791	146.5	6.2	385	2	US-09-248-796A-17306	Sequence 17306, A
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720	154	6.5	1461	3	US-10-884-115-86	Sequence 86, Appli	793	146.5	6.2	717	2	US-08-910-925-1	Sequence 1, Appli
721	153	6.5	561	1	US-08-642-255-52	Sequence 52, Appli	794	146.5	6.2	918	2	US-09-041-886-11	Sequence 11, Appli
722	152.5	6.5	166	2	US-09-270-767-41190	Sequence 41190, A	795	146	6.2	84	1	US-08-175-155-17	Sequence 17, Appli
723	152.5	6.5	166	2	US-09-270-767-56406	Sequence 56406, A	796	146	6.2	84	1	US-08-477-509B-52	Sequence 52, Appli
724	152.5	6.5	195	2	US-09-270-767-44458	Sequence 44458, A	797	146	6.2	84	1	US-08-707-237A-23	Sequence 23, Appli
725	152.5	6.5	284	2	US-09-431-887-24	Sequence 24, Appli	798	146	6.2	84	2	US-08-482-085B-52	Sequence 52, Appli
726	152.5	6.5	336	2	US-09-270-767-43241	Sequence 43241, A	799	146	6.2	185	2	US-09-710-239-20	Sequence 20, Appli
727	152.5	6.5	504	2	US-09-821-687-11	Sequence 11, Appli	800	146	6.2	219	2	US-09-380-015B-2	Sequence 2, Appli
728	152.5	6.5	504	2	US-09-219-849-3	Sequence 3, Appli	801	146	6.2	415	2	US-09-328-352-6430	Sequence 6430, Ap
729	152.5	6.5	790	2	US-09-328-352-4283	Sequence 4283, Ap	802	146	6.2	467	2	US-09-949-016-7779	Sequence 7779, Ap
730	152.5	6.5	1395	2	US-09-252-991A-30345	Sequence 30345, A	803	146	6.2	467	2	US-09-949-016-7779	Sequence 7779, Ap
731	152	6.4	1010	2	US-09-248-796A-16379	Sequence 16379, A	804	146	6.2	1328	2	US-09-830-230A-631	Sequence 631, App
732	152	6.4	1417	2	US-08-900-230-3	Sequence 3, Appli	805	145.5	6.2	99	2	US-09-072-967-255	Sequence 255, App
733	151.5	6.4	461	1	US-08-186-222-2	Sequence 2, Appli	806	145.5	6.2	99	2	US-09-072-967-260	Sequence 260, App
734	151	6.4	313	2	US-09-949-016-9265	Sequence 9265, Ap	807	145.5	6.2	99	2	US-10-193-002-255	Sequence 255, App
735	150.5	6.4	162	2	US-09-575-574-4	Sequence 4, Appli	808	145.5	6.2	99	2	US-10-084-843-260	Sequence 260, App
736	150.5	6.4	251	1	US-08-209-747-8	Sequence 8, Appli	809	145.5	6.2	743	2	US-09-910-925-3	Sequence 3, Appli
737	150.5	6.4	251	1	US-08-458-298-8	Sequence 8, Appli	810	145.5	6.2	743	2	US-09-949-016-1261	Sequence 6261, Ap
738	150.5	6.4	447	2	US-09-916-109-5	Sequence 5, Appli	811	145.5	6.2	870	2	US-09-605-703B-1686	Sequence 1686, Ap
739	150.5	6.4	447	2	US-10-211-412B-5	Sequence 5, Appli	812	145.5	6.2	970	2	US-09-270-767-42741	Sequence 42741, A
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741	150.5	6.4	483	2	US-10-211-412B-4	Sequence 4, Appli	814	145	6.1	328	1	US-08-229-287-4	Sequence 4, Appli
742	150.5	6.4	483	2	US-09-538-092-1162	Sequence 1162, Ap	815	145	6.1	553	2	US-09-083-351-2	Sequence 2, Appli
743	150	6.3	72	2	US-09-513-999C-5563	Sequence 5563, Ap	816	145	6.1	553	2	US-09-083-352-2	Sequence 2, Appli
744	150	6.3	72	2	US-09-513-999C-5564	Sequence 5564, Ap	817	145	6.1	553	2	US-09-612-809B-2	Sequence 2, Appli
745	150	6.3	207	2	US-10-029-180-70	Sequence 70, Appli	818	145	6.1	572	2	US-09-489-039A-11826	Sequence 11826, A
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747	150	6.3	423	1	US-08-999-336-2	Sequence 2, Appli	820	145	6.1	633	2	US-09-821-687-10	Sequence 10, Appli
748	149.5	6.3	423	5	PCT-US96-01427-2	Sequence 2, Appli	821	145	6.1	720	2	US-09-756-071B-2	Sequence 20, Appli
749	149.5	6.3	121	2	US-09-072-967-253	Sequence 253, App	822	145	6.1	720	2	US-09-252-991A-25823	Sequence 25823, A
750	149.5	6.3	121	2	US-09-072-967-258	Sequence 258, App	823	145	6.1	909	2	US-09-982-616-11	Sequence 11, Appli
751	149.5	6.3	121	2	US-10-193-002-253	Sequence 253, App	824	145	6.1	919	2	US-09-538-032-895	Sequence 895, App
752	149.5	6.3	121	2	US-10-084-843-258	Sequence 258, App	825	145	6.1	923	2	US-09-497-822C-19	Sequence 19, Appli
753	149.5	6.3	148	2	US-10-190-902B-11	Sequence 11, Appli	826	145	6.1	1186	1	US-08-861-464-8	Sequence 8, Appli
754	149.5	6.3	145	2	US-09-252-991A-24354	Sequence 24354, A	827	145	6.1	1186	1	US-08-396-001-8	Sequence 8, Appli
755	149.5	6.3	1060	2	US-08-911-393-2	Sequence 2, Appli	828	145	6.1	1186	2	US-09-323-433A-8	Sequence 8, Appli
756	149.5	6.3	1060	2	US-09-955-909-2	Sequence 2, Appli	829	145	6.1	1186	2	US-09-826-752-8	Sequence 8, Appli

830	145	6.1	2314	2	US-09-268-347-49	Sequence 49, Appl	903	141	6.0	211	5	PCT-US93-08364-16	Sequence 16, Appl
831	145	6.1	2763	2	US-08-496-944-2	Sequence 24, Appl	904	141	6.0	211	5	PCT-US95-08743-34	Sequence 34, Appl
832	145	6.1	3907	2	US-10-029-217A-24	Sequence 2, Appl	905	141	6.0	293	2	US-08-438-745-4	Sequence 4, Appl
833	144.5	6.1	258	2	US-09-248-796A-23723	Sequence 23723, A	906	141	6.0	293	2	US-08-438-745-6	Sequence 6, Appl
834	144.5	6.1	302	2	US-09-657-013-49	Sequence 49, Appl	907	141	6.0	293	2	US-09-219-019-4	Sequence 4, Appl
835	144.5	6.1	302	2	US-09-949-016-6893	Sequence 6893, Ap	908	141	6.0	293	2	US-09-219-019-6	Sequence 6, Appl
836	144.5	6.1	411	2	US-09-657-013-57	Sequence 57, Appl	909	141	6.0	293	5	PCT-US94-05669A-4	Sequence 4, Appl
837	144.5	6.1	411	2	US-09-949-016-6439	Sequence 6439, Ap	910	141	6.0	293	5	PCT-US94-05669A-6	Sequence 6, Appl
838	144.5	6.1	477	2	US-09-863-901-5	Sequence 5, Appl	911	141	6.0	319	2	US-09-884-767A-215	Sequence 215, App
839	144.5	6.1	477	2	US-10-307-389-5	Sequence 5, Appl	912	141	6.0	378	2	US-09-395-017B-1	Sequence 1, Appl
840	144.5	6.1	906	2	US-09-863-901-6	Sequence 6, Appl	913	141	6.0	434	2	US-09-270-767-61286	Sequence 61286, A
841	144.5	6.1	906	2	US-10-307-389-6	Sequence 6, Appl	914	141	6.0	884	2	US-09-823-240A-9	Sequence 9, Appl
842	144	6.1	91	2	US-09-270-767-3789	Sequence 3789, A	915	141	6.0	1059	2	US-09-270-767-45764	Sequence 45764, A
843	144	6.1	91	2	US-07-609-716-103	Sequence 55006, A	916	141	6.0	2284	2	US-09-252-991A-23547	Sequence 23547, A
844	144	6.1	123	1	US-08-475-411A-103	Sequence 103, App	917	140.5	5.9	200	2	US-09-710-239-28	Sequence 28, Appl
845	144	6.1	123	2	US-08-475-411A-103	Sequence 103, App	918	140.5	5.9	435	3	US-10-000-512-18	Sequence 18, Appl
846	144	6.1	123	2	US-08-478-028A-103	Sequence 29, Appl	919	140.5	5.9	456	2	US-09-252-991A-19417	Sequence 19417, A
847	144	6.1	375	2	US-09-600-932-29	Sequence 2, Appl	920	140.5	5.9	462	2	US-09-248-796A-14808	Sequence 17, Appl
848	144	6.1	391	2	US-09-395-017B-2	Sequence 20683, A	921	140.5	5.9	484	3	US-10-347-252-17	Sequence 17, Appl
849	144	6.1	402	2	US-09-252-991A-20683	Sequence 1160, Ap	922	140.5	5.9	506	2	US-09-949-016-11518	Sequence 11518, A
850	144	6.1	1475	2	US-09-538-092-1160	Sequence 9450, Ap	923	140.5	5.9	569	2	US-09-252-991A-24513	Sequence 24513, A
851	144	6.1	1712	2	US-09-949-016-9450	Sequence 4, Appl	924	140.5	5.9	1776	2	US-09-556-877-179	Sequence 179, App
852	144	6.1	1833	2	US-08-621-944A-4	Sequence 4, Appl	925	140.5	5.9	1776	2	US-09-556-877-179	Sequence 179, App
853	144	6.1	1833	2	US-08-945-567D-4	Sequence 3, Appl	926	140.5	5.9	1776	2	US-09-620-412C-179	Sequence 179, App
854	144	6.1	1992	2	US-08-621-944A-3	Sequence 3, Appl	927	140.5	5.9	1776	2	US-09-598-419-179	Sequence 179, App
855	144	6.1	1992	2	US-08-945-567D-3	Sequence 3, Appl	928	140.5	5.9	3969	2	US-08-061-376-5	Sequence 5, Appl
856	144	6.1	2123	2	US-08-968-685A-10	Sequence 10, Appl	929	140	5.9	101	2	US-08-556-978B-22	Sequence 22, Appl
857	143.5	6.1	482	2	US-09-509-031-16	Sequence 16, Appl	930	140	5.9	101	2	US-08-556-978B-62	Sequence 62, Appl
858	143.5	6.1	527	2	US-09-712-363-156	Sequence 156, Ap	931	140	5.9	101	2	US-09-247-806-5	Sequence 5, Appl
859	143.5	6.1	563	2	US-09-949-016-10153	Sequence 10153, A	932	140	5.9	101	2	US-09-247-806-7	Sequence 7, Appl
860	143.5	6.1	2142	2	US-09-540-236-3459	Sequence 3459, Ap	933	140	5.9	101	2	US-09-863-859-11	Sequence 11, Appl
861	143	6.1	165	2	US-09-270-767-59895	Sequence 59895, A	934	140	5.9	101	2	US-09-861-597-5	Sequence 5, Appl
862	143	6.1	263	1	US-08-242-188-3	Sequence 3, Appl	935	140	5.9	101	2	US-09-861-597-7	Sequence 7, Appl
863	143	6.1	263	1	US-08-509-261A-3	Sequence 3, Appl	936	140	5.9	101	2	US-10-414-760-11	Sequence 11, Appl
864	143	6.1	263	1	US-08-660-626-9	Sequence 9, Appl	937	140	5.9	148	2	US-09-248-796A-26837	Sequence 26837, A
865	143	6.1	263	1	US-08-692-892-3	Sequence 3, Appl	938	140	5.9	137	2	US-09-710-239-24	Sequence 24, Appl
866	143	6.1	263	1	US-08-713-939A-3	Sequence 3, Appl	939	140	5.9	264	1	US-08-642-255-51	Sequence 51, Appl
867	143	6.1	263	1	US-08-868-162A-23	Sequence 23, Appl	940	140	5.9	705	2	US-09-252-991A-30792	Sequence 30792, A
868	143	6.1	263	2	US-09-031-168-9	Sequence 9, Appl	941	140	5.9	892	2	US-09-336-447A-5	Sequence 5, Appl
869	143	6.1	263	2	US-09-036-579-3	Sequence 3, Appl	942	140	5.9	892	2	US-09-336-467B-5	Sequence 5, Appl
870	143	6.1	263	2	US-09-550-374-3	Sequence 3, Appl	943	140	5.9	956	2	US-09-949-016-8159	Sequence 8159, Ap
871	143	6.1	263	2	US-09-943-906-3	Sequence 3, Appl	944	139.5	5.9	219	2	US-09-809-517A-24	Sequence 24, Appl
872	143	6.1	263	2	US-09-669-516C-9	Sequence 9, Appl	945	139.5	5.9	219	2	US-09-809-517A-27	Sequence 27, Appl
873	143	6.1	263	2	US-10-435-602-3	Sequence 3, Appl	946	139.5	5.9	234	2	US-10-830-792A-16	Sequence 36, Appl
874	143	6.1	264	2	US-09-627-218B-11	Sequence 11, Appl	947	139.5	5.9	237	2	US-10-830-792A-37	Sequence 37, Appl
875	143	6.1	544	2	US-09-252-991A-27138	Sequence 27138, A	948	139.5	5.9	237	2	US-10-830-792A-43	Sequence 43, Appl
876	142.5	6.0	3969	2	US-09-538-092-1262	Sequence 412, Ap	949	139.5	5.9	253	2	US-09-927-394-2	Sequence 2, Appl
877	142	6.0	137	2	US-09-270-767-56792	Sequence 56792, A	950	139.5	5.9	449	1	US-08-927-394-2	Sequence 2, Appl
878	142	6.0	269	2	US-09-538-092-412	Sequence 16628, A	951	139.5	5.9	449	2	US-09-538-092-1372	Sequence 1372, Ap
879	142	6.0	367	2	US-09-252-991A-16628	Sequence 22945, A	952	139.5	5.9	449	2	US-09-949-016-6604	Sequence 6604, Ap
880	142	6.0	424	2	US-09-252-991A-22945	Sequence 21, Appl	953	139.5	5.9	467	2	US-09-252-991A-31427	Sequence 31427, A
881	142	6.0	1135	2	US-09-294-298A-21	Sequence 6, Appl	954	139.5	5.9	489	2	US-09-366-009-8	Sequence 8, Appl
882	142	6.0	1325	2	US-09-294-298A-6	Sequence 4, Appl	955	139.5	5.9	489	2	US-08-705-964-8	Sequence 8, Appl
883	142	6.0	1376	2	US-09-294-298A-4	Sequence 2, Appl	956	139.5	5.9	489	2	US-09-879-156B-8	Sequence 8, Appl
884	142	6.0	1423	2	US-09-294-298A-2	Sequence 2, Appl	957	139.5	5.9	537	2	US-09-252-991A-27024	Sequence 27024, A
885	141.5	6.0	222	2	US-10-830-792A-40	Sequence 40, Appl	958	139.5	5.9	653	2	US-09-345-473B-50	Sequence 50, Appl
886	141.5	6.0	233	1	US-08-458-568A-4	Sequence 4, Appl	959	139.5	5.9	743	2	US-09-862-027-50	Sequence 50, Appl
887	141.5	6.0	474	2	US-09-702-705-1812	Sequence 1812, Ap	960	139.5	5.9	2291	2	US-09-252-991A-28327	Sequence 28327, A
888	141.5	6.0	474	2	US-09-736-457-1812	Sequence 1812, Ap	961	139.5	5.9	2291	2	US-09-252-991A-28154	Sequence 28154, A
889	141.5	6.0	474	2	US-09-671-325-1812	Sequence 1812, Ap	962	139	5.9	257	2	US-09-155-794-3	Sequence 3, Appl
890	141.5	6.0	474	2	US-09-538-092-1279	Sequence 1279, Ap	963	139	5.9	393	2	US-09-252-991A-10202	Sequence 30202, A
891	141.5	6.0	474	2	US-10-017-754-1812	Sequence 1812, Ap	964	139	5.9	481	2	US-09-252-991A-16955	Sequence 16955, A
892	141.5	6.0	487	2	US-03-386-962C-14	Sequence 14, Appl	965	138.5	5.9	282	2	US-09-605-703B-888	Sequence 888, App
893	141.5	6.0	487	2	US-09-386-959-65	Sequence 65, Appl	966	138.5	5.9	415	2	US-09-605-703B-890	Sequence 890, App
894	141	6.0	211	1	US-08-276-852-34	Sequence 34, Appl	967	138.5	5.9	421	2	US-09-252-991A-27669	Sequence 27669, A
895	141	6.0	211	1	US-08-133-011-16	Sequence 16, Appl	968	138.5	5.9	437	2	US-09-252-991A-32326	Sequence 32326, A
896	141	6.0	211	1	US-08-323-730A-16	Sequence 16, Appl	969	138.5	5.9	1261	2	US-09-921-099A-17	Sequence 17, Appl
897	141	6.0	211	1	US-08-387-874-16	Sequence 16, Appl	970	138.5	5.9	1261	2	US-09-473-716-2	Sequence 2, Appl
898	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	971	138.5	5.9	1497	2	US-10-175-158-2	Sequence 2, Appl
899	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	972	138	5.8	1497	2	US-09-060-854B-2	Sequence 2, Appl
900	141	6.0	211	1	US-08-383-619-16	Sequence 16, Appl	973	138	5.8	1815	2	US-09-529-904-3	Sequence 3, Appl
901	141	6.0	211	2	US-08-907-739-16	Sequence 16, Appl	974	138	5.8	2736	2	US-09-270-767-46554	Sequence 46554, A
902	141	6.0	211	2	US-09-729-597-16	Sequence 16, Appl	975	138	5.8	2736	2	US-09-252-991A-30227	Sequence 30227, A

976	137.5	5.8	263	2	US-09-252-991A-31863	Sequence 31863, A	1049	134	5.7	387	2	US-09-252-991A-23334	Sequence 23334, A
977	137.5	5.8	371	2	US-09-252-991A-30926	Sequence 30926, A	1050	134	5.7	1043	2	US-08-851-567B-61	Sequence 61, Appl
978	137.5	5.8	425	2	US-09-252-991A-31834	Sequence 31834, A	1051	134	5.7	1298	2	US-09-252-991A-30579	Sequence 30579, A
979	137.5	5.8	518	2	US-09-252-991A-25203	Sequence 25203, A	1052	134	5.7	2048	2	US-09-266-347-48	Sequence 48, Appl
980	137.5	5.8	745	2	US-09-841-334A-38	Sequence 38, Appl	1053	133.5	5.6	148	1	US-08-207-904-45	Sequence 15, Appl
981	137.5	5.8	745	2	US-09-837-969A-38	Sequence 38, Appl	1054	133.5	5.6	378	7	5171843-9	Patent No. 5171843
982	137.5	5.8	1419	2	US-10-197-220-173	Sequence 173, App	1055	133.5	5.6	442	2	US-09-538-092-1123	Sequence 1123, Ap
983	137.5	5.8	1805	1	US-07-853-913-2	Sequence 2, Appli	1056	133.5	5.6	862	2	US-09-958-359-35	Sequence 35, Appl
984	137	5.8	838	3	US-10-420-191-2	Sequence 2, Appli	1057	133	5.6	141	2	US-09-252-991A-23427	Sequence 23427, A
985	137	5.8	867	2	US-09-540-236-2676	Sequence 2676, Ap	1058	133	5.6	486	2	US-09-710-279-788	Sequence 788, Appl
986	137	5.8	995	2	US-09-252-991A-22297	Sequence 22297, A	1059	133	5.6	513	2	US-09-252-991A-18177	Sequence 18177, A
987	136.5	5.8	159	2	US-10-190-902B-10	Sequence 10, Appl	1060	133	5.6	855	2	US-09-902-540-14518	Sequence 14518, A
988	136.5	5.8	177	2	US-10-830-792A-17	Sequence 17, Appl	1061	133	5.6	1742	3	US-09-958-359-33	Sequence 23, Appl
989	136.5	5.8	219	2	US-10-153-469A-44	Sequence 44, Appl	1062	132.5	5.6	80	2	US-09-148-796A-23892	Sequence 23892, A
990	136.5	5.8	219	2	US-10-153-469A-46	Sequence 46, Appl	1063	132.5	5.6	91	2	US-10-148-306A-18	Sequence 18, Appl
991	136.5	5.8	219	2	US-10-104-889-44	Sequence 44, Appl	1064	132.5	5.6	182	2	US-09-488-039A-8301	Sequence 8301, Ap
992	136.5	5.8	219	2	US-10-104-889-46	Sequence 46, Appl	1065	132.5	5.6	247	2	US-09-199-637A-363	Sequence 363, App
993	136.5	5.8	223	2	US-09-248-796A-27735	Sequence 27735, A	1066	132.5	5.6	301	2	US-08-466-318-142	Sequence 142, App
994	136.5	5.8	464	1	US-08-836-854-19	Sequence 19, Appl	1067	132.5	5.6	301	2	US-08-466-609A-142	Sequence 142, App
995	136.5	5.8	464	2	US-09-366-009-7	Sequence 7, Appli	1068	132.5	5.6	301	2	US-08-446-872A-142	Sequence 142, App
996	136.5	5.8	464	2	US-08-809-156B-7	Sequence 7, Appli	1069	132.5	5.6	301	2	US-08-762-227A-142	Sequence 142, App
997	136.5	5.8	464	2	US-09-775-364-7	Sequence 7, Appli	1070	132.5	5.6	301	5	PCT-US95-01185-142	Sequence 142, App
998	136.5	5.8	703	2	US-08-910-925-4	Sequence 4, Appli	1071	132.5	5.6	394	3	US-09-980-862B-22	Sequence 22, Appl
999	136.5	5.8	850	2	US-09-129-603-2	Sequence 2, Appli	1072	132.5	5.6	396	2	US-09-980-862B-19	Sequence 19, Appl
1000	136.5	5.8	1064	2	US-10-104-047-3830	Sequence 3830, Ap	1073	132.5	5.6	466	2	US-09-134-001C-4749	Sequence 4749, Ap
1001	136.5	5.8	1113	2	US-09-252-991A-24385	Sequence 24385, A	1074	132.5	5.6	468	2	US-09-252-991A-24394	Sequence 24394, A
1002	136.5	5.8	1290	2	US-09-150-460B-6	Sequence 6, Appli	1075	132.5	5.6	706	2	US-09-270-767-40994	Sequence 40994, A
1003	136.5	5.8	1376	2	US-09-252-991A-30344	Sequence 30344, A	1076	132.5	5.6	706	2	US-09-270-767-40994	Sequence 56210, A
1004	136.5	5.8	1388	2	US-09-463-048A-6	Sequence 6, Appli	1077	132.5	5.6	722	2	US-09-714-865-3	Sequence 3, Appli
1005	136.5	5.8	1388	3	US-10-617-962-6	Sequence 6, Appli	1078	132	5.6	186	2	US-09-366-009-6	Sequence 6, Appli
1006	136	5.8	50	2	US-09-863-901-22	Sequence 22, Appl	1079	132	5.6	186	2	US-08-809-156B-6	Sequence 6, Appli
1007	136	5.8	50	2	US-10-307-389-22	Sequence 22, Appl	1080	132	5.6	186	2	US-09-775-964-6	Sequence 6, Appli
1008	136	5.8	139	2	US-08-506-553C-8	Sequence 8, Appli	1081	132	5.6	430	2	US-09-252-991A-22599	Sequence 22599, A
1009	136	5.8	247	2	US-09-252-991A-21412	Sequence 21412, A	1082	132	5.6	455	2	US-09-270-767-45531	Sequence 45531, A
1010	136	5.8	339	2	US-09-252-991A-32096	Sequence 32096, A	1083	132	5.6	580	2	US-09-252-991A-29979	Sequence 29979, A
1011	135.5	5.7	260	2	US-09-431-887-6	Sequence 6, Appli	1084	132	5.6	615	2	US-09-252-991A-23203	Sequence 23203, A
1012	135.5	5.7	400	2	US-09-086-010-2	Sequence 2, Appli	1085	132	5.6	700	2	US-09-714-865-5	Sequence 5, Appli
1013	135.5	5.7	400	2	US-09-879-312A-2	Sequence 2, Appli	1086	132	5.6	929	2	US-09-252-991A-19203	Sequence 19203, A
1014	135.5	5.7	590	2	US-09-252-991A-19127	Sequence 19127, A	1087	131.5	5.6	136	2	US-09-270-767-6188	Sequence 46188, A
1015	135	5.7	139	2	US-09-050-739-68	Sequence 68, Appl	1088	131.5	5.6	256	2	US-09-431-887-31	Sequence 31, Appl
1016	135	5.7	139	2	US-09-804-980-68	Sequence 68, Appl	1089	131.5	5.6	257	2	US-09-431-887-30	Sequence 30, Appl
1017	135	5.7	332	1	US-08-893-853-3	Sequence 3, Appli	1090	131.5	5.6	268	2	US-08-961-083-140	Sequence 140, App
1018	135	5.7	302	2	US-09-451-921-3	Sequence 3, Appli	1091	131.5	5.6	268	2	US-09-536-784-140	Sequence 140, App
1019	135	5.7	302	2	US-09-451-067-3	Sequence 3, Appli	1092	131.5	5.6	268	2	US-09-765-271-140	Sequence 140, App
1020	135	5.7	302	3	US-10-086-208-3	Sequence 3, Appli	1093	131.5	5.6	268	2	US-09-765-272A-140	Sequence 140, App
1021	135	5.7	310	2	US-08-845-258-19	Sequence 19, Appl	1094	131.5	5.6	269	2	US-09-252-991A-25667	Sequence 25667, A
1022	135	5.7	310	2	US-08-990-571-19	Sequence 19, Appl	1095	131.5	5.6	388	2	US-09-252-991A-30608	Sequence 30608, A
1023	135	5.7	310	2	US-08-723-142A-19	Sequence 19, Appl	1096	131.5	5.6	647	1	US-08-770-761A-8	Sequence 8, Appli
1024	135	5.7	310	2	US-09-528-784A-19	Sequence 19, Appl	1097	131.5	5.6	705	1	US-08-770-761A-7	Sequence 7, Appli
1025	135	5.7	310	2	US-09-569-098A-19	Sequence 19, Appl	1098	131.5	5.6	709	2	US-09-702-705-335	Sequence 335, App
1026	135	5.7	345	2	US-09-252-991A-30910	Sequence 30910, A	1099	131.5	5.6	709	2	US-09-736-457-335	Sequence 335, App
1027	135	5.7	558	2	US-09-199-637A-277	Sequence 277, App	1100	131.5	5.6	709	2	US-09-614-124B-335	Sequence 335, App
1028	135	5.7	2516	2	US-08-374-077C-2	Sequence 2, Appli	1101	131.5	5.6	709	2	US-09-671-325-335	Sequence 335, App
1029	135	5.7	2516	2	US-08-895-590-2	Sequence 2, Appli	1102	131.5	5.6	709	2	US-09-589-184-335	Sequence 335, App
1030	135	5.7	2516	2	US-09-539-879A-2	Sequence 2, Appli	1103	131.5	5.6	709	2	US-09-658-824-335	Sequence 335, App
1031	134.5	5.7	101	2	US-08-556-878B-20	Sequence 20, Appli	1104	131.5	5.6	709	2	US-10-017-754-335	Sequence 335, App
1032	134.5	5.7	101	2	US-09-247-806-3	Sequence 3, Appli	1105	131.5	5.6	709	2	US-09-651-563-335	Sequence 335, App
1033	134.5	5.7	101	2	US-09-863-859-10	Sequence 10, Appl	1106	131.5	5.6	709	2	US-09-519-642-335	Sequence 335, App
1034	134.5	5.7	101	2	US-09-861-597-3	Sequence 3, Appli	1107	131.5	5.6	713	2	US-09-714-865-4	Sequence 4, Appli
1039	134.5	5.7	634	2	US-08-257-073-3	Sequence 3, Appli	1111	131	5.5	1728	2	US-09-252-991A-23166	Sequence 23166, A
1040	134.5	5.7	984	1	US-08-184-009-120	Sequence 120, App	1113	131	5.5	456	2	US-09-495-980A-11	Sequence 11, Appl
1041	134.5	5.7	984	1	US-08-458-356-120	Sequence 120, App	1114	131	5.5	613	2	US-09-605-703B-1310	Sequence 1310, Ap
1042	134.5	5.7	984	2	US-08-460-736-120	Sequence 120, App	1115	131	5.5	707	2	US-10-094-749-2443	Sequence 2443, Ap
1043	134.5	5.7	984	2	US-09-535-370-120	Sequence 120, App	1116	130.5	5.5	72	1	US-07-609-716-35	Sequence 35, Appl
1044	134.5	5.7	984	2	US-09-663-667-120	Sequence 120, App	1117	130.5	5.5	72	1	US-08-175-155-32	Sequence 32, Appl
1045	134.5	5.7	2703	2	US-08-189-432-19	Sequence 19, Appl	1118	130.5	5.5	72	1	US-08-477-509B-87	Sequence 87, Appl
1046	134.5	5.7	2703	2	US-08-895-232-4	Sequence 4, Appli	1119	130.5	5.5	72	1	US-08-707-237A-60	Sequence 60, Appl
1047	134.5	5.7	2703	2	US-09-121-457-4	Sequence 4, Appli	1120	130.5	5.5	72	2	US-08-482-085B-87	Sequence 87, Appl
1048	134	5.7	104	2	US-09-219-849-33	Sequence 33, Appli	1121	130.5	5.5	72	2	US-08-475-411A-35	Sequence 35, Appl



1122	130.5	5.5	72	2	US-08-478-029A-35	Sequence 35, Appl	1195	128.5	5.4	1610	2	US-09-548-473B-4	Sequence 4, Appl1
1123	130.5	5.5	72	2	US-09-444-791A-87	Sequence 87, Appl	1196	128.5	5.4	2596	2	US-09-548-473B-6	Sequence 6, Appl1
1124	130.5	5.5	128	2	US-08-806-029-13	Sequence 13, Appl	1197	128.5	5.4	2630	3	US-10-077-130-2	Sequence 2, Appl1
1125	130.5	5.5	223	2	US-09-248-796A-24067	Sequence 24067, A	1198	128.5	5.4	7968	3	US-10-077-130-5	Sequence 5, Appl1
1126	130.5	5.5	301	2	US-09-252-991A-28663	Sequence 28663, A	1199	128	5.4	198	2	US-10-830-792A-42	Sequence 42, Appl
1127	130.5	5.5	362	2	US-09-252-991A-17884	Sequence 17884, A	1200	128	5.4	297	2	US-09-252-991A-27909	Sequence 27909, A
1128	130.5	5.5	365	2	US-09-252-991A-30166	Sequence 30166, A	1201	128	5.4	376	2	US-09-056-556-202	Sequence 202, App
1129	130.5	5.5	803	2	US-09-252-991A-23614	Sequence 23614, A	1202	128	5.4	376	2	US-09-072-596-197	Sequence 197, App
1130	130.5	5.5	2508	2	US-09-627-650B-7	Sequence 7, Appl1	1203	128	5.4	376	2	US-09-072-596-197	Sequence 202, App
1131	130.5	5.5	2508	2	US-09-436-063C-7	Sequence 7, Appl1	1204	128	5.4	376	2	US-10-193-002-197	Sequence 197, App
1132	130.5	5.5	2544	2	US-09-627-650B-3	Sequence 3, Appl1	1205	128	5.4	376	2	US-10-084-843-202	Sequence 202, App
1133	130.5	5.5	2544	2	US-09-436-063C-3	Sequence 3, Appl1	1206	128	5.4	499	2	US-09-252-991A-28010	Sequence 28010, A
1134	130.5	5.5	2601	2	US-09-627-650B-9	Sequence 9, Appl1	1207	128	5.4	555	2	US-09-252-991A-28734	Sequence 28734, A
1135	130.5	5.5	2601	2	US-09-436-063C-9	Sequence 9, Appl1	1208	128	5.4	1145	2	US-09-758-759-167	Sequence 167, App
1136	130	5.5	176	2	US-09-252-991A-28622	Sequence 28622, A	1209	128	5.4	1145	2	US-09-902-540-12627	Sequence 12627, A
1137	130	5.5	176	2	US-09-328-352-6964	Sequence 6964, Ap	1210	128	5.4	1970	2	US-09-538-092-1005	Sequence 1005, Ap
1138	130	5.5	180	2	US-10-830-792A-18	Sequence 18, Appl	1211	127.5	5.4	192	2	US-09-902-540-10307	Sequence 10307, A
1139	130	5.5	223	2	US-09-206-676C-1	Sequence 1, Appl1	1212	127.5	5.4	324	2	US-09-107-433-4143	Sequence 4143, Ap
1140	130	5.5	253	2	US-09-431-887-16	Sequence 16, Appl	1213	127.5	5.4	375	2	US-09-252-991A-31128	Sequence 31128, A
1141	130	5.5	253	2	US-09-431-887-18	Sequence 18, Appl	1214	127.5	5.4	391	2	US-09-538-092-1097	Sequence 1097, Ap
1142	130	5.5	278	2	US-09-260-283-2	Sequence 2, Appl1	1215	127.5	5.4	394	2	US-09-949-016-8507	Sequence 8507, Ap
1143	130	5.5	425	2	US-09-252-991A-22321	Sequence 22321, A	1216	127.5	5.4	406	2	US-09-252-991A-19702	Sequence 19702, A
1144	130	5.5	441	2	US-09-252-991A-24366	Sequence 24366, A	1217	127.5	5.4	630	2	US-08-653-648A-15	Sequence 15, Appl
1145	130	5.5	510	2	US-09-252-991A-17695	Sequence 17695, A	1218	127.5	5.4	878	2	US-09-564-418-8	Sequence 8, Appl1
1146	130	5.5	514	2	US-09-252-991A-18306	Sequence 18306, A	1219	127.5	5.4	165	2	US-10-830-792A-20	Sequence 20, Appl
1147	130	5.5	635	2	US-09-487-558B-302	Sequence 302, App	1220	127	5.4	253	1	US-08-242-188-2	Sequence 2, Appl1
1148	130	5.5	941	2	US-09-336-447A-9	Sequence 9, Appl1	1221	127	5.4	253	1	US-08-509-261A-2	Sequence 2, Appl1
1149	130	5.5	941	2	US-09-952-267B-9	Sequence 9, Appl1	1222	127	5.4	253	1	US-08-660-626-8	Sequence 8, Appl1
1150	130	5.5	1618	1	US-07-853-913-4	Sequence 4, Appl1	1223	127	5.4	253	1	US-08-692-892-2	Sequence 2, Appl1
1151	130	5.5	1618	1	US-09-538-092-1143	Sequence 1143, Ap	1224	127	5.4	253	1	US-08-713-939A-2	Sequence 2, Appl1
1152	130	5.5	1618	2	US-09-731-255-2	Sequence 2, Appl1	1225	127	5.4	253	1	US-08-868-162A-22	Sequence 22, Appl
1153	130	5.5	1618	2	US-10-136-891-2	Sequence 2, Appl1	1226	127	5.4	253	2	US-09-031-168-8	Sequence 8, Appl1
1154	130	5.5	103	1	US-08-209-747-4	Sequence 4, Appl1	1227	127	5.4	253	2	US-09-128-450-20	Sequence 20, Appl
1155	129.5	5.5	103	1	US-08-458-298-4	Sequence 4, Appl1	1228	127	5.4	253	2	US-09-036-579-2	Sequence 2, Appl1
1156	129.5	5.5	103	1	US-08-556-978B-60	Sequence 60, Appl	1229	127	5.4	253	2	US-09-823-494-20	Sequence 20, Appl
1157	129.5	5.5	119	2	US-09-247-806-9	Sequence 9, Appl1	1230	127	5.4	253	2	US-09-550-374-2	Sequence 2, Appl1
1158	129.5	5.5	119	2	US-09-861-597-9	Sequence 9, Appl1	1231	127	5.4	253	2	US-09-431-887-1	Sequence 1, Appl1
1159	129.5	5.5	119	2	US-08-591-685-13	Sequence 13, Appl	1232	127	5.4	253	2	US-09-431-887-2	Sequence 2, Appl1
1160	129.5	5.5	368	2	US-09-252-991A-27333	Sequence 27333, A	1233	127	5.4	253	2	US-09-431-887-3	Sequence 3, Appl1
1161	129.5	5.5	423	2	US-09-949-016-6628	Sequence 6628, Ap	1234	127	5.4	253	2	US-09-431-887-4	Sequence 4, Appl1
1162	129.5	5.5	564	2	US-09-949-016-11035	Sequence 11035, A	1235	127	5.4	253	2	US-09-431-887-8	Sequence 8, Appl1
1163	129.5	5.5	569	2	US-09-252-991A-25632	Sequence 25632, A	1236	127	5.4	253	2	US-09-943-906-2	Sequence 2, Appl
1164	129.5	5.5	577	2	US-09-336-447A-13	Sequence 13, Appl	1237	127	5.4	253	2	US-09-669-518C-8	Sequence 8, Appl1
1165	129.5	5.5	865	2	US-09-925-991A-18683	Sequence 18683, A	1238	127	5.4	253	2	US-10-435-602-2	Sequence 2, Appl1
1166	129.5	5.5	873	2	US-09-925-267B-13	Sequence 13, Appl	1239	127	5.4	253	2	US-09-155-794-4	Sequence 4, Appl1
1167	129.5	5.5	873	2	US-09-925-267B-13	Sequence 13, Appl	1240	127	5.4	253	2	US-09-155-794-5	Sequence 5, Appl1
1168	129.5	5.5	1236	2	US-09-669-787-109	Sequence 109, App	1241	127	5.4	253	2	US-09-431-887-29	Sequence 29, Appl
1169	129.5	5.5	1705	2	US-08-669-785-4	Sequence 4, Appl1	1242	127	5.4	253	2	US-08-122-458D-11	Sequence 11, Appl
1170	129.5	5.5	1705	2	US-09-907-951-4	Sequence 4, Appl1	1243	127	5.4	257	2	US-09-270-767-31877	Sequence 31877, A
1171	129.5	5.5	1794	7	5183745-6	Patent No. 5183745	1244	127	5.4	298	2	US-09-270-767-45830	Sequence 45830, A
1172	129	5.5	45	2	US-09-863-901-25	Sequence 25, Appl	1245	127	5.4	331	2	US-09-270-767-45830	Sequence 4, Appl1
1173	129	5.5	45	2	US-10-307-389-25	Sequence 25, Appl	1246	127	5.4	370	2	US-09-248-796A-23614	Sequence 23614, A
1174	129	5.5	122	2	US-08-956-307B-19	Sequence 19, Appl	1247	127	5.4	374	2	US-09-252-991A-24378	Sequence 24378, A
1175	129	5.5	256	2	US-09-128-450-22	Sequence 22, Appl	1248	127	5.4	886	2	US-09-252-991A-25804	Sequence 25804, A
1176	129	5.5	256	2	US-09-823-494-22	Sequence 22, Appl	1249	127	5.4	1004	2	US-09-270-767-31877	Sequence 31877, A
1177	129	5.5	256	2	US-09-155-794-1	Sequence 1, Appl1	1250	127	5.4	217	2	US-09-270-767-47094	Sequence 47094, A
1178	129	5.5	334	2	US-09-949-016-11006	Sequence 11006, A	1251	126.5	5.4	217	2	US-09-248-796A-23661	Sequence 23661, A
1179	129	5.5	452	2	US-10-094-749-2809	Sequence 2809, Ap	1252	126.5	5.4	219	2	US-09-431-887-25	Sequence 25, Appl
1180	129	5.5	456	2	US-09-919-172-31	Sequence 31, Appl	1253	126.5	5.4	256	2	US-09-252-991A-29678	Sequence 29678, A
1181	129	5.5	707	2	US-09-919-039-278	Sequence 278, App	1254	126.5	5.4	405	2	US-09-166-265-1	Sequence 1, Appl1
1182	129	5.5	707	2	US-09-538-092-993	Sequence 993, App	1255	126.5	5.4	427	2	US-09-252-991A-16736	Sequence 16736, A
1183	129	5.5	724	2	US-09-714-865-2	Sequence 2, Appl1	1256	126.5	5.4	439	2	US-09-252-991A-25804	Sequence 25804, A
1184	129	5.5	729	2	US-09-949-016-10790	Sequence 10790, A	1257	126.5	5.4	451	2	US-09-252-991A-17887	Sequence 17887, A
1185	129	5.5	729	2	US-09-949-016-10791	Sequence 10791, A	1258	126.5	5.4	476	2	US-09-830-230A-679	Sequence 679, App
1186	128.5	5.4	76	2	US-10-148-306-3	Sequence 3, Appl1	1259	126.5	5.4	567	2	US-10-104-047-3772	Sequence 3772, Ap
1187	128.5	5.4	226	2	US-09-206-676C-2	Sequence 2, Appl1	1260	126.5	5.4	650	2	US-09-252-991A-28145	Sequence 28145, A
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1189	128.5	5.4	365	2	US-09-252-991A-32337	Sequence 32337, A	1262	126.5	5.4	1011	2	US-09-538-092-1142	Sequence 1142, Ap
1190	128.5	5.4	441	2	US-09-794-422-4	Sequence 4, Appl1	1263	126.5	5.4	2142	2		
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1193	128.5	5.4	975	2	US-09-270-767-42040	Sequence 42040, A	1266	126.5	5.4				
1194	128.5	5.4	1351	2	US-09-548-473B-1	Sequence 1, Appl1	1267	126.5	5.4				



1268	126.5	5.4	2142	2	US-09-949-002-371	Sequence 371, App	1341	124	5.2	469	2	US-09-252-991A-26584	Sequence 26584, A
1269	126.5	5.4	2442	2	US-09-514-247A-10	Sequence 10, Appl	1342	124	5.2	482	2	US-09-270-767-43292	Sequence 43292, A
1270	126.5	5.4	2442	2	US-09-538-092-1370	Sequence 1370, Ap	1343	124	5.2	586	2	US-09-252-991A-24512	Sequence 24512, A
1271	126	5.3	97	1	US-07-609-716-99	Sequence 99, Appl	1344	124	5.2	1249	2	US-09-964-899-33	Sequence 33, Appl
1272	126	5.3	97	2	US-08-475-411A-99	Sequence 99, Appl	1345	123.5	5.2	229	2	US-09-248-796A-24631	Sequence 24631, A
1273	126	5.3	97	2	US-08-478-029A-99	Sequence 99, Appl	1346	123.5	5.2	325	2	US-09-902-540-13678	Sequence 13678, A
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1275	126	5.3	208	2	US-09-128-450-18	Sequence 18, Appl	1348	123.5	5.2	704	2	US-09-270-767-46262	Sequence 46262, A
1276	126	5.3	208	2	US-09-823-494-18	Sequence 18, Appl	1349	123.5	5.2	742	2	US-09-949-016-17729	Sequence 7729, Ap
1277	126	5.3	253	2	US-09-919-172-57	Sequence 57, Appl	1350	123.5	5.2	783	2	US-09-252-991A-18035	Sequence 18035, A
1278	126	5.3	253	2	US-09-976-594-72	Sequence 72, Appl	1351	123.5	5.2	1403	1	US-08-387-942C-3	Sequence 3, Appl
1279	126	5.3	374	2	US-09-949-016-7191	Sequence 7191, Ap	1352	123.5	5.2	2283	2	US-10-172-002-8	Sequence 4, Appl
1280	126	5.3	383	2	US-09-252-991A-22283	Sequence 22283, A	1353	123	5.2	129	2	US-10-190-002B-9	Sequence 9, Appl
1281	126	5.3	584	2	US-09-252-991A-21071	Sequence 21071, A	1354	123	5.2	144	2	US-10-190-002B-7	Sequence 7, Appl
1282	126	5.3	819	2	US-09-303-518D-185	Sequence 185, App	1355	123	5.2	179	2	US-09-270-767-57837	Sequence 57837, A
1283	126	5.3	819	2	US-09-252-991A-19569	Sequence 19569, App	1356	123	5.2	208	2	US-09-252-991A-27661	Sequence 27661, A
1284	126	5.3	891	2	US-09-949-016-7798	Sequence 7798, Ap	1357	123	5.2	252	2	US-09-431-887-17	Sequence 17, Appl
1285	126	5.3	1394	2	US-09-902-540-16497	Sequence 16497, A	1358	123	5.2	321	2	US-08-485-511A-4	Sequence 4, Appl
1286	126	5.3	1400	2	US-08-630-915A-37	Sequence 37, Appl	1359	123	5.2	496	3	US-09-958-359-29	Sequence 29, Appl
1287	126	5.3	1400	2	US-09-879-957-37	Sequence 37, Appl	1360	123	5.2	522	2	US-09-538-092-1096	Sequence 1096, Ap
1288	126	5.3	2017	3	US-10-114-270-86	Sequence 86, Appl	1361	123	5.2	524	2	US-09-252-991A-23801	Sequence 23801, A
1289	125.5	5.3	226	2	US-09-155-794-8	Sequence 8, Appl	1362	123	5.2	588	2	US-09-252-991A-18578	Sequence 18578, A
1290	125.5	5.3	232	7	5171843-7	Patent No. 5171843	1363	123	5.2	801	1	US-07-906-449A-6	Sequence 6, Appl
1291	125.5	5.3	333	1	US-08-712-948-1	Sequence 1, Appl	1364	123	5.2	1620	2	US-08-542-363-2	Sequence 2, Appl
1292	125.5	5.3	334	1	US-07-941-523-24	Sequence 24, Appl	1365	123	5.2	1620	2	US-09-100-089-2	Sequence 2, Appl
1293	125.5	5.3	556	2	US-09-252-991A-27601	Sequence 27601, A	1366	123	5.2	1620	2	US-09-670-827-2	Sequence 2, Appl
1294	125.5	5.3	757	2	US-09-252-991A-25918	Sequence 25918, A	1367	123	5.2	1620	2	US-09-827-949-2	Sequence 2, Appl
1295	125.5	5.3	933	2	US-08-293-728-2	Sequence 2, Appl	1368	122.5	5.2	155	1	US-08-209-747-15	Sequence 15, Appl
1296	125.5	5.3	933	2	US-09-421-868-2	Sequence 2, Appl	1369	122.5	5.2	155	1	US-08-458-298-15	Sequence 15, Appl
1297	125.5	5.3	933	2	US-09-679-643-2	Sequence 2, Appl	1370	122.5	5.2	189	2	US-09-710-279-2692	Sequence 2692, Ap
1298	125.5	5.3	936	2	US-08-956-171E-5249	Sequence 5249, Ap	1371	122.5	5.2	203	2	US-09-270-767-35336	Sequence 35336, A
1299	125	5.3	936	2	US-08-781-986A-5249	Sequence 5249, Ap	1372	122.5	5.2	226	2	US-09-252-991A-23893	Sequence 23893, A
1300	125	5.3	165	2	US-10-830-792A-26	Sequence 26, Appl	1373	122.5	5.2	226	2	US-09-252-991A-23901	Sequence 23901, A
1301	125	5.3	254	2	US-09-128-450-26	Sequence 26, Appl	1374	122.5	5.2	528	2	US-09-270-767-42594	Sequence 42594, A
1302	125	5.3	254	2	US-09-823-494-26	Sequence 26, Appl	1375	122.5	5.2	601	2	US-09-252-991A-22594	Sequence 22594, A
1303	125	5.3	254	2	US-09-155-794-6	Sequence 6, Appl	1376	122.5	5.2	606	2	US-09-248-796A-14276	Sequence 14276, A
1304	125	5.3	349	2	US-08-469-318-151	Sequence 151, App	1377	122.5	5.2	684	2	US-09-303-518D-721	Sequence 721, App
1305	125	5.3	349	2	US-08-468-609A-151	Sequence 151, App	1378	122.5	5.2	763	2	US-09-252-991A-30146	Sequence 30146, A
1306	125	5.3	349	2	US-08-468-609A-151	Sequence 151, App	1379	122.5	5.2	930	2	US-09-198-452A-470	Sequence 470, App
1307	125	5.3	349	2	US-08-762-227A-151	Sequence 151, App	1380	122.5	5.2	938	2	US-09-438-185A-448	Sequence 448, App
1308	125	5.3	432	5	PCT-US95-01185-151	Sequence 151, App	1381	122.5	5.2	1085	2	US-09-841-334A-39	Sequence 39, Appl
1309	125	5.3	432	2	US-09-248-796A-16450	Sequence 16450, A	1382	122.5	5.2	1085	2	US-09-837-969A-39	Sequence 39, Appl
1310	125	5.3	712	2	US-09-248-796A-14274	Sequence 14274, A	1383	122.5	5.2	1633	2	US-09-902-540-12892	Sequence 12892, A
1311	125	5.3	716	2	US-09-107-532A-5208	Sequence 5208, Ap	1384	122	5.2	253	2	US-09-431-887-7	Sequence 7, Appl
1312	124.5	5.3	60	2	US-08-469-318-195	Sequence 195, App	1385	122	5.2	253	2	US-09-431-887-9	Sequence 9, Appl
1313	124.5	5.3	60	2	US-08-468-609A-195	Sequence 195, App	1386	122	5.2	253	2	US-09-431-887-10	Sequence 10, Appl
1314	124.5	5.3	60	2	US-08-468-609A-195	Sequence 195, App	1387	122	5.2	253	2	US-09-431-887-11	Sequence 11, Appl
1315	124.5	5.3	60	2	US-08-762-227A-195	Sequence 195, App	1388	122	5.2	253	2	US-09-431-887-12	Sequence 12, Appl
1316	124.5	5.3	60	5	PCT-US95-01185-195	Sequence 195, App	1389	122	5.2	253	2	US-09-431-887-14	Sequence 14, Appl
1317	124.5	5.3	184	2	US-09-270-767-59165	Sequence 59165, A	1390	122	5.2	256	2	US-09-431-887-26	Sequence 26, Appl
1318	124.5	5.3	281	2	US-09-252-991A-21873	Sequence 21873, A	1391	122	5.2	302	2	US-10-029-180-18	Sequence 18, Appl
1319	124.5	5.3	281	2	US-09-270-767-43772	Sequence 43772, A	1392	122	5.2	304	2	US-09-252-991A-23016	Sequence 23016, A
1320	124.5	5.3	349	2	US-08-468-609A-139	Sequence 139, App	1393	122	5.2	311	2	US-09-949-016-8142	Sequence 8142, Ap
1321	124.5	5.3	349	2	US-08-468-609A-139	Sequence 139, App	1394	122	5.2	380	2	US-09-270-767-43626	Sequence 43626, A
1322	124.5	5.3	349	2	US-08-446-872A-139	Sequence 139, App	1395	122	5.2	392	2	US-09-949-016-6078	Sequence 6078, Ap
1323	124.5	5.3	349	2	US-08-762-227A-139	Sequence 139, App	1396	122	5.2	466	2	US-09-215-221-24	Sequence 24, Appl
1324	124.5	5.3	349	5	PCT-US95-01185-139	Sequence 139, App	1397	122	5.2	471	2	US-09-538-092-837	Sequence 837, App
1325	124.5	5.3	425	2	US-09-252-991A-24223	Sequence 24223, A	1398	122	5.2	476	2	US-09-248-796A-18994	Sequence 18994, A
1326	124.5	5.3	425	2	US-09-252-991A-19054	Sequence 19054, A	1399	122	5.2	551	1	US-09-033-537A-1	Sequence 1, Appl
1327	124.5	5.3	510	2	US-09-252-991A-33084	Sequence 33084, A	1400	122	5.2	552	2	US-09-252-991A-25589	Sequence 25589, A
1328	124.5	5.3	534	2	US-09-252-991A-20468	Sequence 20468, A	1401	122	5.2	639	2	US-09-252-991A-28453	Sequence 28453, A
1329	124.5	5.3	757	2	US-09-252-991A-23569	Sequence 23569, A	1402	122	5.2	735	2	US-09-949-016-10120	Sequence 10120, A
1330	124.5	5.3	1261	2	US-09-248-796A-16620	Sequence 16620, A	1403	122	5.2	989	2	US-08-213-4198-2	Sequence 2, Appl
1331	124.5	5.3	1665	2	US-09-858-664A-2	Sequence 2, Appl	1404	122	5.2	989	2	US-08-213-4198-4	Sequence 4, Appl
1332	124.5	5.3	1665	2	US-10-274-978-2	Sequence 2, Appl	1405	122	5.2	1239	1	US-08-937-331-2	Sequence 2, Appl
1333	124.5	5.3	1665	2	US-10-697-263-2	Sequence 2, Appl	1406	122	5.2	1239	2	US-09-285-502-2	Sequence 2, Appl
1334	124	5.2	76	1	US-08-089-862-10	Sequence 10, Appl	1407	122	5.2	1239	2	US-09-709-126-2	Sequence 2, Appl
1335	124	5.2	76	1	US-08-587-333-17	Sequence 17, Appl	1408	122	5.2	1239	2	US-09-871-385A-2	Sequence 2, Appl
1336	124	5.2	76	5	PCT-US94-07776-15	Sequence 15, Appl	1409	122	5.2	2150	3	US-10-135-322-17	Sequence 17, Appl
1337	124	5.2	155	2	US-09-252-991A-27532	Sequence 27532, A	1410	121.5	5.1	75	1	US-07-609-716-39	Sequence 39, Appl
1338	124	5.2	212	2	US-09-252-991A-24512	Sequence 24512, A	1411	121.5	5.1	75	2	US-08-475-411A-39	Sequence 39, Appl
1339	124	5.2	212	2	US-09-252-991A-27887	Sequence 27887, A	1412	121.5	5.1	75	2	US-08-478-029A-39	Sequence 39, Appl
1340	124	5.2	216	2	US-10-830-792A-35	Sequence 35, Appl	1413	121.5	5.1	86	1	US-07-609-716-102	Sequence 102, App



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Db      241  SSNSGGSGSGSGSGSGSGNDNNSSSGSGSSSGSGSGSGSGSGSGS 300
Qy      301  RGDGSESSSWGSSSTGSSSGNHGSGGNGHKPGCEKPGNEARSGESG1QGFRCGYVSN 360
Db      301  RGDGSESSSWGSSSTGSSSGNHGSGGNGHKPGCEKPGNEARSGESG1QGFRCGYVSN 360
Qy      361  MREISKGNRLLGSGDNYRGQSSSWGSGGDAVGVNTVNSETSPGMFNFDTFWKNPKS 420
Db      361  MREISKGNRLLGSGDNYRGQSSSWGSGGDAVGVNTVNSETSPGMFNFDTFWKNPKS 420
Qy      421  KLGFIMWDALKDQSSRIP 440
Db      421  KLGFIMWDALKDQSSRIP 440
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## RESULT 2

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US-10-015-389A-52
; Sequence 52, Application US/10015389A
; Patent No. 6936436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-389A-52
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Query Match      100.0%; Score 2363; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 4.7e-159;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKFGPLACLIALCLSGGAGPLQSGESTGTNIGALGHGLGDALSEGVKAIKREAG 60
Db      1  MKFGPLACLIALCLSGGAGPLQSGESTGTNIGALGHGLGDALSEGVKAIKREAG 60
Qy      61  GAAGSVSEALGGCTREAVGTGVRQVPGFAADALGNRVEAAHALGNTGHEIGROADV 120
Db      61  GAAGSVSEALGGCTREAVGTGVRQVPGFAADALGNRVEAAHALGNTGHEIGROADV 120
Qy      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Db      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Qy      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Db      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Qy      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
Db      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
Qy      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
Db      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
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Db      241  SSNSGGSGSGSGSGSGSGNDNNSSSGSGSSSGSGSGSGSGSGSGSGSGSGSGS 300
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Db      301  RGDGSESSSWGSSSTGSSSGNHGSGGNGHKPGCEKPGNEARSGESG1QGFRCGYVSN 360
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Db      301  RGDGSESSSWGSSSTGSSSGNHGSGGNGHKPGCEKPGNEARSGESG1QGFRCGYVSN 360
Qy      361  MREISKGNRLLGSGDNYRGQSSSWGSGGDAVGVNTVNSETSPGMFNFDTFWKNPKS 420
Db      361  MREISKGNRLLGSGDNYRGQSSSWGSGGDAVGVNTVNSETSPGMFNFDTFWKNPKS 420
Qy      421  KLGFIMWDALKDQSSRIP 440
Db      421  KLGFIMWDALKDQSSRIP 440
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## RESULT 3

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US-10-006-768A-52
; Sequence 52, Application US/10006768A
; Patent No. 6936697
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC10
; CURRENT APPLICATION NUMBER: US/10/006,768A
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-768A-52
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Query Match      100.0%; Score 2363; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 4.7e-159;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKFGPLACLIALCLSGGAGPLQSGESTGTNIGALGHGLGDALSEGVKAIKREAG 60
Db      1  MKFGPLACLIALCLSGGAGPLQSGESTGTNIGALGHGLGDALSEGVKAIKREAG 60
Qy      61  GAAGSVSEALGGCTREAVGTGVRQVPGFAADALGNRVEAAHALGNTGHEIGROADV 120
Db      61  GAAGSVSEALGGCTREAVGTGVRQVPGFAADALGNRVEAAHALGNTGHEIGROADV 120
Qy      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Db      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Qy      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Db      121  IRRHADAVRGSMQGVPHSGAMETSGGHGIFGSGGGLGGQGGNPGGLGTPWVHYPGNS 180
Qy      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
Db      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
Qy      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
Db      181  AGSFGMNPQGAAPMGQGGNGPVPNFNTQGAVAAPGYGVASVANSNNEGCTNPPPSGGG 240
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Db      241  SSNSGGSGSGSGSGSGSGNDNNSSSGSGSSSGSGSGSGSGSGSGSGSGSGSGS 300
Qy      241  SSNSGGSGSGSGSGSGSGNDNNSSSGSGSSSGSGSGSGSGSGSGSGSGSGSGS 300
Db      241  SSNSGGSGSGSGSGSGSGNDNNSSSGSGSSSGSGSGSGSGSGSGSGSGSGSGS 300
Qy      301  RGDGSESSSWGSSSTGSSSGNHGSGGNGHKPGCEKPGNEARSGESG1QGFRCGYVSN 360
Db      301  RGDGSESSSWGSSSTGSSSGNHGSGGNGHKPGCEKPGNEARSGESG1QGFRCGYVSN 360
Qy      361  MREISKGNRLLGSGDNYRGQSSSWGSGGDAVGVNTVNSETSPGMFNFDTFWKNPKS 420
Db      361  MREISKGNRLLGSGDNYRGQSSSWGSGGDAVGVNTVNSETSPGMFNFDTFWKNPKS 420
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Db 361 MREISKENRLLGGSGDNRYGQSSWGSGGDAVGVNTVNSSETSPGMFNFDTEFWKNFKS 420  
 QY 421 KLGFINDAINKDORSSRIP 440  
 Db 421 KLGFINDAINKDORSSRIP 440

RESULT 4  
 US-10-015-671A-52  
 ; Sequence 52, Application US/10015671A  
 ; Patent No. 6946263  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Baton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2830P1C47  
 ; CURRENT APPLICATION NUMBER: US/10/015,671A  
 ; PRIOR FILING DATE: 2001-12-11  
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 52  
 ; LENGTH: 440  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-015-671A-52

Query Match 100.0%; Score 2363; DB 2; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-159;  
 Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 61 GAAGSKVSEALGGGTREAVGTGVRQVPGFAADALGNRVGEAAHALGNTGHEIGROAEDV 120  
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 Db 121 IRRGADAVRGSWGVPGHSGAMETSGHGIFGSGQGLGGQCGNPGIGTIPWVHYGPNS 180  
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 Db 121 IRRGADAVRGSWGVPGHSGAMETSGHGIFGSGQGLGGQCGNPGIGTIPWVHYGPNS 180  
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 Db 181 AGSFQANPQGAIPWGQGGNGGPPNFGTNTQGAVAOPGYASVNASNNEGCTNPPPSGSGG 240  
 QY 241 SSNSGGSGSGSSG 300  
 Db 241 SSNSGGSG 300  
 QY 301 RGDSSSESSWSSSTGSSSGNHGSGGQGNHKGCEKPGNEARSGSGESGIGFRGQGVSSN 360  
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 QY 361 MREISKENRLLGGSGDNRYGQSSWGSGGDAVGVNTVNSSETSPGMFNFDTEFWKNFKS 420  
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 QY 421 KLGFINDAINKDORSSRIP 440  
 Db 421 KLGFINDAINKDORSSRIP 440

Db 421 KLGFINDAINKDORSSRIP 440

RESULT 5  
 US-10-015-393A-52  
 ; Sequence 52, Application US/10015393A  
 ; Patent No. 6951737  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Baton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2830P1C46  
 ; CURRENT APPLICATION NUMBER: US/10/015,393A  
 ; PRIOR FILING DATE: 2002-06-10  
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 52  
 ; LENGTH: 440  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-015-393A-52

Query Match 100.0%; Score 2363; DB 2; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-159;  
 Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKFGQPLACLIALCLGSGEAGPLOSSESTGTINIGELGHLGDLSEGVKAIKKEAG 60  
 Db 1 MKFGQPLACLIALCLGSGEAGPLOSSESTGTINIGELGHLGDLSEGVKAIKKEAG 60  
 QY 61 GAAGSKVSEALGGGTREAVGTGVRQVPGFAADALGNRVGEAAHALGNTGHEIGROAEDV 120  
 Db 61 GAAGSKVSEALGGGTREAVGTGVRQVPGFAADALGNRVGEAAHALGNTGHEIGROAEDV 120  
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 Db 121 IRRGADAVRGSWGVPGHSGAMETSGHGIFGSGQGLGGQCGNPGIGTIPWVHYGPNS 180  
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 Db 121 IRRGADAVRGSWGVPGHSGAMETSGHGIFGSGQGLGGQCGNPGIGTIPWVHYGPNS 180  
 QY 181 AGSFQANPQGAIPWGQGGNGGPPNFGTNTQGAVAOPGYASVNASNNEGCTNPPPSGSGG 240  
 Db 181 AGSFQANPQGAIPWGQGGNGGPPNFGTNTQGAVAOPGYASVNASNNEGCTNPPPSGSGG 240  
 QY 241 SSNSGGSG 300  
 Db 241 SSNSGGSG 300  
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 Db 301 RGDSSSESSWSSSTGSSSGNHGSGGQGNHKGCEKPGNEARSGSGESGIGFRGQGVSSN 360  
 QY 361 MREISKENRLLGGSGDNRYGQSSWGSGGDAVGVNTVNSSETSPGMFNFDTEFWKNFKS 420  
 Db 361 MREISKENRLLGGSGDNRYGQSSWGSGGDAVGVNTVNSSETSPGMFNFDTEFWKNFKS 420  
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 Db 421 KLGFINDAINKDORSSRIP 440

RESULT 6



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APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC19
CURRENT APPLICATION NUMBER: US/10/012,064A
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 477
LENGTH: 440
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-064A-52

Query Match      100.0%; Score 2363; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 4.7e-159;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKFQGPLACLLALCLGSGEAGPLQSGESTGTNIGALGHGLDGLSEGVKAIKXKAG 60
QY 61 GAAGSKVSEALGQGTREAVGTGVRQVPGGAADALGNRVGEAAHALGNTGHEIGROADV 120
DB 61 GAAGSKVSEALGQGTREAVGTGVRQVPGGAADALGNRVGEAAHALGNTGHEIGROADV 120
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DB 121 IRHGADAVRSGWGVPRHSGAMETSGHGIFGSGGLGQGGQGNPGGIGTPTWVHGYPNS 180
QY 181 AGSFGNMPQGAHPMGQGNPGPNTGTQGAVAOPGVGSVYASNONEGCTNPPPSGSGG 240
DB 181 AGSFGNMPQGAHPMGQGNPGPNTGTQGAVAOPGVGSVYASNONEGCTNPPPSGSGG 240
QY 241 SSNSGGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 300
DB 241 SSNSGGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 300
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DB 301 RGSQSGSSSSWGSSTGSSSGNHGSGGNGKPKCEKPGNEARGSGESGIGTFRQGVSSN 360
QY 361 MRISKEGNRLILGSGGNYRGQSSWGSQGGDAVGNTVNSPQMFNFDTPWKNPKS 420
DB 361 MRISKEGNRLILGSGGNYRGQSSWGSQGGDAVGNTVNSPQMFNFDTPWKNPKS 420
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DB 361 MRISKEGNRLILGSGGNYRGQSSWGSQGGDAVGNTVNSPQMFNFDTPWKNPKS 420
QY 421 KLGFINMDAINKDQSSSRIP 440
DB 421 KLGFINMDAINKDQSSSRIP 440

RESULT 9
US-10-015-392A-52
Sequence 52, Application US/10015392A
Patent No. 6972186
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC58
CURRENT APPLICATION NUMBER: US/10/015,392A
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 477
LENGTH: 440
TYPE: PRT
ORGANISM: Homo sapiens
US-10-015-392A-52

Query Match      100.0%; Score 2363; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 4.7e-159;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFQGPLACLLALCLGSGEAGPLQSGESTGTNIGALGHGLDGLSEGVKAIKXKAG 60
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QY 61 GAAGSKVSEALGQGTREAVGTGVRQVPGGAADALGNRVGEAAHALGNTGHEIGROADV 120
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Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GAAGSKVSEALGCGTREA VGTGVROVPFGAADALGNRYGEAAHALGNTGHEIGHQAE DV 120

QY 121 IRHGADAVRGSWQVPGHSGAMETSGGHGIFGSGGGLGGQGGNPGGLCTPWVHGYPGNS 180  
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QY 181 AGSFQMANPQAGPWCQGGNGGPPNFTGTNQGAVAOFGYGSVRASNONNECTNPPPSGSGGG 240  
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QY 241 SSNSGGGSG 300  
Db 241 SSNSGGGSG 300

QY 301 RGDSSSESSWGSSTGSSSGNHGSGGNGHKGPKCEKPGNEARGSGESGIGFRGQGVSSN 360  
Db 301 RGDSSSESSWGSSTGSSSGNHGSGGNGHKGPKCEKPGNEARGSGESGIGFRGQGVSSN 360

QY 361 MREISKENRLLGSGGDNRYRGQSSWGSQGGDVA VGVNTVNSSETSPGMFNFDTFWKXNFS 420  
Db 361 MREISKENRLLGSGGDNRYRGQSSWGSQGGDVA VGVNTVNSSETSPGMFNFDTFWKXNFS 420

QY 421 KLGFINDAINKDQSSRIP 440  
Db 421 KLGFINDAINKDQSSRIP 440

RESULT 12  
US-10-012-121A-52  
; Sequence 52, Application US/10012121A  
; Patent No. 7022817  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C20  
; CURRENT APPLICATION NUMBER: US/10/012, 121A  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 52  
; LENGTH: 440  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-012-121A-52

Query Match 100.0%; Score 2363; DB 3; Length 440;  
Best Local Similarity 100.0%; Pred. No. 4.7e-159;  
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKFGPLACLLALCLSGSEAGPLQSGESTGTNI GEALGHGLDALSEGVKAIGKENG 60  
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Db 61 GAAGSKVSEALGCGTREA VGTGVROVPFGAADALGNRYGEAAHALGNTGHEIGHQAE DV 120

QY 121 IRHGADAVRGSWQVPGHSGAMETSGGHGIFGSGGGLGGQGGNPGGLCTPWVHGYPGNS 180  
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QY 181 AGSFQMANPQAGPWCQGGNGGPPNFTGTNQGAVAOFGYGSVRASNONNECTNPPPSGSGGG 240  
Db 181 AGSFQMANPQAGPWCQGGNGGPPNFTGTNQGAVAOFGYGSVRASNONNECTNPPPSGSGGG 240

QY 241 SSNSGGGSG 300  
Db 241 SSNSGGGSG 300

QY 301 RGDSSSESSWGSSTGSSSGNHGSGGNGHKGPKCEKPGNEARGSGESGIGFRGQGVSSN 360  
Db 301 RGDSSSESSWGSSTGSSSGNHGSGGNGHKGPKCEKPGNEARGSGESGIGFRGQGVSSN 360

QY 361 MREISKENRLLGSGGDNRYRGQSSWGSQGGDVA VGVNTVNSSETSPGMFNFDTFWKXNFS 420  
Db 361 MREISKENRLLGSGGDNRYRGQSSWGSQGGDVA VGVNTVNSSETSPGMFNFDTFWKXNFS 420

QY 421 KLGFINDAINKDQSSRIP 440  
Db 421 KLGFINDAINKDQSSRIP 440

RESULT 13  
US-10-006-485A-52  
; Sequence 52, Application US/10006485A  
; Patent No. 7026448  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C9  
; CURRENT APPLICATION NUMBER: US/10/006, 485A  
; CURRENT FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
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; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09







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;; PRIOR FILING DATE: 1998-10-20  
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;; PRIOR APPLICATION NUMBER: 60/105266  
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;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

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DB 241 SSNSGGSG 300  
QY 301 RGDGSEBSWSSSTGSSSGNHNHGGGQGGHGPCKEPNERGSGESGSIQGFROGVASN 360  
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DB 361 MREISKEGNRLGSGGNDYRGSGSSWSSGCGDAVGVTVVNSSETSPGFNFDTFWKJNS 420  
QY 421 KLGFIMNDAINKQSSRIIP 440  
DB 421 KLGFIMNDAINKQSSRIIP 440

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RESULT 15
US-10-012-752A-52
; Sequence 52, Application US/10012752A
; Patent No. 7026455
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C24
; CURRENT APPLICATION NUMBER: US/10/012,752A
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-752A-52

; Query Match          100.0%; Score 2363; DB 3; Length 440;
; Best Local Similarity 100.0%; Pred. No. 4.7e-159;
; Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 KLGFIMWDALNKDQSSSRIP 440
DB 421 KLGFIMWDALNKDQSSSRIP 440

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Job time : 52 secs